

# SEARCH REQUEST FORM

5-54

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_

Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 5-7-98  
 Searcher: MARK  
 Terminal time: 6  
 Elapsed time: prep 10  
 CPU time: \_\_\_\_\_  
 Total time: 16  
 Number of Searches: 1  
 Number of Databases: 11

Search Site  
☐ STIC  
☒ CM-1  
☐ Pre-S  
 Type of Search  
☒ N.A. Sequence  
☒ A.A. Sequence  
☐ Structure  
☐ Bibliographic

Vendors  
☒ MPSRCH  
☐ STN  
☐ Dialog  
☐ APS  
☐ Geninfo  
☐ SDC  
☐ DARC/Questel  
☐ Other



\*\*\*\*\*  
WIREIMAGE (TM)  
\*\*\*\*\*

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.  
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MPSEARCH protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:18:28 1998; Maspar time 3.90 Seconds  
375.094 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-2

Description: (1-256) from US0804166.pep

Perfect Score: 1994

Sequence: 1 SRTSLALFGLLCIPWQEG.....GFKVENHTGCHCTCYTHKS 256

Scoring table: PAM 150  
Gap 11

Searched: 62627 segs, 5720858 residues

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database:

a-issued  
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCT90  
10:PCIT91 11:PCIT92 12:PCIT93 13:PCIT94 14:PCIT95 15:PCIT96

Statistics: Mean 29.680; Variance 124.309; scale 0.239

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1124	56.4	455	7	US-08-321-	Sequence 2, Applicatio	1.28e-100
2	1124	56.4	455	7	US-08-050-	Sequence 25, Applicati	1.28e-100
3	1115	55.9	199	7	US-08-050-	Sequence 48, Applicati	1.05e-99
4	996	49.9	167	7	US-08-050-	Sequence 2, Applicatio	1.15e-87
5	996	49.9	167	7	US-08-050-	Sequence 57, Applicati	1.15e-87
6	981	49.2	124	7	US-08-050-	Sequence 4, Applicatio	3.78e-86
7	800	40.1	157	7	US-08-050-	Sequence 50, Applicati	6.45e-68
8	666	33.4	158	7	US-08-050-	Sequence 54, Applicati	8.82e-36
9	477	23.9	153	7	US-08-050-	Sequence 35, Applicati	2.30e-22
10	339	17.0	41	7	US-08-050-	Sequence 26, Applicati	6.30e-21
11	324	16.2	40	7	US-08-050-	Sequence 31, Applicati	2.36e-20
12	318	15.9	43	7	US-08-050-	Sequence 2, Applicatio	1.31e-11
13	225	11.3	325	5	US-08-292-	Sequence 2, Applicatio	3.06e-11
14	225	11.3	325	5	US-08-292-	Sequence 4, Applicatio	3.06e-11
15	221	11.1	326	10	PCT-US91-0	Sequence 4, Applicatio	3.06e-11
16	221	11.1	326	10	PCT-US91-0	Sequence 4, Applicatio	3.06e-11
17	212	10.6	474	1	5395760-4	Patent No. 5395760.	2.05e-10
18	210	10.5	355	5	US-08-292-	Sequence 6, Applicatio	3.12e-10
19	183	9.2	283	15	PCT-US96-1	Sequence 2, Applicatio	8.68e-08
20	183	9.2	283	15	PCT-US96-1	Sequence 2, Applicatio	8.68e-08
21	183	9.2	283	15	PCT-US96-1	Sequence 2, Applicatio	8.68e-08
22	181	9.1	228	12	PCT-US93-0	Sequence 8, Applicatio	1.31e-07

23	181	9.1	228	13	PCT-US94-0	Sequence 4, Applicatio	1.31e-07
24	181	9.1	228	14	PCT-US95-0	Sequence 4, Applicatio	1.31e-07
25	181	9.1	228	7	US-08-188-	Sequence 8, Applicatio	1.31e-07
26	181	9.1	228	7	US-08-453-	Sequence 8, Applicatio	1.31e-07
27	180	9.0	461	7	US-08-385-	Sequence 2, Applicatio	1.61e-07
28	180	9.0	461	7	US-08-443-	Sequence 1, Applicatio	1.61e-07
29	180	9.0	486	7	US-08-243-	Sequence 4, Applicatio	1.61e-07
30	180	9.0	518	7	US-08-385-	Sequence 4, Applicatio	1.61e-07
31	169	8.5	333	12	PCT-US93-0	Sequence 12, Applicati	1.53e-06
32	169	8.5	333	7	US-08-453-	Sequence 12, Applicati	1.53e-06
33	169	8.5	333	7	US-08-453-	Sequence 10, Applicati	1.53e-06
34	169	8.5	399	12	PCT-US93-0	Sequence 10, Applicati	1.53e-06
35	167	8.4	70	4	US-07-920-	Sequence 24, Applicati	2.30e-06
36	167	8.4	71	6	US-08-314-	Sequence 24, Applicati	2.30e-06
37	167	8.4	93	7	US-08-445-	Sequence 2, Applicatio	2.30e-06
38	167	8.4	93	7	US-08-343-	Sequence 2, Applicatio	2.30e-06
39	165	8.3	186	4	US-08-089-	Sequence 6, Applicatio	3.46e-06
40	160	8.0	177	6	US-08-187-	Sequence 5, Applicatio	9.51e-06
41	160	8.0	198	6	US-08-187-	Sequence 5, Applicatio	9.51e-06
42	160	8.0	217	6	US-08-187-	Sequence 4, Applicatio	9.51e-06
43	156	7.8	206	5	US-08-097-	Sequence 7, Applicatio	2.13e-05
44	156	7.8	438	5	US-08-097-	Sequence 11, Applicati	2.13e-05
45	139	7.0	335	14	PCT-US95-1	Sequence 2, Applicatio	6.25e-04

ALIGNMENT'S

RESULT 1  
ID US-08-321-668-2 STANDARD; PRT; 455 AA.  
AC xxxxxx  
XX  
DT 01-JAN-1900  
DE Sequence 2, Application US/08321668.  
XX  
CC Sequence 2, Application US/08321668  
CC Patent No. 5665859  
CC GENERAL INFORMATION:  
CC APPLICANT: WALLACH, David  
CC APPLICANT: BRAKEBUSH, Cord  
CC APPLICANT: VAREFOLOMEV, Eugene  
CC APPLICANT: BARKIN, Michael  
CC TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
CC NUMBER OF SEQUENCES: 42  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: BROWDY AND NEIMARK  
CC STREET: 419 Seventh Street, N.W., Suite 300  
CC CITY: Washington  
CC STATE: D.C.  
CC COUNTRY: USA  
CC ZIP: 20004  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/321.668  
CC FILING DATE: 12-OCT-1994  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: IL 107268  
CC FILING DATE: 12-OCT-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: BROWDY, Roger L.  
CC REGISTRATION NUMBER: 25,618  
CC REFERENCE/DOCKET NUMBER: WALLACH-13  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 202-628-5197  
CC TELEFAX: 202-737-3528  
CC TELEX: 246633

CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 455 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 455 AA; 50494 MW; 1048031 CN;

Query Match 56.4%; Score 1124; DB 7; Length 455;  
Best Local Similarity 99.3%; Pred. No. 1,28e-100;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 DSVCPGKTYIHPNNNSICTCKHKGTYLYNDCCPGPGDDTDCRECSGSGFTASENHLRCL 100  
|||  
QY 23 DSVCPGKTYIHPNNNSICTCKHKGTYLYNDCCPGPGDDTDCRECSGSGFTASENHLRCL 82  
|||

Db 101 SCSCKRKMGEVIEISCTVDYDTCGCKRKNQRYHWSENLFCFCNCSLCLNGTVHLSCOE 160  
|||  
QY 83 SCSCKRKMGEVIEISCTVDYDTCGCKRKNQRYHWSENLFCFCNCSLCLNGTVHLSCOE 142  
|||

Db 161 KONTVCTCHAGFLRENECVSCS 183  
|||  
QY 143 KONTVCTCHAGFLRENECVSCA 165  
|||

RESULT 2  
ID US-08-050-319B-25 STANDARD; PRT; 455 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 25, Application US/08050319B.  
CC  
CC Sequence 25, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M. Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbings  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbings, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 25:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 455 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 455 AA; 50579 MW; 1048388 CN;

Query Match 56.4%; Score 1124; DB 7; Length 455;  
Best Local Similarity 99.3%; Pred. No. 1,28e-100;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 DSVCPGKTYIHPNNNSICTCKHKGTYLYNDCCPGPGDDTDCRECSGSGFTASENHLRCL 100  
|||  
QY 23 DSVCPGKTYIHPNNNSICTCKHKGTYLYNDCCPGPGDDTDCRECSGSGFTASENHLRCL 82  
|||

Db 101 SCSCKRKMGEVIEISCTVDYDTCGCKRKNQRYHWSENLFCFCNCSLCLNGTVHLSCOE 160  
|||  
QY 83 SCSCKRKMGEVIEISCTVDYDTCGCKRKNQRYHWSENLFCFCNCSLCLNGTVHLSCOE 142  
|||

Db 161 KONTVCTCHAGFLRENECVSCS 183  
|||  
QY 143 KONTVCTCHAGFLRENECVSCA 165  
|||

RESULT 3  
ID US-08-050-319B-48 STANDARD; PRT; 199 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 48, Application US/08050319B.  
CC  
CC Sequence 48, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M. Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbings  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbings, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 48:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 199 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 199 AA; 22186 MW; 195553 CN;

Query Match 55.9%; Score 1115; DB 7; Length 199;  
Best Local Similarity 98.6%; Pred. No. 1,05e-99;  
Matches 141; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 41 DSVCPGKTYIHPNNNSICTCKHKGTYLYNDCCPGPGDDTDCRECSGSGFTASENHLRCL 100  
|||  
QY 23 DSVCPGKTYIHPNNNSICTCKHKGTYLYNDCCPGPGDDTDCRECSGSGFTASENHLRCL 82  
|||



RESULT	4		STANDARD:	PRT:	167 AA.
ID	US -08-050-319B-2				
XX	xxxxxx				
XX	01-JAN-1900				
DE	Sequence 2, Application US/08050319B.				
XX					
CC	Sequence 2, Application US/08050319B				
CC	Patent No. 5633145				
CC	GENERAL INFORMATION:				
CC	APPLICANT: M.J.C. Turner, F.M. Brennan				
CC	TITLE OF INVENTION: Modified human TNFalpha (Tumor				
CC	Necrosis Factor alpha) Receptor				
CC	NUMBER OF SEQUENCES: 57				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: Reed & Robins				
CC	STREET: 635 Bryant Street				
CC	CITY: Palo Alto				
CC	STATE: California				
CC	COUNTRY: USA				
CC	ZIP: 94301				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: PatentIn Release #1.0, version #1.25				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/050,319B				
CC	FILING DATE: 10-May-1993				
CC	CLASSIFICATION: 435				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Robbins, Roberta L.				
CC	REGISTRATION NUMBER: 33,208				
CC	REFERENCE/DOCKET NUMBER: 5150-0030				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: (415) 617-8999				
CC	TELEFAX: (415) 327-3231				
CC	INFORMATION FOR SEQ ID NO: 2:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 167 amino acids				
CC	TYPE: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
CC	SEQUENCE: 167 AA; 18626 MW; 139513 CN;				
SQ					
DB	Query Match	49.9%;	Score 996;	DB 7;	Length 167;
OY	Best Local Similarity 100.0%;	Pred. No. 1.15e-87;			
DB	Matches 127; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
DB	41 DSVCPGKXIHPPNNSICTCHKGTYLYNDPCPGPDTCRECESGSFASENHLRCL	100			
OY	23 DSYCPQGKXIHPPNNSICTCHKGTYLYNDPCPGDTCRECESGSFASENHLRCL	82			
DB	101 SCSCKRKMGVEISSCTVDSDVCGCRKNQRYRHYSSENLFCQFNCSICLNGTVHLSQE	160			
OY	83 SCSCKRKMGVEISSCTVDSDVCGCRKNQRYRHYSSENLFCQFNCSICLNGTVHLSQE	142			
DB	161 KONTVCT 167				
OY	143 KONTVCT 149				

RESULT	5	STANDARD;	PRT;	167	AA.
ID	US-08-050-319B-57				
XX	xxxxxx				
XX	01-JAN-1900				
XX					
DE	Sequence 57, Application US/08050319B.				
XX					
CC	Sequence 57, Application US/08050319B				
CC	Patent No. 5633145				
CC	GENERAL INFORMATION:				
CC	APPLICANT: M.Feldmann, P.W. Gray,				
CC	APPLICANT: M.J.C. Turner, F.M Brennan				
CC	TITLE OF INVENTION: Modified human TNFalpha (Tumor				
CC	TITLE OF INVENTION: Necrosis Factor alpha) Receptor				
CC	NUMBER OF SEQUENCES: 57				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: Reed & Robbins				
CC	STREET: 635 Bryant Street				
CC	City: Palo Alto				
CC	STATE: California				
CC	COUNTRY: USA				
CC	ZIP: 94301				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: PatentIn Release #1.0, version #1.25				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/050,319B				
CC	FILING DATE: 10-May-1993				
CC	CLASSIFICATION: 435				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Robbins, Roberta L.				
CC	REGISTRATION NUMBER: 33,208				
CC	REFERENCE/DOCKET NUMBER: 5150-0030				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: (415) 617-8999				
CC	TELEFAX: (415) 327-3231				
CC	INFORMATION FOR SEQ ID NO:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 167 amino acids				
CC	TYPE: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
SO	SEQUENCE 167 AA; 18626 MW; 139513 CN;				
	Query Match	49.9%;	Score 996;	DB 7;	Length 167;
	Best Local Similarity 100.0%;	Pred. No. 1,15e-87;			
	Matches 127; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Db	41 DSVCPQGGKYIHPNNSICCTCKHKGTYLYNDCCPGPGDTCDCRECSGSGFTASENHLRHCL 100				
Oy	23 DSVCPQGGKYIHPNNSICCTCKHKGTYLYNDCCPGPGDTCDCRECSGSGFTASENHLRHCL 82				
Db	101 SCSCKRKMGGVEIISCTVDRDTCGCGRKNQYRIYASENLFCQFNCGLCLNGTVHLSQCE 160				
Oy	83 SCSCKRKMGGVEIISCTVDRDTCGCGRKNQYRIYASENLFCQFNCGLCLNGTVHLSQCE 142				
Db	161 KONTVCT 167				
Oy	143 KONTVCT 149				
RESULT	6	STANDARD;	PRT;	124	AA.
ID	US-08-050-319B-4				
XX	xxxxxx				
XX	01-JAN-1900				
XX					

DE Sequence 4, Application US/08050319B.  
XX  
CC Sequence 4, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 4:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 124 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 124 AA; 14047 MW; 75840 CN;  
SQ  
  
Query Match 49.2%; Score 981; DB 7; Length 124;  
Best Local Similarity 100.0%; Pred. No. 3.78e-86;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
DB 1 VCPGKTIHPNNISICGCKHGTLYNDGPGODTDCRCESGFTASNNHLRHCLSC 60  
QY 25 VCPGKTIHPNNISICGCKHGTLYNDGPGODTDCRCESGFTASNNHLRHCLSC 84  
DB 61 SKCRKMGQVEISSCTVDRTVCGCRKNQRYRHYSENLFQCFNCSLCLNGTVHLSCQEKQ 120  
QY 85 SKCRKMGQVEISSCTVDRTVCGCRKNQRYRHYSENLFQCFNCSLCLNGTVHLSCQEKQ 144  
DB 121 NTVC 124  
QY 145 NTVC 148  
  
RESULT 7  
ID US-08-050-319B-50 STANDARD; PRT: 157 AA.  
XX  
AC xxxxxx  
XX 01-JAN-1900  
DE Sequence 50, Application US/08050319B.  
XX  
CC Sequence 50, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 50:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 157 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 157 AA; 17570 MW; 122247 CN;  
SQ

CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 50:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 157 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 157 AA; 17570 MW; 122247 CN;  
SQ  
  
Query Match 40.1%; Score 800; DB 7; Length 157;  
Best Local Similarity 96.2%; Pred. No. 6.45e-68;  
Matches 102; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
DB 36 DREKCEGSGFTASENNLRHCLSCSKRKMGOVEISSCTVDRTVCGCRKNQRYRHY 95  
QY 60 DTDREBESGFTASENNLRHCLSCSKRKMGOVEISSCTVDRTVCGCRKNQRYRHY 119  
DB 96 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFLRENECVSCS 141  
QY 120 ENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFLRENECVSCA 165  
  
RESULT 8  
ID US-08-050-319B-54 STANDARD; PRT: 158 AA.  
XX  
AC xxxxxx  
XX 01-JAN-1900  
DE Sequence 54, Application US/08050319B.  
XX  
CC Sequence 54, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 50:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 157 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 157 AA; 17570 MW; 122247 CN;  
SQ



Matches 41: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCRKNQRYHWSENLFQCFNCISCLNGTVHLSCQEKONTVC 41  
108 GCRKNQRYHWSENLFQCFNCISCLNGTVHLSCQEKONTVC 148

Query 11  
US-08-050-319B-26 STANDARD; PRT; 40 AA.

xxxxxx  
01-JAN-1900

Sequence 26, Application US/08050319B.

Sequence 26, Application US/08050319B  
Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M.Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M.Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
NUMBER OF SEQUENCES: 57  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robblins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robblins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE 40 AA; 4459 MW; 7536 CN;

Query Match 16.2%; Score 324; DB 7; Length 40;  
Best Local Similarity 100.0%; Pred. No. 6,30e-21;  
Matches 40: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VCPQGYIHPQNNISICCTCKHGTLYLNDPCPGQDPTDCR 40  
25 VCPQGYIHPQNNISICCTCKHGTLYLNDPCPGQDPTDCR 64

RESULT 12  
ID US-08-050-319B-31 STANDARD; PRT; 43 AA.  
AC xxxxxx  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 31, Application US/08050319B.

XX Sequence 31, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robblins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robblins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE 43 AA; 4767 MW; 9758 CN;

Query Match 15.9%; Score 318; DB 7; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2.36e-20;  
Matches 43: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ECSSGFTASSENHLRHCSCSKCKEMGVEISSCTVDRTVC 43  
65 ECSSGFTASSENHLRHCSCSKCKEMGVEISSCTVDRTVC 107

RESULT 13  
ID US-08-292-549-2 STANDARD; PRT; 325 AA.  
AC xxxxxx  
AC xxxxxx  
DT 01-JAN-1900  
DE Sequence 2, Application US/08292549.  
XX Sequence 2, Application US/08292549  
CC Patent No. 5464938  
CC GENERAL INFORMATION:  
CC APPLICANT: Smith, Craig A.  
CC APPLICANT: Goodwin, Raymond G.  
CC TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists  
CC NUMBER OF SEQUENCES: 10  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Immunex Corporation  
CC STREET: 51 University Street  
CC CITY: Seattle  
CC STATE: Washington  
CC COUNTRY: USA  
CC ZIP: 98101

```
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/292,549  
CC FILING DATE:  
CC CLASSIFICATION: 530  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 07/963,330  
CC FILING DATE: 10/19/92  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Perkins, Patricia A.  
CC REGISTRATION NUMBER: 34,633  
CC REFERENCE/DOCKET NUMBER: 2603-A  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (206) 587-0430  
CC TELEFAX: (206) 233-0644  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 325 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 325 AA; 35132 MW; 591446 CN;  
  
Cc Query Match 11.3%; Score 225; DB 5; Length 325;  
Cc Best Local Similarity 34.8%; Pred.No. 1,31e-11;  
Cc Matches 39; Conservative 21; Mismatches 45; Indels 7; Gaps 6;  
  
Db 4 LIAL-LVGVYVVYGDVDVFPSSNOGKCGGHDEKGLGCASCHPEFYASRLC-GFGSNIVC 61  
Qy 6 LIALGLCLLPLVLQESADSVCPQKKYI-HP-QNNSICCTCKHKGTYLYNDPCPGGPOTDC 63  
Dd 62 SPCEGTFTASTNHAPACVSCRGSGTGHLSQS--PDQRTHDRYCNCSTGY 111  
Qy 64 RECSEGSTASENHLRHCLSC-SKRCKEMGOVEISSCTVDPRDYVGGRKNQY 114  
  
RESULT 14  
ID PCR-US91-02207-2 STANDARD: PRT; 325 AA.  
Ac xxxxxx  
Xx 01-JAN-1900  
Xx  
De Sequence 2, Application PC/TUS9102207.  
Xx  
Cc GENERAL INFORMATION:  
Cc APPLICANT: Smith, Craig A.  
Cc APPLICANT: Goodwin, Raymond G.  
Cc TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists  
Cc NUMBER OF SEQUENCES: 4  
Cc CORRESPONDENCE ADDRESSES:  
Cc ADDRESSEE: Immunex Corporation  
Cc STREET: 51 University Street  
Cc CITY: Seattle  
Cc STATE: Washington  
Cc COUNTRY: USA  
Cc ZIP: 98101  
Cc COMPUTER READABLE FORM:  
Cc MEDIUM TYPE: Floppy disk  
Cc OPERATING SYSTEM: IBM PC compatible  
Cc SOFTWARE: PatentIn Release #1.24  
Cc CURRENT APPLICATION DATA:  
Cc APPLICATION NUMBER: PCT/US91/02207  
Cc FILING DATE: 19910329  
Cc CLASSIFICATION: 435  
Cc ATTORNEY/AGENT INFORMATION:  
Cc NAME: Wight, Christopher L.
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CC      REGISTRATION NUMBER: 31,680
CC      REFERENCE/DOCKET NUMBER: 2602
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (206) 587-0430
CC      TELEFAX: (206) 587-0606
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 325 amino acids
CC          TYPE: AMINO ACID
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 325 AA; 35132 MW; 591446 CN;
CC
DB      QUERY MATCH 11.3%; Score 225; DB 10; Length 325;
DB      Best Local Similarity 34.8%; Pred. No. 1,31e-11;
DB      Matches 39; Conservative 21; Mismatches 45; Indels 7; Gaps 6;
DB
DB      4 LIAL-LYCVVYVYGDDPVYSNMOGKGGHDXEKGLGCASCHPEFYSLRC-GPGSITVC 61
DB      6 LIAFLDLPLPMQDSADSVCPGRKYI-HP-QNNISICCTCHKGTLYNDPCPGGDTC 63
DB      62 SPCEGRTTASTINHPACVSCRGPCHTGLSESQ--PCDRTHDRYCNCSTGN Y 111
DB      |||:||||| || :||: | :||: | :||: | :||: | :||: | :||: |
DB      64 RECCEGSPTASENHRLRCLSC-SKCRREMGEVLSSCTVDRIYCGCKKNQ Y 114
DB
DE      RESULT 15
DE      ID US-08-292-549-4 STANDARD; PRT; 326 AA.
DE      XX xxxxxx
DE      DT 01-JAN-1900
DE
XX      Sequence 4, Application US/08292549.
XX
CC      Sequence 4, Application US/08292549
CC      Patent No. 5464938
CC      GENERAL INFORMATION:
CC      APPLICANT: Smith, Craig A.
CC      APPLICANT: Goodwin, Raymond G.
CC      TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
CC      NUMBER OF SEQUENCES: 10
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Immunex Corporation
CC      STREET: 51 University Street
CC      CITY: Seattle
CC      STATE: Washington
CC      COUNTRY: USA
CC      ZIP: 98101
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/292,549
CC      FILING DATE:
CC      CLASSIFICATION: 530
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/963,330
CC      FILING DATE: 10/19/92
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Perkins, Patricia A.
CC      REGISTRATION NUMBER: 34,693
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (206) 587-0430
CC      TELEFAX: (206) 233-0644
CC      INFORMATION FOR SEQ ID NO: 4:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 326 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
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CC LENGTH: 2062 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 155..1519  
SQ Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

Query Match 40.4%; Score 424; DB 7; Length 2062;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 275 GATAGTGTGTCCCAAGAAATATATCCACCCTCAAAATATTCATTGCTGTACC 334  
Qy 344 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATATTCATTGCTGTACC 403  
Db 335 AAGTGCACCAAGAAAGAACTACTTGTACAAATGACTGTCCAGGCCGGGCGAGATACGAGC 394  
Qy 404 AAGTGCACCAAGAAAGAACTACTTGTACAAATGACTGTCCAGGCCGGGCGAGATACGAGC 463  
Db 395 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAGAAAACCACTGAGACACTGCCTC 454  
Qy 464 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAGAAAACCACTGAGACACTGCCTC 523  
Db 455 AGTGTCTCCAAATGCGGAAGAAATGGGTGAGTGTGAGATCTCTTGTGCACAGTGGAC 514  
Qy 524 AGTGTCTCCAAATGCGGAAGAAATGGGTGAGTGTGAGATCTCTTGTGCACAGTGGAC 583  
Db 515 CGGGACACCGTGTGTGCTGTGCAGGAAGAACCACTGACCGGCATTATTGAGTGAACCTT 574  
Qy 584 CGGGACACCGTGTGTGCTGTGCAGGAAGAACCACTGACCGGCATTATTGAGTGAACCTT 643  
Db 575 TTCCAGTCTTCAATTGGACGCTCTGCTCAATGGAGCGGTCACCTCTCCGCCAGGAG 634  
Qy 644 TTCCAGTCTTCAATTGGACGCTCTGCTCAATGGAGCGGTCACCTCTCCGCCAGGAG 703  
Db 635 AAACGAACACCGTGTGTGACCTGCGCATGAGTTCTTCTTAAGAGAAACGAGTGTGC 694  
Qy 704 AAACGAACACCGTGTGTGACCTGCGCATGAGTTCTTCTTAAGAGAAACGAGTGTGC 763  
Db 695 TCCGTGT 700  
Qy 764 TCCGTGT 769

RESULT 2  
ID US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP.

XX xxxxxx  
AC  
XX 01-JAN-1900  
DT  
XX  
DE Sequence 1, Application US/08321668.  
XX  
CC Sequence 1, Application US/08321668  
CC Patent No. 565859  
CC GENERAL INFORMATION:  
CC APPLICANT: WALLACH, David  
CC APPLICANT: BRAKEBUSH, Cord  
CC APPLICANT: VARFOLOMEV, Eugene  
CC APPLICANT: BATKIN, Michael  
CC TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
CC TITLE OF INVENTION: THE INF RECEPTORS, THEIR PREPARATION AND THEIR USE  
CC NUMBER OF SEQUENCES: 42  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: BROMDY AND NEIMARK  
CC STREET: 419 Seventh Street, N.W., Suite 300  
CC CITY: Washington  
CC STATE: D.C.  
CC COUNTRY: USA

CC ZIP: 20004  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/321,668  
CC FILING DATE: 12-OCT-1994  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: IL 107268  
CC FILING DATE: 12-OCT-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: BROMDY, Roger L.  
CC REGISTRATION NUMBER: 25,618  
CC REFERENCE/DOCKET NUMBER: WALLACH-13  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 202-628-5197  
CC TELEFAX: 202-737-3528  
CC TELEX: 248633  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2175 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 256..1620  
SQ Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

Query Match 40.4%; Score 424; DB 7; Length 2175;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 376 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATATTCATTGCTGTACC 435  
Qy 344 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATATTCATTGCTGTACC 403  
Db 436 AAGTGCACCAAGAAAGAACTACTTGTACAAATGACTGTCCAGGCCGGGCGAGATACGAGC 495  
Qy 404 AAGTGCACCAAGAAAGAACTACTTGTACAAATGACTGTCCAGGCCGGGCGAGATACGAGC 463  
Db 496 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAGAAAACCACTGACACTGCCTC 555  
Qy 464 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAGAAAACCACTGACACTGCCTC 523  
Db 556 AGTGTCTCCAAATGCGGAAGAAATGGGTGAGTGTGAGATCTCTTGTGCACAGTGGAC 615  
Qy 524 AGTGTCTCCAAATGCGGAAGAAATGGGTGAGTGTGAGATCTCTTGTGCACAGTGGAC 583  
Db 616 CGGGACACCGTGTGTGCTGTGCAGGAAGAACCACTGACCGCATTTATGAGTGAACCTT 675  
Qy 584 CGGGACACCGTGTGTGCTGTGCAGGAAGAACCACTGACCGCATTTATGAGTGAACCTT 643  
Db 676 TTCCAGTCTTCAATTGGACGCTCTGCTCAATGGAGCGGTCACCTCTCTGCCAGGAG 735  
Qy 644 TTCCAGTCTTCAATTGGACGCTCTGCTCAATGGAGCGGTCACCTCTCTGCCAGGAG 703  
Db 736 AAACGAACACCGTGTGTGACCTGCGCATGAGTTCTTCTTAAGAGAAACGAGTGTGC 795  
Qy 704 AAACGAACACCGTGTGTGACCTGCGCATGAGTTCTTCTTAAGAGAAACGAGTGTGC 763  
Db 796 TCCGTGT 801  
Qy 764 TCCGTGT 769

RESULT 3  
ID US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.



XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 2, Application US/08286740.  
XX  
CC Sequence 2, Application US/08286740  
CC Patent No. 5561053  
CC GENERAL INFORMATION:  
CC APPLICANT: Crowley, Craig W.  
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING  
CC TITLE OF INVENTION: HOST CELLS  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Genentech, Inc.  
CC STREET: 460 Point San Bruno Blvd  
CC CITY: South San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94080  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: patin (Genentech)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/286,740  
CC FILING DATE: 05-AUG-1994  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lee, Wendy M.  
CC REGISTRATION NUMBER:  
CC REFERENCE/DOCKET NUMBER: 798  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-1994  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6889 bases  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;  
SQ  
Query Match 40.4%; Score 424; DB 6; Length 6889;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1725 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTTGCTGTACC 1784  
QY |||||||  
CC 344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTTGCTGTACC 403  
CC |||||||  
Db 1785 AAGTGCACAAAGAACCTTACTTGTACATGATGCTCCAGGCCGGGGCAGATACGAGAC 1844  
QY |||||||  
CC 404 AAGTGCACAAAGAACCTTACTTGTACATGATGCTCCAGGCCGGGGCAGATACGAGAC 463  
CC |||||||  
Db 1845 TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAGAAAACACCTCAGACACTGCCTC 1904  
QY |||||||  
CC 464 TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAGAAAACACCTCAGACACTGCCTC 523  
CC |||||||  
Db 1905 AGCTGCTCCAAATGCGCAAGGAATGGCTCAGGTGAGATGCTTCTTGACAGTGGAC 1964  
QY |||||||  
CC 524 AGCTGCTCCAAATGCGCAAGGAATGGCTCAGGTGAGATGCTTCTTGACAGTGGAC 583  
CC |||||||  
Db 1965 CGGAGACACCGTGTGCTGTCAGAGAAACCATGACCGGCTATTTGAGTGAATGAACTT 2024  
QY |||||||  
CC 584 CGGAGACACCGTGTGCTGTCAGAGAAACCATGACCGGCTATTTGAGTGAATGAACTT 643  
CC |||||||

Db 2025 TTCAGTGTCTTCAATTCGACGCTGTGCTCAATGGAGCGGACCTCTCTGCCAGAG 2084  
QY |||||||  
CC 644 TTCAGTGTCTTCAATTCGACGCTGTGCTCAATGGAGCGGACCTCTCTGCCAGAG 703  
CC |||||||  
Db 2085 AAACGAAACACCGTGTGTCACCTGTCATGATGAGTTTCTTCTTAAGAGAAAAGAGTGTGC 2144  
QY |||||||  
CC 704 AAACGAAACACCGTGTGTCACCTGTCATGATGAGTTTCTTCTTAAGAGAAAAGAGTGTGC 763  
CC |||||||  
Db 2145 TCCTGT 2150  
QY |||||||  
CC 764 TCCTGT 769  
CC |||||||  
RESULT 4  
ID PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 2, Application PC/TUS9509576.  
XX  
CC Sequence 2, Application PC/TUS9509576  
CC GENERAL INFORMATION:  
CC APPLICANT: GENENTECH, INC.  
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING  
CC TITLE OF INVENTION: HOST CELLS  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Genentech, Inc.  
CC STREET: 460 Point San Bruno Blvd  
CC CITY: South San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94080  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: patin (Genentech)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/09576  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/286740  
CC FILING DATE: 05-AUG-1994  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lee, Wendy M.  
CC REGISTRATION NUMBER: 00,000  
CC REFERENCE/DOCKET NUMBER: 798PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-1994  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6889 bases  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;  
SQ  
Query Match 40.4%; Score 424; DB 14; Length 6889;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1725 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTTGCTGTACC 1784  
QY |||||||  
CC 344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTTGCTGTACC 403  
CC |||||||  
Db 1785 AAGTGCACAAAGAACCTTACTTGTACATGATGCTCCAGGCCGGGGCAGATACGAGAC 1844  
CC |||||||

|||||  
OY 404 AAGTCCACAAAGAAACCTACTTTGATCAATGACTGCCAGGCCGGGCGAGATACGGAC 463  
DB 1845 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACACCTCAGACACTGCCCTC 1904  
OY 464 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACACCTCAGACACTGCCCTC 523  
DB 1905 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGCAGATCTTCTTGCACAGTGAC 1964  
OY 524 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGCAGATCTTCTTGCACAGTGAC 583  
DB 1965 GGGAGACCGTGTGGCTGCGAGGAAAGAACAGTACCGGATTTATGGAGTAAAACTT 2024  
OY 584 CGGAGACCGTGTGGCTGCGAGGAAAGAACAGTACCGGATTTATGGAGTAAAACTT 643  
DB 2025 TTCCAGTGTCAATTTGACGCTCTGCTCAATGGAGACCGTCACTCTGCGCAGAG 2084  
OY 644 TTCCAGTGTCAATTTGACGCTCTGCTCAATGGAGACCGTCACTCTGCGCAGAG 703  
DB 2085 AAACAGAACCCGTGTGCACCTGCCATGCGAGTTCTTCTTAAGAGAAAAAGAGTGTGC 2144  
OY 704 AAACAGAACCCGTGTGCACCTGCCATGCGAGTTCTTCTTAAGAGAAAAAGAGTGTGC 763  
DB 2145 TCCTGT 2150  
OY 764 TCCTGT 769

RESULT 5  
ID US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

xxxxxx  
XX 01-JAN-1900  
DT  
DE Sequence 47, Application US/08050319B.  
XX  
CC Sequence 47, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 47:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 600 base pairs  
CC TYPE: nucleic acid

CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..597  
SQ Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;  
Query Match 40.0%; Score 420; DB 7; Length 600;  
Best Local Similarity 99.3%; Pred. No. 0.00e+00;  
Matches 423; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
DB 121 GATAGTGTGTGTCACAGAGAAATATATCCACCTCAAAATATTCGATTGCTGTAC 180  
OY 344 GATAGTGTGTGTCACAGAGAAATATATCCACCTCAAAATATTCGATTGCTGTAC 403  
DB 181 AAGTGCACAAAGAAAGAACTACTTTGATCAATGACTGTCCAGGCGCGGAGATACGGAC 240  
OY 404 AAGTGCACAAAGAAAGAACTACTTTGATCAATGACTGTCCAGGCGCGGAGATACGGAC 463  
DB 241 TGCAGGAGTGTGAGAGGGGCTCTTCAACCGCTTCAGAAACCACTCAGACACTGCCCTC 300  
OY 464 TGCAGGAGTGTGAGAGGGGCTCTTCAACCGCTTCAGAAACCACTCAGACACTGCCCTC 523  
DB 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGCAGATCTTCTTGCACAGTGAC 360  
OY 524 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGCAGATCTTCTTGCACAGTGAC 583  
DB 361 CGGAGACCGTGTGGCTGCGAGGAAAGAACAGTACCGGATTTATGGAGTAAAACTT 420  
OY 584 CGGAGACCGTGTGGCTGCGAGGAAAGAACAGTACCGGATTTATGGAGTAAAACTT 643  
DB 421 TTCCAGTGTCAATTTGACGCTCTGCTCAATGGAGACCGTCACTCTGCGCAGAG 480  
OY 644 TTCCAGTGTCAATTTGACGCTCTGCTCAATGGAGACCGTCACTCTGCGCAGAG 703  
DB 481 AAACAGAACCCGTGTGCACCTGCCATGCGAGTTCTTCTTAAGAGAAAAAGAGTGTGC 540  
OY 704 AAACAGAACCCGTGTGCACCTGCCATGCGAGTTCTTCTTAAGAGAAAAAGAGTGTGC 763  
DB 541 TCCTGT 546  
OY 764 TCCTGT 769

RESULT 6  
ID US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

xxxxxx  
XX 01-JAN-1900  
DT  
DE Sequence 56, Application US/08050319B.  
XX  
CC Sequence 56, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 56:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 504 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..501  
SQ Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

Query Match 36.3%; Score 381; DB 7; Length 504;  
Best Local Similarity 99.7%; Pred. No. 1.31e-290;  
Matches 382; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCCTCAAAATATGATTGCTGTACC 180  
|||  
Qy 344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCCTCAAAATATGATTGCTGTACC 403  
|||  
Db 181 AAGTCCCAAGAGAACCTACTGTACATGACTGTCCAGGCCGGGGCAGATACGGAC 240  
|||  
Qy 404 AAGTCCCAAGAGAACCTACTGTACATGACTGTCCAGGCCGGGGCAGATACGGAC 463  
|||  
Db 241 TGCAGGAGTGTGAGACGGGCTCTTACAGCCTTCAGAAAACCACTCAGACACTGCCTC 300  
|||  
Qy 464 TGCAGGAGTGTGAGACGGGCTCTTACAGCCTTCAGAAAACCACTCAGACACTGCCTC 523  
|||  
Db 301 AGCTGCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTTCTTGCACAGTGGAC 360  
|||  
Qy 524 AGCTGCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTTCTTGCACAGTGGAC 583  
|||  
Db 361 CGGGACACCGTGTGCTGCTCAGAGAACCAAGTACCGGATTTATGAGTGAATACCTT 420  
|||  
Qy 584 CGGGACACCGTGTGCTGCTCAGAGAACCAAGTACCGGATTTATGAGTGAATACCTT 643  
|||  
Db 421 TTCAGTGTTCATTTGACAGCTCTGCCTCAATGGAGCCGTGCACTCTCTGCGCAGAG 480  
|||  
Qy 644 TTCAGTGTTCATTTGACAGCTCTGCCTCAATGGAGCCGTGCACTCTCTGCGCAGAG 703  
|||  
Db 481 AAACAGAACACCGTGTGACCTG 503  
|||  
Qy 704 AAACAGAACACCGTGTGACCTG 726  
|||

RESULT 7  
ID US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.

XX xxxxxx  
XX 01-JAN-1900  
XX  
DE Sequence 1, Application US/08050319B.  
CC  
CC Sequence 1, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan

CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 501 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..501  
SQ Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

Query Match 36.1%; Score 379; DB 7; Length 501;  
Best Local Similarity 99.7%; Pred. No. 6.34e-289;  
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCCTCAAAATATGATTGCTGTACC 180  
|||  
Qy 344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCCTCAAAATATGATTGCTGTACC 403  
|||  
Db 181 AAGTCCCAAGAGAACCTACTGTACATGACTGTCCAGGCCGGGGCAGATACGGAC 240  
|||  
Qy 404 AAGTCCCAAGAGAACCTACTGTACATGACTGTCCAGGCCGGGGCAGATACGGAC 463  
|||  
Db 241 TGCAGGAGTGTGAGACGGGCTCTTACAGCCTTCAGAAAACCACTCAGACACTGCCTC 300  
|||  
Qy 464 TGCAGGAGTGTGAGACGGGCTCTTACAGCCTTCAGAAAACCACTCAGACACTGCCTC 523  
|||  
Db 301 AGCTGCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTTCTTGCACAGTGGAC 360  
|||  
Qy 524 AGCTGCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTTCTTGCACAGTGGAC 583  
|||  
Db 361 CGGGACACCGTGTGCTGCTCAGAGAACCAAGTACCGGATTTATGAGTGAATACCTT 420  
|||  
Qy 584 CGGGACACCGTGTGCTGCTCAGAGAACCAAGTACCGGATTTATGAGTGAATACCTT 643  
|||  
Db 421 TTCAGTGTTCATTTGACAGCTCTGCCTCAATGGAGCCGTGCACTCTCTGCGCAGAG 480  
|||  
Qy 644 TTCAGTGTTCATTTGACAGCTCTGCCTCAATGGAGCCGTGCACTCTCTGCGCAGAG 703  
|||  
Db 481 AAACAGAACACCGTGTGACCTG 501  
|||  
Qy 704 AAACAGAACACCGTGTGACCTG 724  
|||

RESULT 8  
ID US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.

XX AC xxxxxx  
XX DT 01-JAN-1900  
XX DE Sequence 3, Application US/08050319B.  
XX CC Sequence 3, Application US/08050319B.  
XX CC Patent No. 5633145  
XX CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 372 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..372  
CC Sequence 372 BP; 102 C; 95 G; 77 T; 0 other;  
SQ  
Query Match 35.3%; Score 370; DB 7; Length 372;  
Best Local Similarity 99.7%; Pred. No. 2,44e-281;  
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 1 GGTGTCCCAAGAAATATATCCACCTCAAAATTAATTCATTGCTGTACCAAGTGC 60  
Oy 350 GTGTGCCCCAAGAAATATATCCACCTCAAAATTAATTCATTGCTGTACCAAGTGC 409  
Db 61 CACAAAGAACTACTGTGACATGACTCTCCAGGCCGGGGGAGATACGGACTCGAG 120  
Oy 410 CACAAAGAACTACTGTGACATGACTCTCCAGGCCGGGGGAGATACGGACTCGAG 469  
Db 121 GAGTGTGAGAGGGCTCTCTACCGCTTCAGAAAACCACTCAGACAGCTCAGACTGC 180  
Oy 470 GAGTGTGAGAGGGCTCTCTACCGCTTCAGAAAACCACTCAGACAGCTCAGACTGC 529  
Db 161 TCCAAATGCCGAAGAAATGGGTGAGTGTGAGATCTCTTCTTGCACTGAGACCGGAG 240  
Oy 530 TCCAAATGCCGAAGAAATGGGTGAGTGTGAGATCTCTTCTTGCACTGAGACCGGAG 589  
Db 241 ACCGTGTGCTGTCGAGGAAGAACGATACCGGATATTGGAGTAAACCTTTTCAG 300  
|||||

Oy 590 ACCGTGTGCTGTCGAGGAAGAACGATACCGGATATTGGAGTAAACCTTTTCAG 649  
Db 301 TGTCTCAATTGACAGCCTTGCTTCAATGGAGCGTGCACCTCTCCGCGAGGAACAG 360  
Oy 650 TGTCTCAATTGACAGCCTTGCTTCAATGGAGCGTGCACCTCTCCGCGAGGAACAG 709  
Db 361 AACACCGTGTGC 372  
Oy 710 AACACCGTGTGC 721  
RESULT 9  
ID US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.  
XX AC xxxxxx  
XX DT 01-JAN-1900  
XX DE Sequence 49, Application US/08050319B.  
XX CC Sequence 49, Application US/08050319B.  
XX CC Patent No. 5633145  
XX CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 49:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 474 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..471  
CC Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;  
SQ  
Query Match 28.8%; Score 302; DB 7; Length 474;  
Best Local Similarity 97.8%; Pred. No. 3.55e-224;  
Matches 309; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Db 105 GGACAGGGAGAGAGAGTGTGAGAGGGCTTCACCGCTTCAGAAAACCACTCTAG 164  
Oy 454 GGTACGGACTCAGAGAGATGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTCTAG 513  
Db 165 ACACCTGCTCAGCTGTCCAAATGCCGAAGAAATGGGTGAGTGTGAGATCTCTCTTG 224  
|||||

|||||  
QY 514 ACAGTCGCTGAGTGTCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTTTG 573  
DB 225 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGCATTATGGAG 284  
QY 574 CACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGCATTATGGAG 633  
DB 285 TGAAGACCTTTTCAGTGTCTCAATTGCAAGCCCTGCTCAATGGAGCGGTGACCTCTC 344  
QY 634 TGAAGACCTTTTCAGTGTCTCAATTGCAAGCCCTGCTCAATGGAGCGGTGACCTCTC 693  
DB 345 CTGCGAGGAGAAACAGAACACCGTGTGCACCTGCACATGACGTTTCTTCAAGAGAAAA 404  
QY 694 CTGCGAGGAGAAACAGAACACCGTGTGCACCTGCACATGACGTTTCTTCAAGAGAAAA 753  
DB 405 CGAGTGTCTCTCTCT 420  
QY 754 CGAGTGTCTCTCTCT 769

RESULT 10  
ID US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.

XX xxxxxx  
XX 01-JAN-1900  
XX Sequence 5, Application US/08273411.  
XX Sequence 5, Application US/08273411.  
CC Patent No. 5625124  
CC GENERAL INFORMATION:  
CC APPLICANT: Falk, Per  
CC APPLICANT: Gordon, Jeffrey I.  
CC TITLE OF INVENTION: Animal Model for Gastro-Intestinal  
CC NUMBER OF SEQUENCES: 10  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Patrea L. Pabst  
CC STREET: 1100 Peachtree Street, Suite 2800  
CC CITY: Atlanta  
CC STATE: Georgia  
CC COUNTRY: USA  
CC ZIP: 30309-4530  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/273,411  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Pabst, Patrea L.  
CC REGISTRATION NUMBER: 31,284  
CC REFERENCE/DOCKET NUMBER: WU106  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (404) 815-6508  
CC TELEFAX: (404) 815-6555  
CC INFORMATION FOR SEQ ID NO: 5:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2771 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Sweetser, et al.  
CC JOURNAL: Genes & Dev.

CC VOLUME: 2  
CC PAGES: 1318-1332  
CC DATE: 1988  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 561 TO 629  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Seeburg, et al.  
CC JOURNAL: DNA  
CC VOLUME: 1  
CC PAGES: 239-249  
CC DATE: 1982  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 620 TO 2771  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Sweetser, et al.  
CC JOURNAL: J. Biol. Chem.  
CC VOLUME: 261  
CC PAGES: 5553-5561  
CC DATE: 1986  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 617  
CC SEQUENCE 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;

Query Match 28.6%; Score 300; DB 7; Length 2771;  
Best Local Similarity 97.3%; Pred. No. 1,69e-222;  
Matches 329; Conservative 0; Mismatches 5; Indels 4; Gaps 2;

DB 680 ATGGCTACAGGTAAAGCGCCCTAAATCCCTTGGGACACAATGTCTGAGGGAGAG 739  
QY 6 ATGGCTACAGGTAAAGCGCCCTAAATCCCTTGGGACACAATGTCTGAGGGAGAG 65  
DB 740 CACGACCTGTAGATGGACGGGGGACCTAACCTCAGGTTGGGCTTCTGAATG--AG 797  
QY 66 CACGACCTGTAGATGGACGGGGGACCTAACCTCAGGTTGGGCTTCTGAATG--AG 125  
DB 798 TATGCCATGTAAAGCCAGTAT--GGCCAAATCTCAGAAAGCTCTGCTCCCTGGAGGAT 855  
QY 126 TATGCCATGTAAAGCCAGTAT--GGCCAAATCTCAGAAAGCTCTGCTCCCTGGAGGAT 185  
DB 856 GGAGAGAGAAACAAACAGCTCTGGAGAGGAGAGAGTGGCTTGTCTCCGCG 915  
QY 186 GGAGAGAGAAACAAACAGCTCTGGAGAGGAGAGAGTGGCTTGTCTCCGCG 245  
DB 916 TCCCTGTGTGCCCCCTGTGTTTCTCCCAAGGCTCCCGAGCTCCTGCTGCTTTT 975  
QY 246 TCCCTGTGTGCCCCCTGTGTTTCTCCCAAGGCTCCCGAGCTCCTGCTGCTTTT 305  
DB 976 GCCTGCTGCTGCTCCCTGCTGCTTCAAGAGGGAGTGC 1013  
QY 306 GCCTGCTGCTGCTCCCTGCTGCTTCAAGAGGGAGTGC 343

RESULT 11  
ID US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.

XX xxxxxx  
XX 01-JAN-1900  
XX Sequence 3, Application US/08343401A.  
XX Sequence 3, Application US/08343401A.  
CC Patent No. 5661132  
CC GENERAL INFORMATION:  
CC APPLICANT: Swain, William F  
CC APPLICANT: Macklin, Michael D  
CC APPLICANT: Eriksson, Eloff  
CC APPLICANT: Andree, Christophe  
CC TITLE OF INVENTION: Improved Wound Healing  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Quarles & Brady  
CC STREET: PO Box 2113  
CC CITY: Madison  
CC STATE: WI





Job time : 122 secs.

QY 661 CAGCCTCTGCTCAATGAGGACGTCACCTCTCTCTCCAGAGAAACAGACCTGTG 720  
DB 360 CACCTGCCATGACGAGTTTCTTTCTTAAGAGAAAACGAGTGTCTCTGT 408  
QY 721 CACCTGCCATGACGAGTTTCTTTCTTAAGAGAAAACGAGTGTCTCTGT 769

## RESULT 15

ID US-08-187-756C-3 STANDARD; DNA; UNC; 534 BP.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 3, Application US/08187756C.

CC Sequence 3, Application US/08187756C

CC Patent No. 5597709

CC GENERAL INFORMATION:

CC APPLICANT: ROSEN, ET AL.

CC TITLE OF INVENTION: Human Growth Hormone

CC NUMBER OF SEQUENCES: 7

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: CECCHI, BYRNE, BAIN, GILFILLAN,

CC STREET: 6 BECKER FARM ROAD

CC CITY: ROSELAND

CC STATE: NEW JERSEY

CC COUNTRY: USA

CC ZIP: 07068

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: 3.5 INCH DISKETTE

CC COMPUTER: IBM PS/2

CC OPERATING SYSTEM: MS-DOS

CC SOFTWARE: WORD PERFECT 5.1

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/187,756C

CC FILING DATE: January 27, 1994

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER:

CC FILING DATE:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: FERRARO, GREGORY D.

CC REGISTRATION NUMBER: 36,134

CC REFERENCE/DOCKET NUMBER: 325800-55

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 201-994-1700

CC TELEFAX: 201-994-1744

CC INFORMATION FOR SEQ ID NO: 3:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 534 BASE PAIRS

CC TYPE: NUCLEIC ACID

CC STRANDEDNESS: SINGLE

CC TOPOLOGY: LINEAR

CC MOLECULE TYPE: CDNA

CC Sequence 534 BP; 108 A; 166 C; 143 G; 117 T; 0 other;

SQ Query Match 6.6%; Score 69; DB 6; Length 534;

Best Local Similarity 98.6%; P-Val. 9.14e-34;

Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 8 CAGGCTCCCGAGAGTCCCTGCTGCTTTGGCTGCTGCTGCTGCTGCTGCTCAAG 67






QY 273 CAGGCTCCCGAGAGTCCCTGCTGCTTTGGCTGCTGCTGCTGCTGCTCAAG 332

DB 68 AGGCGAGTGCC 78

QY 333 AGGCGAGTGCC 343

Search completed: Wed May 6 10:02:47 1998



Release 3.0.5AA John F. Collins, Blocomputing Research Unit  
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```

Mpsrich_pp      protein - protein database search, using Smith-Mateman algorithm
Run on:         Wed May 6 08:27:00 1998;      MasPar time 4.88 seconds
Tabular output not generated.      394.142 Million cell updates/sec

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Title: >US-08-804-166-8
Description: (1-336) from US08804166 pep
Perfect Score: 2541
Sequence: 1 SRTSLLAFLGLCLPMTQES.....PELSPSPKRPGBSDPTPIPQ 336
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Scoring table: PAM 150  
Gap 11

Searched: 62627 seqs, 5720858 residues

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Post-processing: Minimum Match 08
Listing first 45 summaries
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Database:

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Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PT90
10:PT91 11:PT92 12:PT93 13:PT94 14:PT95 15:PT96
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Statistics: Mean 30.838; Variance 140.153; scale 0.220

**Pred. No.** Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1332	52.0	455	7	US-08-321-	Sequence 2, Applicatio	1.11e-11
2	1332	52.0	455	7	US-08-050-	Sequence 25, Applicati	1.11e-11
3	1233	48.9	199	7	US-08-050-	Sequence 48, Applicati	2.75e-10
4	1025	40.3	145	6	US-08-425-	Sequence 2, Applicatio	6.14e-83
5	1025	40.3	145	6	US-08-425-	Sequence 1, Applicatio	6.14e-83
6	1020	40.1	145	6	US-08-298-	Sequence 1, Applicatio	1.17e-82
7	995	39.2	145	6	US-08-425-	Sequence 10, Applicati	3.81e-80
8	996	39.2	167	7	US-08-050-	Sequence 57, Applicati	3.07e-80
9	996	39.2	167	7	US-08-050-	Sequence 2, Applicatio	3.07e-80
10	981	38.5	124	7	US-08-050-	Sequence 4, Applicatio	7.64e-79
11	928	36.5	157	7	US-08-425-	Sequence 50, Applicatio	6.44e-74
12	760	29.1	114	6	US-08-425-	Sequence 9, Applicatio	1.61e-56
13	724	28.9	114	6	US-08-425-	Sequence 7, Applicatio	5.77e-56
14	714	28.1	117	6	US-08-425-	Sequence 11, Applicati	4.01e-54
15	664	26.9	114	6	US-08-425-	Sequence 8, Applicatio	2.31e-51
16	666	26.2	158	7	US-08-050-	Sequence 54, Applicati	1.04e-49
17	651	25.6	117	6	US-08-425-	Sequence 12, Applicati	2.47e-48
18	613	24.1	149	6	US-08-425-	Sequence 5, Applicatio	7.49e-45
19	605	23.8	153	7	US-08-050-	Sequence 52, Applicati	4.04e-44
20	339	13.3	41	7	US-08-050-	Sequence 36, Applicati	3.84e-20
21	324	12.8	40	7	US-08-050-	Sequence 26, Applicati	8.05e-19
22	318	12.5	43	7	US-08-050-	Sequence 31, Applicati	2.71e-18

23	298	11.7	39	7	US-08-050-	Sequence 40,	Applicati	1.53e-16
24	296	11.6	445	1	5451527-1	Patent No. 5451527.		1.28e-15
25	287	11.3	111	6	US-08-435-	Sequence 4,	Applicatio	1.39e-15
26	287	11.3	111	6	US-08-435-	Sequence 3,	Applicatio	1.39e-15
27	282	11.1	112	6	US-08-425-	Sequence 6,	Applicatio	3.77e-15
28	268	10.5	445	5	US-08-086-	Sequence 14,	Applicati	6.14e-14
29	261	10.3	46	5	US-08-086-	Sequence 12,	Applicati	2.47e-13
30	260	10.2	131	1	5177193-3	Patent No. 5177193.		3.01e-13
31	249	9.8	46	5	US-08-086-	Sequence 11,	Applicati	2.65e-12
32	249	9.8	46	5	US-08-086-	Sequence 13,	Applicati	2.65e-12
33	230	9.1	41	5	US-08-086-	Sequence 17,	Applicati	1.10e-10
34	227	8.9	34	1	5451527-4	Patent No. 5451527.		1.98e-10
35	227	8.9	39	1	5451527-8	Patent No. 5451527.		1.98e-10
36	227	8.9	39	1	5451527-12	Patent No. 5451527.		1.98e-10
37	227	8.9	39	13	PT-US94-0	Sequence 29,	Applicati	1.98e-10
38	225	8.9	325	5	US-08-292-	Sequence 2,	Applicatio	2.93e-10
39	225	8.9	325	10	PT-US91-0	Sequence 2,	Applicatio	2.93e-10
40	221	8.7	326	5	US-08-292-	Sequence 4,	Applicatio	6.38e-10
41	221	8.7	326	10	PT-US91-0	Sequence 4,	Applicatio	6.38e-10
42	212	8.3	41	5	US-08-086-	Sequence 15,	Applicati	3.65e-09
43	210	8.3	355	5	US-08-292-	Sequence 6,	Applicatio	5.38e-09
44	212	8.3	474	1	5395760-4	Patent No. 5395760.		3.65e-09
45	209	8.2	36	1	5451527-5	Patent No. 5451527.		6.52e-09

## ALIGNMENTS

RESULT 1  
 ID US-08-321-668-2 STANDARD; PRT; 455 AA.  
 XX  
 AC xxxxxx  
 XX  
 DT 01-JAN-1900  
 XX  
 DE Sequence 2, Application US/08321668.  
 XX  
 CC Sequence 2, Application US/08321668  
 CC Patent No. 5665859  
 CC GENERAL INFORMATION:  
 CC APPLICANT: WALLACH, David  
 CC APPLICANT: BRAKEBUSCH, Cord  
 CC APPLICANT: VARFOLOMEEV, Eugene  
 CC APPLICANT: BAYKIN, Michael  
 CC TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
 CC TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
 CC NUMBER OF SEQUENCES: 42  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: BROWDY AND NEWMARK  
 CC STREET: 419 Seventh Street, N.W., Suite 300  
 CC City: Washington  
 CC STATE: D.C.  
 CC COUNTRY: USA  
 CC Zip: 20004  
 CC  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/321,668  
 CC FILING DATE: 12-OCT-1994  
 CC CLASSIFICATION: 435  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: IL 107268  
 CC FILING DATE: 12-OCT-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: BROWDY, Roger L.  
 CC REGISTRATION NUMBER: 25,618  
 CC REFERENCE/DOCKET NUMBER: WALLACH-13  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 202-628-5197  
 CC TELEFAX: 202-737-3528  
 CC TELEX: 248633

CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 455 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 455 AA; 50494 MW; 1048031 CN;

Query Match 52.0%; Score 1322; DB 7; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.11e-110;  
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 41 DSVCPQGYIHPNNSICTCKHGTLYINDCPGPGQDTDCRECSGSFTASENHLRCL 100  
OY 23 DSVCPQGYIHPNNSICTCKHGTLYINDCPGPGQDTDCRECSGSFTASENHLRCL 82

Db 101 SCSKCRKMGVEISSCTVDRTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSOE 160  
OY 83 SCSKCRKMGVEISSCTVDRTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSOE 142

Db 161 KONTVCTCHAGFFLRENECVSCSNCKSLSECTKLCPLQIENVKGTEDSGTT 211  
OY 143 KONTVCTCHAGFFLRENECVSCSNCKSLSECTKLCPLQIENVKGTEDSGTT 193

RESULT 2  
ID US-08-050-319B-25 STANDARD; PRT; 455 AA.  
AC xxxxxx  
XX 01-JAN-1900  
DE Sequence 25, Application US/08050319B.  
XX  
CC Sequence 25, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC INFORMATION FOR SEQ ID NO: 25:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 25:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 455 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 455 AA; 50579 MW; 1048388 CN;

Query Match 52.0%; Score 1322; DB 7; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1.11e-110;  
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 41 DSVCPQGYIHPNNSICTCKHGTLYINDCPGPGQDTDCRECSGSFTASENHLRCL 100  
OY 23 DSVCPQGYIHPNNSICTCKHGTLYINDCPGPGQDTDCRECSGSFTASENHLRCL 82

Db 101 SCSKCRKMGVEISSCTVDRTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSOE 160  
OY 83 SCSKCRKMGVEISSCTVDRTVCGCRKNQYRHYSENLFQCFNCSICLNGTVHLSOE 142

Db 161 KONTVCTCHAGFFLRENECVSCSNCKSLSECTKLCPLQIENVKGTEDSGTT 211  
OY 143 KONTVCTCHAGFFLRENECVSCSNCKSLSECTKLCPLQIENVKGTEDSGTT 193

RESULT 3  
ID US-08-050-319B-48 STANDARD; PRT; 199 AA.  
AC xxxxxx  
XX 01-JAN-1900  
DE Sequence 48, Application US/08050319B.  
XX  
CC Sequence 48, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC INFORMATION FOR SEQ ID NO: 48:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 48:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 199 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 199 AA; 22186 MW; 195553 CN;

Query Match 48.9%; Score 1243; DB 7; Length 199;  
Best Local Similarity 99.4%; Pred. No. 2.75e-103;  
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 23 DSVCPQGYIHPNNSICTCKHGTLYINDCPGPGQDTDCRECSGSFTASENHLRCL 82

Db 101 SCSCCKREMGVEISSCTVDRDVTYCGCRKNQRYHWSENIFOCFNSICLNGTVHLSQOE 160  
|||  
QY 83 SCSCCKREMGVEISSCTVDRDVTYCGCRKNQRYHWSENIFOCFNSICLNGTVHLSQOE 142  
Db 161 KONTVCTCHAGFFLRENECVSCSNCKSLCCTVLCPLQI 199  
|||  
QY 143 KONTVCTCHAGFFLRENECVSCSNCKSLCCTVLCPLQI 181

RESULT 4  
ID US-08-425-673-2 STANDARD: PRT: 145 AA.

AC xxxxxx  
XX  
DT 01-JAN-1900  
XX

DE Sequence 2, Application US/08425673.

CC Sequence 2, Application US/08425673  
CC Patent No. 5508261

CC GENERAL INFORMATION:

CC APPLICANT: Moyle, William R.  
CC APPLICANT: Campbell, Robert K.

CC TITLE OF INVENTION: Analogs of glycoprotein Hormones Having

CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and

CC TITLE OF INVENTION: Methods for Preparing and Using Same

CC NUMBER OF SEQUENCES: 12

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Richard R. Muccino

CC STREET: P.O. Box 1267

CC CITY: Princeton

CC STATE: New Jersey

CC COUNTRY: USA

CC ZIP: 08551

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/425,673

CC FILING DATE:

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/717,151

CC FILING DATE: 18-JUN-1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Muccino, Richard R.

CC REGISTRATION NUMBER: 32,538

CC REFERENCE/DOCKET NUMBER: UMD 1.0-004

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (609) 466-3407

CC TELEFAX: (609) 466-2760

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 145 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC HYPOTHETICAL: NO

CC ANTI-SENSE: NO

CC SEQUENCE 145 AA: 15544 MW: 114662 CN:

Query Match 40.3%; Score 1025; DB 6; Length 145;

Best Local Similarity 99.3%; Pred. No. 6.14e-83;

Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7 PRCRPNATLAVERKCPVITVNTICAGYCTMTRVLOGVLPALPQVVCNTRDVAFES 66

QY 198 PRCRPNATLAVERKCPVITVNTICAGYCTMTRVLOGVLPALPQVVCNTRDVAFES 257

Db 67 IRLPGCPRGVNPVSVYAVALSOCALCRSTTDCGPKDHPPLTCDDPFRQDSSSSKAPP 126

QY 258 IRLPGCPRGVNPVSVYAVALSOCALCRSTTDCGPKDHPPLTCDDPFRQDSSSSKAPP 317

QY 258 IRLPGCPRGVNPVSVYAVALSOCALCRSTTDCGPKDHPPLTCDDPFRQDSSSSKAPP 317  
Db 127 SLSPSRRLPGSPDTPILPQ 145  
QY 318 SLSPSRRLPGSPDTPILPQ 336

RESULT 5  
ID US-08-425-673-1 STANDARD: PRT: 145 AA.

AC xxxxxx  
XX  
DT 01-JAN-1900  
XX

DE Sequence 1, Application US/08425673.

CC Sequence 1, Application US/08425673  
CC Patent No. 5508261

CC GENERAL INFORMATION:

CC APPLICANT: Moyle, William R.  
CC APPLICANT: Campbell, Robert K.

CC TITLE OF INVENTION: Analogs of glycoprotein Hormones Having

CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and

CC TITLE OF INVENTION: Methods for Preparing and Using Same

CC NUMBER OF SEQUENCES: 12

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Richard R. Muccino

CC STREET: P.O. Box 1267

CC CITY: Princeton

CC STATE: New Jersey

CC COUNTRY: USA

CC ZIP: 08551

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/425,673

CC FILING DATE:

CC CLASSIFICATION: 514

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/717,151

CC FILING DATE: 18-JUN-1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Muccino, Richard R.

CC REGISTRATION NUMBER: 32,538

CC REFERENCE/DOCKET NUMBER: UMD 1.0-004

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (609) 466-3407

CC TELEFAX: (609) 466-2760

CC INFORMATION FOR SEQ ID NO: 1:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 145 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC HYPOTHETICAL: NO

CC ANTI-SENSE: NO

CC SEQUENCE 145 AA: 15544 MW: 114662 CN:

Query Match 40.3%; Score 1025; DB 6; Length 145;

Best Local Similarity 99.3%; Pred. No. 6.14e-83;

Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 7 PRCRPNATLAVERKCPVITVNTICAGYCTMTRVLOGVLPALPQVVCNTRDVAFES 66

QY 198 PRCRPNATLAVERKCPVITVNTICAGYCTMTRVLOGVLPALPQVVCNTRDVAFES 257

Db 67 IRLPGCPRGVNPVSVYAVALSOCALCRSTTDCGPKDHPPLTCDDPFRQDSSSSKAPP 126

QY 258 IRLPGCPRGVNPVSVYAVALSOCALCRSTTDCGPKDHPPLTCDDPFRQDSSSSKAPP 317

DB 127 SLSPSRLLPGPSDTPILPQ 145  
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OY 318 SLSPSRLLPGPSDTPILPQ 336

RESULT 6  
ID US-08-298-1898-1 STANDARD: PRT: 145 AA.  
XX xxxxxx  
DT 01-JAN-1900

Sequence 1, Application US/082981898.  
XX Sequence 1, Application US/082981898  
CC Patent No. 5674727  
CC GENERAL INFORMATION:  
CC APPLICANT: Dr. Laurence A. Cole and Dr. Andrew Kardana  
CC TITLE OF INVENTION: No. 5674727el Methods for Detecting Reproductive  
CC TITLE OF INVENTION: Cancers or Tumors and Assay Products  
CC NUMBER OF SEQUENCES: 1  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Dr. Laurence A. Cole, c/o Dept. of Obstetrics and  
CC STREET: 333 Cedar Street  
CC CITY: New Haven  
CC STATE: Connecticut  
CC COUNTRY: USA  
CC ZIP: 06510

COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" diskette  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: Windows 95  
CC SOFTWARE: Microsoft Word 7.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/298,1898  
CC FILING DATE: 08/31/94  
CC CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
CC NAME: Brian D. Voyce  
CC REGISTRATION NUMBER: 28,917  
CC REFERENCE/DOCKET NUMBER: DS11  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 919-638-3939 or 803-272-1471  
CC TELEFAX: 919-638-3939 or 803-272-1471  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 145 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: No. 5674727 applicable  
CC TOPOLOGY: Unknown  
CC MOLECULE TYPE: subunit of hormone, specifically the  
CC MOLECULE TYPE: beta subunit of hCG  
CC ORIGINAL SOURCE: human urine  
CC FEATURE:  
CC NAME/KEY: beta subunit of hCG that is nicked by GBNE  
CC LOCATION: hCG  
CC IDENTIFICATION METHOD: N-terminal sequence analysis  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Keutmann et alia  
CC TITLE: "A Receptor-binding Region in Human Choriongonadotropin/Luteop  
CC JOURNAL: Proc Natl Acad Sci USA  
CC VOLUME: 84  
CC ISSUE: No. 5674727 applicable  
CC PAGES: 2038-2042  
CC DATE: 1987

SEQUENCE 145 AA: 15476 MW: 116769 CN;  
SQ

Query Match 40.1%; Score 1020; DB 7; Length 145;  
Best Local Similarity 98.6%; Pred. No. 1,79e-82;  
Matches 137, Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 7 PCRPRINATLAVERGCGPCVITVNTTICAGYCPMTNRVLQGLPALPOVCYCNRYDVRFS 66

OY 198 PCRPRINATLAVERGCGPCVITVNTTICAGYCPMTNRVLQGLPALPOVCYCNRYDVRFS 257  
|||||  
DB 67 IRLPGCGRVGNVNVSYAVALSCCALCKRSTTDCGPRDHPITCDDPFRDSSSSKAPP 126  
|||||  
OY 258 IRLPGCGRVGNVNVSYAVALSCCALCKRSTTDCGPRDHPITCDDPFRDSSSSKAPP 317  
|||||

DB 127 SLSPSRLLPGPSDTPILPQ 145  
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OY 318 SLSPSRLLPGPSDTPILPQ 336

RESULT 7  
ID US-08-425-673-10 STANDARD: PRT: 145 AA.  
XX xxxxxx  
DT 01-JAN-1900

Sequence 10, Application US/08425673.  
XX Sequence 10, Application US/08425673.  
CC Patent No. 5508261  
CC GENERAL INFORMATION:  
CC APPLICANT: Moyle, William R.  
CC APPLICANT: Campbell, Robert K.  
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Richard R. Muccino  
CC STREET: P.O. Box 1267  
CC CITY: Princeton  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 08551

COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/425,673  
CC FILING DATE:  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/717,151  
CC FILING DATE: 18-JUN-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Muccino, Richard R.  
CC REGISTRATION NUMBER: 32,538  
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (609) 466-3407  
CC TELEFAX: (609) 466-2760  
CC INFORMATION FOR SEQ ID NO: 10:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 145 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO

SEQUENCE 145 AA: 15448 MW: 114931 CN;  
SQ

Query Match 39.2%; Score 995; DB 6; Length 145;  
Best Local Similarity 96.4%; Pred. No. 3,81e-80;  
Matches 134, Conservative 1; Mismatches 4; Indels 0; Gaps 0;

DB 7 PCRPRINATLAVERGCGPCVITVNTTICAGYCPMTNRVLQGLPALPOVCYCNRYDVRFS 66  
|||||  
OY 198 PCRPRINATLAVERGCGPCVITVNTTICAGYCPMTNRVLQGLPALPOVCYCNRYDVRFS 257  
|||||



XX Sequence 4, Application US/08050319B.  
DE  
XX  
CC Sequence 4, Application US/08050319B  
CC Patent No. 5633145  
CC  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA: US/08/050, 319B  
CC APPLICATION NUMBER: US/08/050, 319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 4:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 124 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 124 AA: 14047 MW: 75840 CN:  
SQ  
Query Match 38.6%; Score 981; DB 7; Length 124;  
Best Local Similarity 100.0%; Pred. No. 7,64e-79;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 VCPQGYIHPNNSICTCTCHGTYLYXNDPQGGOTDRECESSGFTASENHLRLCLSC 60  
QY 25 VCPQGYIHPNNSICTCTCHGTYLYXNDPQGGOTDRECESSGFTASENHLRLCLSC 84  
Db 61 SSCRKMGVEISSCTVDRTVCGCRKNOYRHWSENLFCQCFNCSICLNGTVHLSCEKQ 120  
QY 85 SSCRKMGVEISSCTVDRTVCGCRKNOYRHWSENLFCQCFNCSICLNGTVHLSCEKQ 144  
Db 121 NTVC 124  
QY 145 NTVC 148  
RESULT 11  
ID US-08-050-319B-50 STANDARD; PRT; 157 AA.  
AC xxxxxx  
XX 01-JAN-1900  
XX  
DE Sequence 50, Application US/08050319B.  
XX  
CC Sequence 50, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan

CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA: US/08/050, 319B  
CC APPLICATION NUMBER: US/08/050, 319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 50:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 157 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 157 AA: 17570 MW: 122247 CN:  
SQ

Query Match 36.5%; Score 928; DB 7; Length 157;  
Best Local Similarity 97.5%; Pred. No. 6,44e-74;  
Matches 119; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 36 DREKRECSGFTASENHLRLCLSCSKRKMGOVEISSCTVDRTVCGCRKNOYRHW 95  
QY 60 DREKRECSGFTASENHLRLCLSCSKRKMGOVEISSCTVDRTVCGCRKNOYRHW 119  
Db 96 ENLFCQCFNCSICLNGTVHLSCEKQNTVCTCHAGFFLRNECVSNCNKSIECTRLCLP 155  
QY 120 ENLFCQCFNCSICLNGTVHLSCEKQNTVCTCHAGFFLRNECVSNCNKSIECTRLCLP 179  
Db 156 QI 157  
QY 180 QI 181

RESULT 12  
ID US-08-425-673-9 STANDARD; PRT; 114 AA.  
AC xxxxxx  
XX 01-JAN-1900  
XX  
DE Sequence 9, Application US/08425673.  
XX  
CC Sequence 9, Application US/08425673  
CC Patent No. 5508261  
CC GENERAL INFORMATION:  
CC APPLICANT: Moyle, William R.  
CC APPLICANT: Campbell, Robert K.  
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Richard R. Muccino  
CC STREET: P.O. Box 1267  
CC CITY: Princeton







\*\*\*\*\*  
MIRAGE  
(TM)  
\*\*\*\*\*

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MParch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 11:17:48 1998; Maspar time 73.35 Seconds

Tabular output not generated. 934.882 Million cell updates/sec

Title: >US-08-804-166-7

Description: (1-1301) from US08804166.seq

Perfect Score: 1301 1 CTCGAGATCGCTACAGCTA.....CACATATAGGATCCCTCGAG 1301

N.A. Sequence: Comp: GAGCTGTACCGATGTCATT.....GTGTATTCCTAGGAGCTC

Scoring table: TABLE default

Match STD : Dbase 0; Query 0

Searched: 102136 segs, 26354296 bases x 2

Post-processing: Minimum Match 0%

Database: n-tssued

1:Back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PCIT90

10:PCIT91 11:PCIT92 12:PCIT93 13:PCIT94 14:PCIT95 15:PCIT96

Statistics: Mean 8.845; Variance 4.678; scale 1.891

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	514	39.5	2062	7	US-08-050-	Sequence 24, Applicati	0.00e+00
2	514	39.5	2175	7	US-08-321-	Sequence 1, Applicatio	0.00e+00
3	514	39.5	6889	6	US-08-286-	Sequence 2, Applicatio	0.00e+00
4	514	39.5	6889	14	PCT-US95-0	Sequence 2, Applicatio	0.00e+00
5	474	36.4	600	7	US-08-050-	Sequence 47, Applicati	0.00e+00
6	383	29.4	504	7	US-08-050-	Sequence 56, Applicati	6.44e-278
7	381	29.3	501	7	US-08-050-	Sequence 1, Applicatio	2.60e-275
8	372	28.6	372	7	US-08-050-	Sequence 3, Applicatio	4.39e-269
9	354	27.2	474	7	US-08-050-	Sequence 49, Applicati	1.22e-254
10	304	23.4	2771	7	US-08-273-	Sequence 5, Applicatio	1.27e-214
11	303	23.3	4283	7	US-08-343-	Sequence 3, Applicatio	7.97e-214
12	303	23.3	4283	7	US-08-445-	Sequence 1, Applicatio	3.56e-177
13	257	19.8	477	7	US-08-050-	Sequence 53, Applicati	1.21e-148
14	221	17.0	462	7	US-08-050-	Sequence 51, Applicati	6.08e-57
15	103	7.9	138	5	US-08-086-	Sequence 2, Applicatio	6.30e-54
16	99	7.6	138	5	US-08-086-	Sequence 14, Applicati	1.00e-42
17	84	6.5	7218	6	US-08-187-	Sequence 3, Applicatio	9.66e-32
18	69	5.3	654	6	US-08-187-	Sequence 1, Applicatio	9.66e-32
19	69	5.3	654	6	US-08-187-	Sequence 1, Applicatio	9.66e-32

20	59	4.5	321	4	US-07-920-	Sequence 23, Applicati	1.37e-24
21	59	4.5	321	6	US-08-314-	Sequence 2, Applicatio	1.37e-24
22	59	4.5	597	7	US-08-187-	Sequence 1, Applicatio	1.08e-19
23	52	4.0	2248	7	US-08-636-	Sequence 1, Applicatio	1.08e-19
24	52	4.0	2248	7	US-08-780-	Sequence 1, Applicatio	1.08e-19
25	52	4.0	2248	6	US-08-369-	Sequence 1, Applicatio	1.08e-19
26	52	4.0	2248	7	US-08-475-	Sequence 1, Applicatio	1.08e-19
27	42	3.2	215	6	US-08-238-	Sequence 5, Applicatio	6.38e-13
28	41	3.2	7218	7	US-08-232-	Sequence 14, Applicati	2.91e-12
29	38	2.9	633	7	US-08-388-	Sequence 1, Applicatio	2.61e-10
30	36	2.8	4810	7	US-08-453-	Sequence 1, Applicatio	4.97e-09
31	36	2.8	4810	13	PCT-US94-0	Sequence 3, Applicatio	4.97e-09
32	36	2.8	4810	12	PCT-US93-0	Sequence 3, Applicatio	4.97e-09
33	36	2.8	4810	14	PCT-US95-0	Sequence 3, Applicatio	4.97e-09
34	36	2.8	4810	7	US-08-188-	Sequence 3, Applicatio	4.97e-09
35	36	2.8	5125	12	PCT-US93-0	Sequence 11, Applicati	4.97e-09
36	36	2.8	5125	7	US-08-453-	Sequence 11, Applicati	4.97e-09
37	36	2.8	5323	7	US-08-453-	Sequence 9, Applicatio	4.97e-09
38	36	2.5	5323	12	PCT-US93-0	Sequence 9, Applicatio	4.97e-09
39	32	2.5	166	1	5177193-2	Patent No. 5177193.	1.56e-06
40	32	2.5	215	6	US-08-238-	Sequence 5, Applicatio	1.56e-06
41	32	2.5	1006	6	US-08-239-	Sequence 1, Applicatio	1.56e-06
42	30	2.3	33	7	US-08-050-	Sequence 14, Applicati	2.53e-05
43	26	2.0	74	14	PCT-US95-1	Sequence 94, Applicati	5.44e-03
44	26	2.0	105	5	US-07-865-	Sequence 13, Applicati	5.44e-03
45	26	2.0	242	7	US-08-273-	Sequence 1, Applicatio	5.44e-03

## ALIGNMENTS

RESULT 1  
ID US-08-050-319B-24 STANDARD; DNA; UNC; 2062 BP.

XX AC xxxxxx  
XX DT 01-JAN-1900  
XX DE Sequence 24, Application US/08050319B.  
XX CC Sequence 24, Application US/08050319B  
XX CC Patent No. 5633145  
XX CC GENERAL INFORMATION:  
XX CC APPLICANT: M.Feldmann, P.W. Gray,  
XX CC APPLICANT: M.J.C. Turner, F.M. Brennan  
XX CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
XX CC NUMBER OF SEQUENCES: 57  
XX CC CORRESPONDENCE ADDRESS:  
XX CC ADDRESSEE: Reed & Robbins  
XX CC STREET: 635 Bryant Street  
XX CC CITY: Palo Alto  
XX CC STATE: California  
XX CC COUNTRY: USA  
XX CC ZIP: 94301  
XX CC COMPUTER READABLE FORM:  
XX CC MEDIUM TYPE: Floppy disk  
XX CC OPERATING SYSTEM: IBM PC compatible  
XX CC SOFTWARE: Patent Release #1.0, version #1.25  
XX CC CURRENT APPLICATION DATA:  
XX CC APPLICATION NUMBER: US/08/050,319B  
XX CC FILING DATE: 10-May-1993  
XX CC CLASSIFICATION: 435  
XX CC ATTORNEY/AGENT INFORMATION:  
XX CC NAME: Robbins, Roberta L.  
XX CC REGISTRATION NUMBER: 33,208  
XX CC TELEPHONE: (415) 617-8999  
XX CC TELEFAX: (415) 327-3231  
XX CC INFORMATION FOR SEQ ID NO: 24:  
XX CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 2062 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 155..1519  
SQ Sequence 2062 BP; 429 A; 617 C; 573 G; 443 T; 0 other;

Query Match 39.5%; Score 514; DB 7; Length 2062;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 275 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCCCTCAAAATTAATTCGATTGCTGTACC 334  
|||  
Qy 345 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCCCTCAAAATTAATTCGATTGCTGTACC 404  
|||  
Db 333 AAGTGCACAAAGAAAGAACTTGTGTACATGACTGTCCAGGCCCGGGGCGAGATACGGAC 394  
|||  
Qy 405 AAGTGCACAAAGAAAGAACTTGTGTACATGACTGTCCAGGCCCGGGGCGAGATACGGAC 464  
|||  
Db 395 TCCAGGAGTGTGAGAGGGGCTCTCCACGGCTTCAGAAACCACTCAGACACTGCTTC 454  
|||  
Qy 465 TCCAGGAGTGTGAGAGGGGCTCTCCACGGCTTCAGAAACCACTCAGACACTGCTTC 524  
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Db 455 AGCTGCTCCAAATGCCGAAGAAATGGGTGTCAGTGTGATCTCTTCCACAGTGGAC 514  
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Qy 525 AGCTGCTCCAAATGCCGAAGAAATGGGTGTCAGTGTGATCTCTTCCACAGTGGAC 584  
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Db 515 CCGGACACCGTGTGTGGCTGTCAGGAAACCAAGTACCGGCATTATTGAGTGAACCTT 574  
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Qy 585 CCGGACACCGTGTGTGGCTGTCAGGAAACCAAGTACCGGCATTATTGAGTGAACCTT 644  
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Db 575 TTCCAGTGTCTTAATTCAGCTCTCTCCCTCAATGGGACCGCTGACCTCTCCCTCCAGGAC 634  
|||  
Qy 645 TTCCAGTGTCTTAATTCAGCTCTCTCCCTCAATGGGACCGCTGACCTCTCCCTCCAGGAC 704  
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Db 635 AAGCAGAACACCGGTGTCAGCTGCTCATGAGGTTCTTCTTAAGAGAAACAGAGTGTTC 694  
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Qy 705 AAGCAGAACACCGGTGTCAGCTGCTCATGAGGTTCTTCTTAAGAGAAACAGAGTGTTC 764  
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Db 695 TCCGTGTAGTACTGTAAAGAAAGCTGTGAGTGCAGAGTGTGCTTACCCAGATGGAG 754  
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Qy 765 TCCGTGTAGTACTGTAAAGAAAGCTGTGAGTGCAGAGTGTGCTTACCCAGATGGAG 824  
|||  
Db 755 AATGTTAAGGCACTGAGACTCAGGCACACACAG 788  
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Qy 825 AATGTTAAGGCACTGAGACTCAGGCACACACAG 858  
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RESULT 2  
ID US-08-321-668-1 STANDARD; DNA; UNC; 2175 BP.

XX xxxxxx  
XX 01-JAN-1900  
XX  
DE Sequence 1, Application US/08321668.  
XX  
CC Sequence 1, Application US/08321668  
CC Patent No. 5665859  
CC GENERAL INFORMATION:  
CC APPLICANT: WALLACH, David  
CC APPLICANT: BRAKEBUSCH, Cord  
CC APPLICANT: VAFLOMEY, Eugene  
CC APPLICANT: BAIKIN, Michael  
CC TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
CC TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
CC NUMBER OF SEQUENCES: 42  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: BROWDY AND NEIMARK

CC STREET: 419 Seventh Street, N.W., Suite 300  
CC CITY: Washington  
CC STATE: D.C.  
CC COUNTRY: USA  
CC ZIP: 20004  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/321,668  
CC FILING DATE: 12-OCT-1994  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: IL 107268  
CC FILING DATE: 12-OCT-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: BROWDY, Roger L.  
CC REGISTRATION NUMBER: 25,618  
CC REFERENCE/DOCKET NUMBER: WALLACH-13  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 202-628-5197  
CC TELEFAX: 202-737-3528  
CC TELEX: 248633  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2175 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 256..1620  
SQ Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;

Query Match 39.5%; Score 514; DB 7; Length 2175;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 376 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCCCTCAAAATTAATTCGATTGCTGTACC 435  
|||  
Qy 345 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCCCTCAAAATTAATTCGATTGCTGTACC 404  
|||  
Db 436 AAGTGCACAAAGAAAGAACTTGTGTACATGACTGTCCAGGCCCGGGGCGAGATACGGAC 495  
|||  
Qy 405 AAGTGCACAAAGAAAGAACTTGTGTACATGACTGTCCAGGCCCGGGGCGAGATACGGAC 464  
|||  
Db 496 TCCAGGAGTGTGAGAGGGGCTCTCCACGGCTTCAGAAACCACTCAGACACTGCTTC 555  
|||  
Qy 465 TCCAGGAGTGTGAGAGGGGCTCTCCACGGCTTCAGAAACCACTCAGACACTGCTTC 524  
|||  
Db 556 AGCTGCTCCAAATGCCGAAGAAATGGGTGTCAGTGTGATCTCTTCCACAGTGGAC 615  
|||  
Qy 525 AGCTGCTCCAAATGCCGAAGAAATGGGTGTCAGTGTGATCTCTTCCACAGTGGAC 584  
|||  
Db 616 CCGGACACCGTGTGTGGCTGTCAGGAAACCAAGTACCGGCATTATTGAGTGAACCTT 675  
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Qy 585 CCGGACACCGTGTGTGGCTGTCAGGAAACCAAGTACCGGCATTATTGAGTGAACCTT 644  
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Db 676 TTCCAGTGTCTTAATTCAGCTCTCTCCCTCAATGGGACCGTGCACCTCTCCCTCCAGGAC 735  
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Qy 645 TTCCAGTGTCTTAATTCAGCTCTCTCCCTCAATGGGACCGTGCACCTCTCTCCCTCCAGGAC 704  
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Db 736 AAGCAGAACACCGGTGTCAGCTGCTCATGAGGTTCTTCTTAAGAGAAACAGAGTGTTC 795  
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Qy 705 AAGCAGAACACCGGTGTCAGCTGCTCATGAGGTTCTTCTTAAGAGAAACAGAGTGTTC 764  
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Db 796 TCCGTGTAGTACTGTAAAGAAAGCTGTGAGTGCAGAGTGTGCTTACCCAGATGGAG 855  
|||  
Qy 765 TCCGTGTAGTACTGTAAAGAAAGCTGTGAGTGCAGAGTGTGCTTACCCAGATGGAG 824  
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Dh 856 AATGTTAAGGCACTGAGACTGAGCACCACAG 889  
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Oy 825 AATGTTAAGGCACTGAGACTGAGCACCACAG 858

RESULT 3  
ID US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.

XX xxxxxx  
XX 01-JAN-1900  
DE Sequence 2, Application US/08286740.  
XX  
CC Sequence 2, Application US/08286740  
CC Patent No. 5561053  
CC GENERAL INFORMATION:  
CC APPLICANT: Crowley, Craig W.  
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING  
CC TITLE OF INVENTION: HOST CELLS  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Genentech, Inc.  
CC STREET: 460 Point San Bruno Blvd  
CC City: South San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94080  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: palin (Genentech)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/286,740  
CC FILING DATE: 05-AUG-1994  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lee, Wendy M.  
CC REGISTRATION NUMBER:  
CC REFERENCE/DOCKET NUMBER: 798  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-1994  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6889 bases  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;  
Query Match 39.5%; Score 514; DB 6; Length 6889;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 1725 GATAGTGTGTGTCCTCCCAAGAAAATATATCCACCTCAAAATAATGATTTGCTGACC 1784  
|||||  
Oy 345 GATAGTGTGTGTCCTCCCAAGAAAATATATCCACCTCAAAATAATGATTTGCTGACC 404  
|||||  
Dh 1785 AAGTGCACAAGAAAGAACTTGTACAAATGATGTCAGGCGCGGGGCAAGATACGAC 1844  
|||||  
Oy 405 AAGTGCACAAGAAAGAACTTGTACAAATGATGTCAGGCGCGGGGCAAGATACGAC 464  
|||||  
Dh 1845 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 1904  
|||||  
Oy 465 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 524  
|||||

Dh 1905 AGCTGCTCCAAATGCCGAAGAAATGGTGCAGTGGATCTCTTCTGCACAGTGAC 1964  
|||||  
Oy 525 AGCTGCTCCAAATGCCGAAGAAATGGTGCAGTGGATCTCTTCTGCACAGTGAC 584  
|||||  
Dh 1965 CGGAGACCGGTGTGTGGCTCAGAGAAACCACTACCGGCATTATGAGTGAACCTT 2024  
|||||  
Oy 585 CGGAGACCGGTGTGTGGCTCAGAGAAACCACTACCGGCATTATGAGTGAACCTT 644  
|||||  
Dh 2025 TTCGAGTGTTCATTTGCACTGACCTCTGCTCAATGGACCGCTCTCTGCGAGAG 2084  
|||||  
Oy 645 TTCGAGTGTTCATTTGCACTGACCTCTGCTCAATGGACCGCTCTCTGCGAGAG 704  
|||||  
Dh 2085 AAACAGAACCGGTGTGACCTGACCTGCATGACGTTTCTTCTAAGAGAAAGAGTGTCT 2144  
|||||  
Oy 705 AAACAGAACCGGTGTGACCTGACCTGCATGACGTTTCTTCTAAGAGAAAGAGTGTCT 764  
|||||  
Dh 2145 TCCTGTAGTACTGTAAAGAAACCTGAGTGCAGAAAGTTGTGCTTACCCAGATTGAG 2204  
|||||  
Oy 765 TCCTGTAGTACTGTAAAGAAACCTGAGTGCAGAAAGTTGTGCTTACCCAGATTGAG 824  
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Dh 2205 AATGTTAAGGCACTGAGACTGAGCACCACAG 2238  
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Oy 825 AATGTTAAGGCACTGAGACTGAGCACCACAG 858  
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RESULT 4  
ID PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.

XX xxxxxx  
XX 01-JAN-1900  
DE Sequence 2, Application PC/TUS9509576.  
XX  
CC Sequence 2, Application PC/TUS9509576  
CC GENERAL INFORMATION:  
CC APPLICANT: GENENTECH, INC.  
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING  
CC TITLE OF INVENTION: HOST CELLS  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Genentech, Inc.  
CC STREET: 460 Point San Bruno Blvd  
CC City: South San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94080  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: palin (Genentech)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/09576  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/286740  
CC FILING DATE: 05-AUG-1994  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lee, Wendy M.  
CC REGISTRATION NUMBER: 00,000  
CC REFERENCE/DOCKET NUMBER: 798PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-1994  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6889 bases  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double

CC TOPOLOGY: linear  
SQ Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other:  
Query Match 39.5%; Score 514; DB 14; Length 6889;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1725 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCTCAAAATATATGATTTGCTGTACC 1784  
|||||  
Qy 345 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCTCAAAATATATGATTTGCTGTACC 404  
|||||

Db 1785 AAGTGCACAAAGGAACCTACTTGTATGATGTCTCCAGGCCCCGGGGGAGATACGGAC 1844  
|||||  
Qy 405 AAGTGCACAAAGGAACCTACTTGTATGATGTCTCCAGGCCCCGGGGGAGATACGGAC 464  
|||||

Db 1845 TGCAGGAGTGTGAGAGCGGCTCCTCAGCGCTTCAGAAACACACTCAGACACTGCTC 1904  
|||||  
Qy 465 TGCAGGAGTGTGAGAGCGGCTCCTCAGCGCTTCAGAAACACACTCAGACACTGCTC 524  
|||||

Db 1905 AGCTGCTCCAAATGCCGAAAGGAATGGGTGAGGTGAGATCTCTTTCAGACAGTGGAC 1964  
|||||  
Qy 525 AGCTGCTCCAAATGCCGAAAGGAATGGGTGAGGTGAGATCTCTTTCAGACAGTGGAC 584  
|||||

Db 1965 CGGGACACCGTGTGTGGCTGCGAGGAAGAACGATACCGGCTATTGAGTGAACCTT 2024  
|||||  
Qy 585 CGGGACACCGTGTGTGGCTGCGAGGAAGAACGATACCGGCTATTGAGTGAACCTT 644  
|||||

Db 2025 TTCACGTGCTTCATATGACACCTCTGCTCAATGAGACCGTGCACCTCTCCAGAG 2084  
|||||  
Qy 645 TTCACGTGCTTCATATGACACCTCTGCTCAATGAGACCGTGCACCTCTCCAGAG 704  
|||||

Db 2085 AAACAGAACACCGTGTGACACCTGCCATGCAAGTTCTTCTTAAGAGAAAAAGAGTGTG 2144  
|||||  
Qy 705 AAACAGAACACCGTGTGACACCTGCCATGCAAGTTCTTCTTAAGAGAAAAAGAGTGTG 764  
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Db 2145 TCCTGTAGTAAGTCTGAAGAAAGCCCTGAGTGTGACGAATGTGCTTACCCGATTTGAG 2204  
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Qy 765 TCCTGTAGTAAGTCTGAAGAAAGCCCTGAGTGTGACGAAGTGTGCTTACCCGATTTGAG 824  
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Db 2205 AATGTTAAGGCACTGAGACCTCAGGACACACAG 2238  
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Qy 825 AATGTTAAGGCACTGAGACCTCAGGACACACAG 858  
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RESULT 5  
ID US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

AC xxxxxx  
XX  
XX 01-JAN-1900  
XX  
DE Sequence 47, Application US/08050319B.  
XX  
XX Sequence 47, Application US/08050319B.  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M. Feldmann, P. W. Gray,  
CC APPLICANT: M. J. C. Turner, F. M. Brennan  
CC TITLE OF INVENTION: Modified human TRFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 47:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 600 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..597  
CC  
SQ Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other:  
Query Match 36.4%; Score 474; DB 7; Length 600;  
Best Local Similarity 99.4%; Pred. No. 0.00e+00;  
Matches 477; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCTCAAAATATATGATTTGCTGTACC 180  
|||||  
Qy 345 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCTCAAAATATATGATTTGCTGTACC 404  
|||||

Db 181 AAGTGCACAAAGGAACCTACTTGTATGATGTCTCCAGGCCCCGGGGGAGATACGGAC 240  
|||||  
Qy 405 AAGTGCACAAAGGAACCTACTTGTATGATGTCTCCAGGCCCCGGGGGAGATACGGAC 464  
|||||

Db 241 TGCAGGAGTGTGAGAGCGGCTCCTCAGCGCTTCAGAAACACACTCAGACACTGCTC 300  
|||||  
Qy 465 TGCAGGAGTGTGAGAGCGGCTCCTCAGCGCTTCAGAAACACACTCAGACACTGCTC 524  
|||||

Db 301 AGCTGCTCCAAATGCCGAAAGGAATGGGTGAGGTGAGATCTCTTTCAGACAGTGGAC 360  
|||||  
Qy 525 AGCTGCTCCAAATGCCGAAAGGAATGGGTGAGGTGAGATCTCTTTCAGACAGTGGAC 584  
|||||

Db 361 CGGGACACCGTGTGTGGCTGCGAGGAAGAACGATACCGGCTATTGAGTGAACCTT 420  
|||||  
Qy 585 CGGGACACCGTGTGTGGCTGCGAGGAAGAACGATACCGGCTATTGAGTGAACCTT 644  
|||||

Db 421 TTCAGTGTCTTCATATGACACCTCTGCTCAATGAGACCGTGCACCTCTCCAGAG 480  
|||||  
Qy 645 TTCAGTGTCTTCATATGACACCTCTGCTCAATGAGACCGTGCACCTCTCCAGAG 704  
|||||

Db 481 AAACAGAACACCGTGTGACACCTGCCATGCAAGTTCTTCTTAAGAGAAAAAGAGTGTG 540  
|||||  
Qy 705 AAACAGAACACCGTGTGACACCTGCCATGCAAGTTCTTCTTAAGAGAAAAAGAGTGTG 764  
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Db 541 TCCTGTAGTAAGTCTGAAGAAAGCCCTGAGTGTGACGAAGTGTGCTTACCCGATTTGAG 600  
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Qy 765 TCCTGTAGTAAGTCTGAAGAAAGCCCTGAGTGTGACGAAGTGTGCTTACCCGATTTGAG 824  
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RESULT 6  
ID US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

AC xxxxxx  
XX  
XX 01-JAN-1900  
XX  
DE Sequence 56, Application US/08050319B.  
XX  
XX Sequence 56, Application US/08050319B.  
CC Patent No. 5633145

CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 56:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 504 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..501  
CC  
SQ Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;

Query Match 29.4%; Score 383; DB 7; Length 504;  
Best Local Similarity 100.0%; Pred. No. 6.44e-278;  
Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180  
|||  
Oy 345 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 404  
|||  
Db 181 AAGTGCACAAAGAAAGAACTTGTACAAATGATGTCAGAGCCCGGGGCGAGATAGGGAC 240  
|||  
Oy 405 AAGTGCACAAAGAAAGAACTTGTACAAATGATGTCAGAGCCCGGGGCGAGATAGGGAC 464  
|||  
Db 241 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 300  
|||  
Oy 465 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 524  
|||  
Db 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGCACAGTGAC 360  
|||  
Oy 525 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGCACAGTGAC 584  
|||  
Db 361 CGGAGACCGGTGTGGCTGTCAGAGAAACCACTACCGGATTTAGTGAATAACCTT 420  
|||  
Oy 585 CGGAGACCGGTGTGGCTGTCAGAGAAACCACTACCGGATTTAGTGAATAACCTT 644  
|||  
Db 421 TTCAGTGTCTTCAATTCAGACCTCTGCTCAATGAGACCGTGCACCTCTCTCTGCGAGAG 480  
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Oy 645 TTCAGTGTCTTCAATTCAGACCTCTGCTCAATGAGACCGTGCACCTCTCTCTGCGAGAG 704  
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Db 481 AAACAGAACCGTGTGCACCTG 503  
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Oy 705 AAACAGAACCGTGTGCACCTG 727  
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RESULT 7  
ID US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 1, Application US/08050319B.  
XX  
CC Sequence 1, Application US/08050319B  
CC Patent No. 5633145  
CC  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 501 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..501  
CC  
SQ Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;

Query Match 29.3%; Score 381; DB 7; Length 501;  
Best Local Similarity 100.0%; Pred. No. 2.60e-276;  
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180  
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Oy 345 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 404  
|||  
Db 181 AAGTGCACAAAGAAAGAACTTGTACAAATGATGTCAGAGCCCGGGGCGAGATAGGGAC 240  
|||  
Oy 405 AAGTGCACAAAGAAAGAACTTGTACAAATGATGTCAGAGCCCGGGGCGAGATAGGGAC 464  
|||  
Db 241 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 300  
|||  
Oy 465 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 524  
|||  
Db 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGCACAGTGAC 360  
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Oy 525 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGCACAGTGAC 584  
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XX	xxxxxx
DT	01-JAN-1900
DE	Sequence 3, Application US/08343401A.
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CC	Sequence 3, Application US/08343401A
CC	Patent No. 5661132
CC	GENERAL INFORMATION:
CC	APPLICANT: Swain, William F
CC	APPLICANT: Macklin, Michael D
CC	APPLICANT: Eriksson, Elof
CC	APPLICANT: Andree, Christophe
CC	TITLE OF INVENTION: Improved Wound Healing
CC	NUMBER OF SEQUENCES: 4
CC	CORRESPONDENCE ADDRESSES:
CC	ADDRESSEE: Quarles & Brady
CC	STREET: PO Box 2113
CC	CITY: Madison
CC	STATE: WI
CC	COUNTRY: USA
CC	ZIP: 53701-2113
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: Patentin Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/343,401A
CC	FILING DATE: 22-NOV-1994
CC	CLASSIFICATION: 514
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Seay, Nicholas J
CC	REGISTRATION NUMBER: 27,386
CC	REFERENCE/DOCKET NUMBER: 11-229-9103-9
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: 608-251-9166
CC	TELEFAX: 608-251-9166
CC	INFORMATION FOR SEQ ID NO: 3:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 4283 base pairs
CC	TYPE: nucleic acid
CC	STRANDEDNESS: double
CC	TOPOLOGY: circular
CC	MOLECULE TYPE: DNA (genomic)
CC	IMMEDIATE SOURCE:
CC	CLONE: pMRG1630
CC	FEATURE:
CC	NAME/KEY: exon
CC	LOCATION: 713..721
CC	FEATURE:
CC	NAME/KEY: exon
CC	LOCATION: 981..1253
CC	FEATURE:
CC	NAME/KEY: CDS
CC	LOCATION: join(713..721, 981..1253)
CC	FEATURE:
CC	NAME/KEY: sig_peptide
CC	LOCATION: 713..1049
CC	Sequence 4283 BP: 1023 A; 1095 C; 1114 G; 1051 T; 0 other;
DB	Query Match
DB	Best Local Similarity 95.6%; Pred. NO. 7.97e-214;
DB	Matches 333; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
DB	713 ATGGCTACAGTAAGCGCCCTAAATTCCTTTGG-CACAAATGTGTCTTGAGGGAGAGG 771
DB	
DB	7 ATGGCTACAGTAAGCGCCCTAAATTCCTTTGGGCAACAATGTGTCTTGAGGGAGAGG 66
DB	
DB	772 CAGGACCTGTAGATGGAGCGGGGCACTAACCTCAGGGGTTGGGGTTTCGATGTGAG 831
DB	
DB	67 CAGGACCTGTAGATGGAGCGGGGCACTAACCTCAGGGGTTGGGGTTTCGATGTGAG 126
DB	

Db	832	TAGCCCATCTTAAGCCCGTATTTTGGGCAATCTCAGAAAGCTCGCTCGGAGGAT	891
Qy	127	TATGCCCATGTAAAGCCCGATTTTGGCCATGTATGAAAGACTCTGTGCTCGTGAGGAT	186
Db	892	GGAGAGAGAAAAACAAACAGCTCCTGGAGCAGGAGAGTGTGGCCTTGCTCCGC	951
Qy	187	GGAGAGAGAAAAAACAAACACTCTCGAGCGAGGAGAGTGTGCTGCTTGCTCCGC	246
Db	952	TCCCTCTGTTCGCTCTGTGTTCTTCTCCCAAGGCTCCCGAGAGTCCCTCTGCTTTG	1011
Qy	247	TCCCTCTGTTCGCTCTGTGTTCTTCTCCCAAGGCTCCCGAGAGTCCCTCTGCTTTG	306
Db	1012	GCTCTGCTGCTGCTGCTGCTGCTTAAAGAGGAGCTGCC	1049
Qy	307	GCTCTGCTGCTGCTGCTGCTGCTTAAAGAGGAGCTGCC	344
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XX	xxxxxx		
XX	01-JAN-1900		
DE	Sequence 1, Application US/08445265A.		
XX			
CC	Sequence 1, Application US/08445265A		
CC	Patent No. 5697901		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Eriksson, Elof		
CC	TITLE OF INVENTION: GENE DELIVERY BY MICRONEEDLE INJECTION		
CC	NUMBER OF SEQUENCES: 4		
CC	CORRESPONDENCE ADDRESSES:		
CC	ADDRESSEE: Quarles & Brady		
CC	STREET: 1 South Plinckney Street		
CC	CITY: Madison		
CC	STATE: WI		
CC	COUNTRY: US		
CC	ZIP: 53703		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/445,265A		
CC	FILING DATE:		
CC	CLASSIFICATION: 604		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Seay, Nicholas J		
CC	REGISTRATION NUMBER: 27386		
CC	REFERENCE/DOCKET NUMBER: 110229.91080		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 608-251-5000		
CC	TELEFAX: 608-251-9166		
CC	INFORMATION FOR SEQ ID NO: 1:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 4283 base pairs		
CC	TYPE: nucleic acid		
CC	STRANDEDNESS: double		
CC	TOPOLOGY: circular		
CC	MOLECULE TYPE: other nucleic acid		
CC	DESCRIPTION: /desc = "Plasmid DNA"		
CC	FEATURE:		
CC	NAME/KEY: CDS		
CC	LOCATION: join(713..721, 981..1250)		
CC	Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;		
Qy	Query Match	23.3%; Score 303; DB 7; Length 4283;	
Matches	Best Local Similarity	95.6%; Pred.No.7.97e-214;	
Matches	333; Conservative	0; Pct.Matches 14; Indels 1; Gaps 1;	





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CC LENGTH: 462 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: double
CC TOPOLOGY: linear
CC MOLECULE TYPE: CDNA to mRNA
CC FEATURE:
CC NAME/KEY: CDS
CC LOCATION: 1..459
SQ Sequence 462 bp; 116 A; 119 C; 121 G; 106 T; 0 other;

Query Match 17.0%; Score 221; DB 7; Length 462;
Best Local Similarity 99.6%; Pred.No.1,21e-148;
Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 240 CTCGAGGAAGAACCAAGTACCGGCAATTATGTGAGTGAAGAAACCTTTTCCAGTGCCTCAATTG 259
|
|
|
QY 602 CTGACGGAAGAACCAAGTACCGGCAATTATGTGAGTGAAGAAACCTTTTCCAGTGCCTCAATTG 661
|
|
|
Db 300 CAGCCTCTGCCTCAATGGAGACGCGACCTCTCTGCGAGGAGAAACAGAACCCGCTG 359
|
|
|
QY 662 CAGCCTCTGCCTCAATGGAGACGCGACCTCTCTGCGAGGAGAAACAGAACCCGCTG 721
|
|
|
Db 360 CACCTGCCATCAGAGTTTCTTTCTTACAGAAAGAGTGTCTCTCTGTAGTAACTGAA 419
|
|
|
QY 722 CACCTGCCATCAGAGTTTCTTTCTTACAGAAAGAGTGTCTCTCTGTAGTAACTGAA 781
|
|
|
Db 420 GAAAGCCTGGAGTGCACGAAAGTTGTGCTTACCCCAAGATTGAG 462
|
|
|
QY 782 GAAAGCCTGGAGTGCACGAAAGTTGTGCTTACCCCAAGATTGAG 824
|
|
|

RESULT 15
ID US-08-086-915-2 STANDARD; DNA; UNC; 138 BP.

XX
AC xxxxxx
XX
XX 01-JAN-1900
DE
XX
DE Sequence 2, Application US/08086915.
XX
XX
Sequence 2, Application US/08086915
Patent No. 5444167
GENERAL INFORMATION:
CC APPLICANT: Pettersson, Kim SI
CC TITLE OF INVENTION: Variant Lutelinizing Hormone Encoding DNA
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Adduct, Mastrianl, Schaunberg & Schilll
CC STREET: 1140 Connecticut Avenue, N.W., Suite 250
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/086,915
CC FILING DATE: 07-JUL-1993
CC CLASSIFICATION: 536
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Kubovcik, Ronald J.
CC REGISTRATION NUMBER: 25,401
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-467-2006
CC TELEFAX: 202-466-2006
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 138 base pairs

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CC      type: nucleic acid
CC      STRANDEDNESS: double
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: DNA (genomic)
CC      HYPOTHETICAL: NO
CC      ANTI-SENSE: NO
CC      ORIGINAL SOURCE:
CC      ORGANISM: Homo sapiens
CC      DEVELOPMENTAL STAGE: Adult
S0      Sequence 138 Bp: 24 A; 51 C; 42 G; 21 T; 0 other;

Query Match      7.9%; Score 103; DB 5; Length 138;
Best Local Similarity 99.0%; Pred. No. 6,08e-57;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      34      CCACGGTGCACACCCATCAATGATCCACCGCTGGCTGTGGAGAAGAGGCTGCCCGGTGTGC 93
          |||||
QY      870     CCACGGTGCACCCGCCCATCATCATGCAACCCCTGGCTGTGGAGAAGAGGAGGCTGCCCGGTGTGC 929

Db      94      ATCACCGTCAACACACACCACATCTGTGCGGGCTACTGCCCCACCATG 138
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QY      930     ATCACCGTCAACACACACCATCTGTGCGGGCTACTGCCCCACCATG 974

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Job time : 85 secs.

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Search completed: Wed May 6 11:19:13 1998  
Job time : 85 secs.

\*\*\*\*\*  
M P E R E H  
(TM)  
\*\*\*\*\*

Release 3.0.5A John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

MParch\_dp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed May 6 08:23:57 1998; MasPar time 4.43 Seconds  
Tabular output not generated. 368.292 Million cell updates/sec

Title: >US-08-804-166-6  
Description: (1-285) from US08804166.pep  
Perfect Score: 2183  
Sequence: 1 SRTSLLAFLGLCLPWLQEG.....GFKYENHTACHSCSTCYHKS 285

Scoring table:  
PAM 150  
Gap 11

Searched: 62627 segs, 5720858 residues

Post-Processing: Minimum Match 0%  
Listing first 45 summaries

Database:

a-issued  
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PC90  
10:PC91 11:PC92 12:PC93 13:PC94 14:PC95 15:PC96

Statistics: Mean 30.064; Variance 126.027; scale 0.239

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1306	59.8	455	7	US-08-321-Sequence 2, Applicatio	7.75e-119
2	1306	59.8	455	7	US-08-050-Sequence 25, Applicati	7.75e-119
3	1227	56.2	199	7	US-08-050-Sequence 48, Applicati	8.08e-111
4	994	45.5	167	7	US-08-050-Sequence 2, Applicatio	3.05e-87
5	994	45.5	167	7	US-08-050-Sequence 57, Applicati	3.05e-87
6	979	44.8	124	7	US-08-050-Sequence 4, Applicatio	9.66e-86
7	912	41.8	157	7	US-08-050-Sequence 50, Applicati	2.50e-54
8	666	30.5	158	7	US-08-050-Sequence 54, Applicati	1.12e-46
9	589	27.0	153	7	US-08-050-Sequence 52, Applicati	4.74e-22
10	337	15.4	41	7	US-08-050-Sequence 36, Applicati	8.28e-21
11	324	14.8	40	7	US-08-050-Sequence 26, Applicati	3.09e-20
12	318	14.6	40	7	US-08-050-Sequence 31, Applicati	5.18e-17
13	284	13.0	39	7	US-08-050-Sequence 40, Applicati	1.64e-11
14	225	10.3	325	5	US-08-292-Sequence 2, Applicatio	1.64e-11
15	225	10.3	325	10	PCT-US91-0 Sequence 2, Applicatio	3.81e-11
16	221	10.1	326	5	US-08-292-Sequence 4, Applicatio	3.81e-11
17	221	10.1	326	10	PCT-US91-0 Sequence 4, Applicatio	3.81e-11
18	212	9.7	474	1	5395760-4 Patent No. 5395760.	2.54e-10
19	210	9.6	355	5	US-08-292-Sequence 6, Applicatio	3.86e-10
20	183	8.4	283	15	PCT-US96-1 Sequence 2, Applicatio	1.06e-07
21	183	8.4	595	7	US-08-570-Sequence 2, Applicatio	1.06e-07
22	183	8.4	595	5	US-08-225-Sequence 2, Applicatio	1.06e-07

RESULT	ID	US-08-321-668-2	STANDARD:	PRT:	455 AA.
AC	xxxxxx				
DT	01-JAN-1900				
DE	Sequence 2, Application US/08321668.				
XX					
CC	Sequence 2, Application US/08321668				
CC	Patent No. 5665859				
CC	GENERAL INFORMATION:				
CC	APPLICANT: WALLACH, David				
CC	APPLICANT: BRAKEBUSCH, Cord				
CC	APPLICANT: VARFOLOMEV, Eugene				
CC	APPLICANT: BARKIN, Michael				
CC	TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF				
CC	TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE				
CC	NUMBER OF SEQUENCES: 42				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: BROWDY AND NEIMARK				
CC	STREET: 419 Seventh Street, N.W., Suite 300				
CC	CITY: Washington				
CC	STATE: D.C.				
CC	COUNTRY: USA				
CC	ZIP: 20004				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/321,668				
CC	FILING DATE: 12-OCT-1994				
CC	CLASSIFICATION: 435				
CC	PRIOR APPLICATION DATA:				
CC	APPLICATION NUMBER: IL 107268				
CC	FILING DATE: 12-OCT-1993				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: BROWDY, Roger L.				
CC	REGISTRATION NUMBER: 25,618				
CC	REFERENCE/DOCKET NUMBER: WALLACH-13				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: 202-628-5197				
CC	TELEFAX: 202-737-3528				
CC	TELEX: 248633				

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CC      INFORMATION FOR SEQ ID NO: 2
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 455 amino acids
CC          TYPE: amino acid
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 455 AA; 50494 MW; 1048031 CN;
SQ
Query Match          59.8%; Score 1306; DB 7; Length 455;
Best Local Similarity 98.8%; Pred. No. 7,75e-119;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db      41 DSVCPQGGYIHPQNNSSICCTCKHGKGYLTLYNDCPPPGQDTCRECESSGFASENHLRHCL 100
      |||
Qy      23 DSVCPQGGYIHPQNNSSICCTCKHGKGYLTLYNDCPPPGQDTCRECESSGFASENHLRHCL 82
      |||

Db      101 SCSCCRKMEGVEIISCTVDTRDVTGCGCRKNQRYHWSENLFCQCFNCSLCLNGTVHLSQOE 160
      |||
Qy      83 SCSCCRKMEGVEIISCTVDTRDVTGCGCRKNQRYHWSENLFCQCFNCSLCLNGTVHLSQOE 142
      |||

Db      161 KQNVCTCHAGFFLRNENCVSCSNCKSLSECTKTLCLPQIENVKGTEDSGTT 211
      |||
Qy      143 KQNVCTCHAGFFLRNENCVSCSNCKSLSECTKTLCLPQIENVKGTEDSGTT 193
      |||

RESULT      2
ID      US-08-050-319B-25          STANDARD;      PRT;      455 AA.
XX      xxxxxx
XX      01-JAN-1900
XX
DE      Sequence 25, Application US/08050319B.
CC      Sequence 25, Application US/08050319B
CC      Patent No. 5633145
CC      GENERAL INFORMATION:
CC      APPLICANT: M. Feldmann, P.W. Gray,
CC      APPLICANT: M.J.C. Turner, F.M. Brennan
CC      TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION: Necrosis factor alpha) Receptor
CC      NUMBER OF SEQUENCES: 57
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Reed & Robblins
CC      STREET: 635 Bryant Street
CC      City: Palo Alto
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94301
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/050,319B
CC      FILING DATE: 10-May-1993
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Robblins, Roberta L.
CC      REGISTRATION NUMBER: 33,208
CC      REFERENCE/DOCKET NUMBER: 5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (415) 617-8999
CC      TELEFAX: (415) 327-3231
CC      INFORMATION FOR SEQ ID NO: 25:
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 455 amino acids
CC          TYPE: amino acid
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 455 AA; 50579 MW; 1048388 CN;
SQ

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Query Match          59.8%; Score 1306; DB 7; Length 455;
Best Local Similarity 98.1%; Pred. No. 7,75e-119;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0

Db      Qy      41 DSVCPGGKTHIPNNNSICTCKHGKGYTLVNDCCPGGDDTCRECSGSFTASENHLRHCL 100
        |||
Qy      23 DSVCPGGKTHIPNNNSICTCKHGKGYTLVNDCCPGGDDTCRECSGSFTASENHLRHCL 82
        |||

Db      Db      101 SCSCKRKMGOVEIISCTVDPRDHYGCGRKNQRYHWSENLTFQCFCNSGLNLGVHLSCOE 160
        |||
Qy      Qy      83 SCSCKRKMGOVEIISCTVDPRDHYGCGRKNQRYHWSENLTFQCFCNTLCINGTVHLSCOE 142
        |||

Db      Db      161 KONTVCCHAGFLRENDCVSCSNCKSLSECTXICLPOIENVKGTEPDSGTT 211
        |||
Qy      Qy      143 KONTVCCHAGFLRENDCVSCSNCKSLSECTKLSPQIENVKGTEPDSGTT 193
        |||

RESULT      3 STANDARD; PRT; 199 AA.
XX US -08 -050-319B-48
XX xxxxxx
XX 01-JAN-1900
XX
DE Sequence 48, Application US/08050319B.
XX
CC Sequence 48, Application US/08050319B
CC Patent No. 5633145
CC GENERAL INFORMATION:
CC APPLICANT: M.Feldmann, P.W.Gray,
CC APPLICANT: M.J.C. Turner, F.M.Brennan
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC NUMBER OF SEQUENCES: 57
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Reed & Robbins
CC STREET: 635 Bryant Street
CC City: Palo Alto
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/050,319B
CC FILING DATE: 10-May-1993
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Robbins, Roberta L.
CC REGISTRATION NUMBER: 33,208
CC REFERENCE/DOCKET NUMBER: 5150-0030
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 617-8999
CC TELEFAX: (415) 327-3231
CC INFORMATION FOR SEQ ID NO: 48:
CC LENGTH: 199 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 199 AA; 22186 MW; 195553 CN;

Qy Query Match          56.2%; Score 1227; DB 7; Length 199;
    Best Local Similarity 98.1%; Pred. No. 8,08e-111;
    Matches 156; Conservative 1; Mismatches 2; Indels 0; Gaps 0

Db      41 DSVCPGTGTHIPNNNSICTCKHGKGYTLVNDCCPGGDDTCRECSGSFTASENHLRHCL 100
        |||
Qy      23 DSVCPGGKTHIPNNNSICTCKHGKGYTLVNDCCPGGDDTCRECSGSFTASENHLRHCL 82
        |||

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DE Sequence 4, Application US/08050319B.  
XX  
CC Sequence 4, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 4:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 124 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 124 AA; 14047 MW; 75840 CN;  
SQ  
Query Match 44.8%; Score 979; DB 7; Length 124;  
Best Local Similarity 99.2%; Pred. No. 9,96e-86;  
Matches 133; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 1 VCPGKTIHPQNNISICCKHGTLYNDGPGGDTCCRECSGFTASENHLRHCLSC 60  
QY 25 VCPGKTIHPQNNISICCKHGTLYNDGPGGDTCCRECSGFTASENHLRHCLSC 84  
Db 61 SKCRKMGQVEISSCTVDRTVCGCRKNQRYHWSENLFOCFNCSLCLNGTVHLSQCEKQ 120  
QY 85 SKCRKMGQVEISSCTVDRTVCGCRKNQRYHWSENLFOCFNCSLCLNGTVHLSQCEKQ 144  
Db 121 NTVC 124  
QY 145 NTVC 148  
RESULT 7  
ID US-08-050-319B-50 STANDARD; PRT: 157 AA.  
XX  
AC xxxxxx  
XX 01-JAN-1900  
XX  
XX Sequence 50, Application US/08050319B.  
XX  
CC Sequence 50, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.W. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor

CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 50:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 157 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 157 AA; 17570 MW; 122247 CN;  
SQ  
Query Match 41.8%; Score 912; DB 7; Length 157;  
Best Local Similarity 95.9%; Pred. No. 5.63e-79;  
Matches 117; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Db 36 DREKRECSGFTASENHLRHCLSCSKCRKMGQVEISSCTVDRTVCGCRKNQRYHWS 95  
QY 60 DTDRECSGFTASENHLRHCLSCSKCRKMGQVEISSCTVDRTVCGCRKNQRYHWS 119  
Db 96 ENLFOCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFLRENECVSCSNCKSLSECTKICLP 155  
QY 120 ENLFOCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFLRENECVSCSNCKSLSECTKICLP 179  
Db 156 QI 157  
QY 180 QI 181  
RESULT 8  
ID US-08-050-319B-54 STANDARD; PRT: 158 AA.  
XX  
AC xxxxxx  
XX 01-JAN-1900  
XX  
XX Sequence 54, Application US/08050319B.  
XX  
CC Sequence 54, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.W. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA

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CC      ZIP: 94301
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/050,319B
CC      FILING DATE: 10-May-1993
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Robbins, Roberta L.
CC      REGISTRATION NUMBER: 33,208
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (415) 617-8999
CC      TELEFAX: (415) 327-3231
CC      INFORMATION FOR SEO ID NO: 54:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 158 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 158 AA; 17375 MW; 124033 CN;

Query Match          30.5%; Score 666; DB 7; Length 158;
Best Local Similarity 97.7%; Pred.No. 2.50e-54;
Matches 86; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db      41 DSVCPQGGYHHPNNSICTCTCHGHTLYLNDCCPFGQDTDCREESGFTASENHLRHCL 100
      |||
QY      23 DSVCPQGGYHHPNNSICTCTCHGHTLYLNDCCPFGQDTDCREESGFTASENHLRHCL 82
      |||

Db      101 SCSKCRKEMGOVEISCTVDRTVCTCH 128
      |||
QY      83 SCSKCRKEMGOVEISCTVDRTVCGCR 110
      |||

RESULT          9
ID      US-08-050-319B-52          STANDARD;          PRT: 153 AA.
XX      xxxxxx
DT      01-JAN-1900
XX      DE
XX      Sequence 52, Application US/08050319B.
CC      Sequence 52, Application US/08050319B
CC      Patent No. 5633145
CC      GENERAL INFORMATION:
CC      APPLICANT: M.Feldmann, P.W. Gray,
CC      APPLICANT: M.J.C. Turner, F.M Brennan
CC      TITLE OF INVENTION: Modified human TNFa1pha (Tumor
CC      TITLE OF INVENTION: Necrosis factor alpha) Receptor
CC      NUMBER OF SEQUENCES: 57
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Reed & Robbins
CC      STREET: 635 Bryant Street
CC      CITY: Palo Alto
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94301
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patentin Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/050,319B
CC      FILING DATE: 10-May-1993
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Robbins, Roberta L.
CC

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[illegible]





CC STREET: 635 Bryant Street  
CC City: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8899  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 40:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 39 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 39 AA; 4335 MW; 8059 CN;

Query Match	13.08;	Score 284;	DB 7;	length 39;
Best Local Similarity	97.48;	Pred. No. 5.18e-17;		
Matches	38;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;

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Db      1 TCHAGFFLRENECVSCSNCKKSLLECTKLCLPQIENVKGT 39
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QY     149 TCHAGFFLRENECVSCSNCKKSLLECTKLCLPQIENVKGT 187
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RESULT	14		PRT;	325	AA.
ID	US-08-292-549-2	STANDARD:			
XX	xxxxxx				
AC					
XX					
DT	01-JAN-1900				
XX					
DE	Sequence 2, Application US/08292549.				
XX					
CC	Sequence 2, Application US/08292549				
CC	Patent No. 5464938				
CC	GENERAL INFORMATION:				
CC	APPLICANT: Smith, Craig A.				
CC	APPLICANT: Goodwin, Raymond G.				
CC	TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists				
CC	NUMBER OF SEQUENCES: 10				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: Immunex Corporation				
CC	STREET: 51 University Street				
CC	CITY: Seattle				
CC	STATE: Washington				
CC	COUNTRY: USA				
CC	ZIP: 98101				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/292,549				
CC	FILING DATE:				
CC	CLASSIFICATION: 530				
CC	PRIOR APPLICATION DATA:				
CC	APPLICATION NUMBER: 07/963,330				

CC FILING DATE: 10/19/92  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Perkins, Patricia A.  
CC REGISTRATION NUMBER: 34,693  
CC REFERENCE/DOCKET NUMBER: 2602-A  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (206) 587-0430  
CC TELEFAX: (206) 233-0644  
CC INFORMATION FOR SEQ. ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 325 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 325 AA; 35132 MW; 591446 CN;

Query Match	10.3%;	Score 225;	DB 5;	Length 325;
Best Local Similarity	34.8%;	Pred. No. 1,64e-11;		
Matches	39;	Mismatches 45;	Indels 7;	Gaps 6;

Db 4 LIAL-LVGVVVYVGGDVPVYSSNKGCGGIDKEDKDLACASGHPFYASRLC-GRGNSVY 61  
 5 LIAAGLLCLFMLEDSADSVCPQKXTI-HP-QNNSICTKHKKTYLYNCPPEPGQDTDC 62  
 Qy 6 LIAAGLLCLFMLEDSADSVCPQKXTI-HP-QNNSICTKHKKTYLYNCPPEPGQDTDC 63  
 Db 62 SPCEDEGTTAATINHAAPACYSCRAQPGTGLHSEQ--PCDRTDRVNCSTQNY 111  
 64 RECGSGGTAASENHLRLCLSC-SKCRKEGGQVEISSCVDDTYCGGRKNQY 114  
 Qy 64 RECGSGGTAASENHLRLCLSC-SKCRKEGGQVEISSCVDDTYCGGRKNQY 115

RESULT	15	
ID	PCT-US91-02207-2	STANDARD; PRT; 325 AA

AC XXXXXXXX

DT 01-JAN-1900

DE Sequence 2, Application PC/TUS9102207.

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CC Sequence 2, Application PC/TUS9102207
CC GENERAL INFORMATION:
CC APPLICANT: Smith, Craig A.
CC APPLICANT: Goodwin, Raymond G.
CC TITLE OF INVENTION: Isolated Viral Protein Cytokine Antagonists
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Immunex Corporation
CC STREET: 51 University Street
CC CITY: Seattle
CC STATE: Washington
CC COUNTRY: USA
CC ZIP: 98101
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.24
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US91/02207
CC FILING DATE: 19910329
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Night, Christopher L.
CC REGISTRATION NUMBER: 31,650
CC REFERENCE/DOCKET NUMBER: 2602
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (206) 587-0430
CC TELEFAX: (206) 587-0606
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 325 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC

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SO SEQUENCE 325 AA; 35132 MW; 591446 CN;

Query Match 10.3%; Score 225; DB 10; Length 325;

Best Local Similarity 34.8%; Pred. No. 1,64e-11;

Matches 39; Conservative 21; Mismatches 45; Indels 7; Gaps 6;

Db 4 LIAL-LVCVYVYGGDDVPYSSNQGCGGHDYERKDGICACSHPGFYASRIQ-GPGSNTVC 61

QY 6 LIAFGILCLPWLEGSADSVCPQGXRI-HP-QNNSICTKCHKGTLYLNDPCPGQDIDC 63

Db 62 SPCEOGTFTASTNNHAPACVSCRGPCGHLSESG--PCDRTHDRCVCMSTGNY 111

QY 64 RECESGFTASENHLRHLCLSC-SKCRKMGQVEISSCTVDRDTCGCRKNQY 114

Search completed: Wed May 6 08:24:12 1998  
Job time : 15 secs.



CC	LENGTH:	2062	base pairs
CC	TYPE:	nucleic acid	
CC	STRANDEDNESS:	double	
CC	TOPOLOGY:	linear	
CC	MOLECULE TYPE:	CDNA to mRNA	
CC	FEATURE:		
CC	NAME/KEY:	CDS	
CC	LOCATION:	155..1519	
CC	Sequence	2062	Bp: 429 A; 617 C; 573 G; 443 T; 0 other;
CC	Query Match	44.1%;	Score 506; DB 7; Length 2062;
CC	Best Local Similarity	98.1%;	Pred. No. 0.00e+00;
CC	Matches	521; Conservative	0; Mismatches 9; Indels 1; Gaps 1;
Db	275	GATAGTGTGTGTCCCAAGAAAATATATATCCACCCTCAAAATATTCGATTGTGCTGACC	334
Oy	344	GATAGTGTGTGTGTCCCAAGAAAATATATATTCACCCTCAAAATATTCGATTGTGCTGACC	403
Db	335	AAGTCCCAAAAGGAACCTACTCTGTACAAATGACTGTCCAGGCCGGGGCAGGANTACGGAC	394
Oy	404	AAGTCCCAAAAGGAACCTACTCTGTACAAATGACTGTCCAGGCCGGGGCAGGANTACGGAC	463
Db	395	TGCAGGGAGTGTGAGAGGGGGCTCCACACGGTTGAGAAAACCACTCAAGACACTGCTC	454
Oy	464	TGCAGGGAGTGTGAGAGGGGGCTCCACACGGTTGAGAAAACCACTCAAGACACTGCTC	523
Db	455	AGCTCTCCAAATGCGGAAGGAAGAAATGGGTGACGTGAGATCTCTTCTTGACAGTGGAC	514
Oy	524	AGCTCTCCAAATGCGGAAGGAAGAAATGGGTGACGTGAGATCTCTTCTTGACAGTGGAC	583
Db	515	CGGGACACCGTGTGTGTGCTGCAGAGAAACCACTACCGGCATTATTGAGTGAACCTT	574
Oy	584	CGGGACACCGTGTGTGTGCTGCAGAGAAACCACTACCGGCATTATTGAGTGAACCTT	643
Db	575	TTCCAGTGTTCAAATGTGACAGCCTCGCCTCAATGGGACCGGTGCACCTCTCCCTCCACGAG	634
Oy	644	TTCCAGTGTTCAAATGTGACAGCCTCGCCTCAATGGGACCGGTGCACCTCTCCCTGTAGAG	703
Db	635	AAACGAACACCGTGTGACACCTGCCATCGAGTTTCTTCTTAAGAGAAACGAGTGTGC	694
Oy	704	AAACGAACACCGTGTGACACCTGCCATCGAGTTTCTTCTTAAGAGAAACGAGTGTGC	763
Db	695	TCCTTAGTACTGTAAAGAAAAGCCTGGAGTGCACGAAAGTTGTGCTACCCCGATTGAG	754
Oy	764	TCCTTAGTACTGTAAAGAAAAGCCTGGAGTGCACGAAAGTTGTGCTACCCCGATTGAG	823
Db	755	AATGTTAAGGGCACTGAGGAGCTCAGGACACCAAGT-GCTGTTGCCCCCGT	804
Oy	824	AATGTTAAGGGCACTGAGGAGCTCAGGACACCAAGTGGCGGTGCTGCCCAAGT	874
RESULT	2		
ID	US-08-321-668-1	STANDARD; DNA; UNC; 2175 Bp.	
AX	xxxxxx		
XX	01-JAN-1900		
XX	Sequence 1, Application	US/08321668.	
XX	Sequence 1, Application	US/08321668	
CC	Patent No.	5665859	
CC	GENERAL INFORMATION:		
CC	APPLICANT:	WALLACH, David	
CC	APPLICANT:	BRAKEBUSCH, Cord	
CC	APPLICANT:	VARFOLOMEV, Eugene	
CC	APPLICANT:	BATKIN, Michael	
CC	TITLE OF INVENTION:	MOLECULES INFLUENCING THE SHEDDING OF	
CC	TITLE OF INVENTION:	THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE	
CC	NUMBER OF SEQUENCES:	42	
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE:	BROWDY AND NEIMARK	

CC	STREET: 419 Seventh Street, N.W., Suite 300
CC	CITY: Washington
CC	STATE: D.C.
CC	COUNTRY: USA
CC	ZIP: 20004
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: Patent Release #1.0, Version #1.30
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/321,668
CC	FILING DATE: 12-OCT-1994
CC	CLASSIFICATION: 435
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: IL 107268
CC	FILING DATE: 12-OCT-1993
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: BROWDY, Roger L.
CC	REGISTRATION NUMBER: 25,618
CC	REFERENCE/DOCKET NUMBER: WALACH-13
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: 202-628-5197
CC	TELEFAX: 202-737-3528
CC	TELEX: 248633
CC	INFORMATION FOR SEQ ID NO: 1:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 2175 base pairs
CC	TYPE: nucleic acid
CC	STRANDEDNESS: single
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: cDNA
CC	FEATURE:
CC	NAME/KEY: CDS
CC	LOCATION: 256..1620
CC	Sequence 2175 Bp: 474 A; 641 C; 604 G; 456 T; 0 other;
CC	50
CC	Query Match 44.1%; Score 506; DB 7; Length 2175;
CC	Best Local Similarity 98.1%; Pred. No. 0.00e+00;
CC	Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1
CC	376 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATAATTGATTGTGTACC 435
CC	344 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATAATTGATTGTGTACC 403
CC	436 AAGTCCCAAAAGGAACCTACTTGTACAAATACATCTGTCCAGGCCGGGGGAGGATACGAGC 495
CC	404 AAGTCCCAAAAGGAACCTACTTGTACAAATACATCTGTCCAGGCCGGGGGAGGATACGAGC 463
CC	436 TGCAGGGAGTGTGAGAGGGGCTCCTTACCGCTTCAGAAAACCACTCAGACACTGGCTC 555
CC	464 TGCAGGGAGTGTGAGAGGGGCTCCTTACCGCTTCAGAAAACCACTCAGACACTGGCTC 523
CC	556 AGCTCTCCAAATGCGGAAAGAAATGGGTGACAGTGTGAGATCTCTTTTGCACAGTGGAC 615
CC	524 AGCTCTCCAAATGCGGAAAGAAATGGGTGACAGTGTGAGATCTCTTTTGCACAGTGGAC 583
CC	616 CGGACACCCGTGTGTGGCTGTGACAGAAACCAATACCGGCAATTATTGGAGTGAACCTT 675
CC	584 CGGACACCCGTGTGTGGCTGTGACAGAAACCAATACCGGCAATTATTGGAGTGAACCTT 643
CC	676 TTCCAGTCTTCAATTGACAGCTGTGACCTCAATGGGACCGGCACTCTCTGTGACAGGAG 735
CC	644 TTCCAGTCTTCAATTGACAGCTGTGACCTCAATGGGACCGGCACTCTCTGTGACAGGAG 703
CC	736 AAACGAACACCCGTGTGACCTGTGCATGACAGTTCTTTTCAAGAGAAAAGAGTGTGTC 795
CC	704 AAACGAACACCCGTGTGACCTGTGCATGACAGTTCTTTTCAAGAGAAAAGAGTGTGTC 763
CC	736 TCCGTAGTAACTGTAGAAAAGCCTGTGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 855
CC	764 TCCGTAGTAACTGTAGAAAAGCCTGTGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 823

ID	RESULT	3	PCT-US95-09576-2	STANDARD	DNA	UNC	6889	BP
Db	886	AAGTAAAGGACACTGAGACTACGACGACCACT	-GCTGTTCCTGCT	905				
Oy	824	AATGTAAAGGACACTGAGACTACGACGACCACT	CGCTGTTCCTGCT	874				
XX	XXXXXX							
DT	01-JAN-1900							
DE	Sequence 2, Application PC/TUS9509576.							
CC	Sequence 2, Application PC/TUS9509576							
CC	GENERAL INFORMATION:							
CC	APPLICANT: GENENTECH, INC.							
CC	TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING							
CC	TITLE OF INVENTION: HOST CELLS							
CC	NUMBER OF SEQUENCES: 4							
CC	CORRESPONDENCE ADDRESS:							
CC	ADDRESSEE: Genentech, Inc.							
CC	STREET: 460 Point San Bruno Blvd							
CC	CITY: South San Francisco							
CC	STATE: California							
CC	COUNTRY: USA							
CC	ZIP: 94080							
CC	COMPUTER READABLE FORM:							
CC	MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk							
CC	COMPUTER: IBM PC compatible							
CC	OPERATING SYSTEM: PC-DOS/MS-DOS							
CC	SOFTWARE: patin (Genentech)							
CC	CURRENT APPLICATION DATA:							
CC	APPLICATION NUMBER: PCT/US95/09576							
CC	FILING DATE:							
CC	CLASSIFICATION:							
CC	PRIOR APPLICATION DATA:							
CC	APPLICATION NUMBER: 08/286740							
CC	FILING DATE: 05-AUG-1994							
CC	ATTORNEY/AGENT INFORMATION:							
CC	NAME: Lee, Wendy M.							
CC	REGISTRATION NUMBER: 00,000							
CC	REFERENCE/DOCKET NUMBER: 798PCT							
CC	TELECOMMUNICATION INFORMATION:							
CC	TELEPHONE: 415/225-1994							
CC	TELEFAX: 415/952-9881							
CC	TELEX: 910/371-7168							
CC	INFORMATION FOR SEQ ID NO: 2:							
CC	SEQUENCE CHARACTERISTICS:							
CC	LENGTH: 6889 bases							
CC	TYPE: nucleic acid							
CC	STRANDEDNESS: double							
CC	TOPOLOGY: linear							
CC	Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;							
Db	Query Match	43.9%	Score 504;	DB 14;	Length 6889;			
Oy	Best Local Similarity	99.0%	Pred. No. 0.00e+00;					
Matches	509; Conservative	0;	Mismatches	5;	Indels	0;	Gaps	0
Db	1725	GATAGTGTGTCTCCCAAGAAATATATATCCACCCCTCAAAATAATTCGATTGCTGTACC	1784					
Oy	344	GATAGTGTGTCTCCCAAGAAATATATATCCACCCCTCAAAATAATTCGATTGCTGTACC	403					
Db	1785	AAGTCCCAAGAAAGAACTACTTGTACATATACATGTCCAGCCCGGGGACAGATACGGAC	1844					
Oy	404	AAGTCCCAAGAAAGAACTACTTGTACATATACATGTCCAGCCCGGGGACAGATACGGAC	463					
Db	1845	TGCAGAGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACACACTCAGACTGCTC	1904					
Oy	464	TGCAGAGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACACACTCAGACTGCTC	523					
Db	1905	AGCTCTCCAAATGCGCAAGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGACAGATGGAC	1964					

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0Y      524  AGCTGCTCAATATCCCAAAAGGAAATGGGTCAGGTGGAGATCTCTTTCGCACAGTGAC 583
Db      1965  CGGGACACCGTGTGTGGCTGCAGAAAGAACCACTACCGGCATTATTTGAGTGAACCTT 2024
0Y      584  CGGACACACCGTGTGTGGCTGCAGAGAACCACTACCGGCATTATTTGAGTGAACCTT 643
Db      2025  TTCCAGTCTTCAATTGACCTCTGACCTCTGCTTCATGGAAGGAGCCGTGACCTCTCTGCGCAGAG 2084
0Y      644  TTCCAGTCTTCAATTGACCTCTGACCTCTGCTTCATGGAAGGAGCCGTGACCTCTCTGCGCAGAG 703
Db      2085  AAACGAACACCGTGTGTGGCTGCAGTGTGCTGCTTCTTCTAAGAGAAACAGTGTGTC 2144
0Y      704  AAACGAACACCGTGTGTGGCTGCAGTGTGCTGCTTCTTCTAAGAGAAACAGTGTGTC 763
Db      2145  TCCTGTAGTACTGTAAAGAAAGCCTGGATGGACGAGTGTGCTTACCCAGATTGAG 2204
0Y      764  TCCTGTAGTACTGTAAAGAAAGCCTGGATGGACGAGTGTGCTTCTAAGAGAAACAGTGTG 823
Db      2205  AATGTTAAGGCACTGAGGACTCAGGCACCCACAG 2238
0Y      824  AATGTTAAGGCACTGAGGACTCAGGCACCCACAG 857

. RESULT      4
ID      US-08-286-740-2 STANDARD; DNA; UNC; 6889 BP.

XX      xxxxxx
XX
XX      01-JAN-1900
XX
XX      Sequence 2, Application US/08286740.
XX
CC      Sequence 2, Application US/08286740
CC      Patent No. 5561053
CC      GENERAL INFORMATION:
CC      APPLICANT: Crowley, Craig W.
CC      TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
CC      TITLE OF INVENTION: HOST CELLS
CC      NUMBER OF SEQUENCES: 4
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Genentech, Inc.
CC      STREET: 460 Point San Bruno Blvd
CC      CITY: South San Francisco
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94080
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: palign (Genentech)
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/286,740
CC      FILING DATE: 05-AUG-1994
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:
CC      FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Lee, Wendy M.
CC      REGISTRATION NUMBER:
CC      REFERENCE/DOCKET NUMBER: 798
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 415/225-1994
CC      TELEFAX: 415/952-9881
CC      TELEX: 910/371-7168
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 6889 bases
CC      TYPE: nucleic acid
CC      STRANDEDNESS: double

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CC TOPOLOGY: linear  
SQ Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;  
Query Match 43.9%; Score 504; DB 6; Length 6889;  
Best Local Similarity 99.0%; Pred. No. 0.00e+00;  
Matches 509; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1725 GATAGTGTGTGTCCTCCAGGAAATATATTCACCTCAAAATTAATTCATTGCTGTAC 1784  
|||||  
Cc 344 GATAGTGTGTGTCCTCCAGGAAATATATTCACCTCAAAATTAATTCATTGCTGTAC 403  
|||||

Db 1785 AAGTGCACCAAGAACTTACTTGTACATGACTCTCCAGGCGGGGACAGATACGAC 1844  
|||||  
Cc 404 AAGTGCACCAAGAACTTACTTGTACATGACTCTCCAGGCGGGGACAGATACGAC 463  
|||||

Db 1845 TGCAAGGAGTGTAGAGGCGCTCTTCCAGGCGGGGACAGATACGAC 1904  
|||||  
Cc 464 TGCAAGGAGTGTAGAGGCGCTCTTCCAGGCGGGGACAGATACGAC 523  
|||||

Db 1905 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 1964  
|||||  
Cc 524 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 583  
|||||

Db 1965 CGGACACCGGTGTGTGCTGACAGGAAACCACTACCGCATTTAGAGTGAACCTT 2024  
|||||  
Cc 584 CGGACACCGGTGTGTGCTGACAGGAAACCACTACCGCATTTAGAGTGAACCTT 643  
|||||

Db 2025 TTCCAGTCTTCATTTGACGCTGCTGCAATGGGACGCTGCACTCTCCGACAGGAG 2084  
|||||  
Cc 644 TTCCAGTCTTCATTTGACGCTGCTGCAATGGGACGCTGCACTCTCCGACAGGAG 703  
|||||

Db 2085 AAACAGAACCCGTGTGTGACCTGCGCATGAGTTCTTCTTACGAAAGAGAGTGTCTC 2144  
|||||  
Cc 704 AAACAGAACCCGTGTGTGACCTGCGCATGAGTTCTTCTTACGAAAGAGAGTGTCTC 763  
|||||

Db 2145 TCCTGTACTAATCTGTAAAGAAAGCTGTGAGTGCACGAAAGTTGCTTACCCAGATTGAG 2204  
|||||  
Cc 764 TCCTGTACTAATCTGTAAAGAAAGCTGTGAGTGCACGAAAGTTGCTTACCCAGATTGAG 823  
|||||

Db 2205 AATGTTAAGGACACTGAGACTCAGGACACACAG 2238  
|||||  
Cc 824 AATGTTAAGGACACTGAGACTCAGGACACACAG 857  
|||||

RESULT 5  
ID US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

XX xxxxxx  
AC  
XX  
DT 01-JAN-1900  
XX

DE Sequence 47, Application US/08050319B.  
XX  
CC Sequence 47, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M. Feldmann, P. W. Gray,  
CC APPLICANT: M. J. C. Turner, F. M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESS: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 47:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 600 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..597  
SQ Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;

Query Match 40.5%; Score 464; DB 7; Length 600;  
Best Local Similarity 98.3%; Pred. No. 0.00e+00;  
Matches 472; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCCTCCAGGAAATATATTCACCTCAAAATTAATTCATTGCTGTAC 180  
|||||  
Cc 344 GATAGTGTGTGTCCTCCAGGAAATATATTCACCTCAAAATTAATTCATTGCTGTAC 403  
|||||

Db 181 AAGTGCACCAAGAACTTACTTGTACATGACTCTCCAGGCGGGGACAGATACGAC 240  
|||||  
Cc 404 AAGTGCACCAAGAACTTACTTGTACATGACTCTCCAGGCGGGGACAGATACGAC 463  
|||||

Db 241 TGCAAGGAGTGTAGAGGCGCTCTTCCAGGCGGGGACAGATACGAC 300  
|||||  
Cc 464 TGCAAGGAGTGTAGAGGCGCTCTTCCAGGCGGGGACAGATACGAC 523  
|||||

Db 301 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 360  
|||||  
Cc 524 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 583  
|||||

Db 361 CGGACACCGGTGTGTGCTGACAGGAAACCACTACCGCATTTAGAGTGAACCTT 420  
|||||  
Cc 584 CGGACACCGGTGTGTGCTGACAGGAAACCACTACCGCATTTAGAGTGAACCTT 643  
|||||

Db 421 TTCCAGTCTTCATTTGACGCTGCTGCAATGGGACGCTGCACTCTCCGACAGGAG 480  
|||||  
Cc 644 TTCCAGTCTTCATTTGACGCTGCTGCAATGGGACGCTGCACTCTCCGACAGGAG 703  
|||||

Db 481 AAACAGAACCCGTGTGTGACCTGCGCATGAGTTCTTCTTACGAAAGAGAGTGTCTC 540  
|||||  
Cc 704 AAACAGAACCCGTGTGTGACCTGCGCATGAGTTCTTCTTACGAAAGAGAGTGTCTC 763  
|||||

Db 541 TCCTGTACTAATCTGTAAAGAAAGCTGTGAGTGCACGAAAGTTGCTTACCCAGATTGAG 600  
|||||  
Cc 764 TCCTGTACTAATCTGTAAAGAAAGCTGTGAGTGCACGAAAGTTGCTTACCCAGATTGAG 823  
|||||

RESULT 6  
ID US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

XX xxxxxx  
AC  
XX  
DT 01-JAN-1900  
XX

DE Sequence 56, Application US/08050319B.  
XX  
CC Sequence 56, Application US/08050319B  
CC Patent No. 5633145

GENERAL INFORMATION:  
APPLICANT: M.Feldmann, P.W. Gray,  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESS: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..501  
Sequence 504 BP; 122 A; 137 C; 138 G; 107 T; 0 other;  
Query Match 32.7%; Score 375; DB 7; Length 504;  
Best Local Similarity 99.0%; Pred. No. 8,54e-293;  
Matches 379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Db 121 GATAGTGTGTGTCCTCCCAAGAAATATATATCCACCTCAAAATATTCGATTGCTGTACC 180  
Oy 344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 403  
Db 181 AAGTGCACAAAGAAACCTACTGTACATGACTGTCCAGGCGCGGAGGATACGAGAC 240  
Oy 404 AAGTGCACAAAGAAACCTACTGTACATGACTGTCCAGGCGCGGAGGATACGAGAC 463  
Db 241 TGCAGGAGTGTGAGAGCGGCTCTCACCCTCAGAAAACCACTCAGACCTGCTC 300  
Oy 464 TGCAGGAGTGTGAGAGCGGCTCTCACCCTCAGAAAACCACTCAGACCTGCTC 523  
Db 301 AGTGTCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTCTTCTTGACAGTGGAC 360  
Oy 524 AGTGTCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTCTTCTTGACAGTGGAC 583  
Db 361 CGGAGACCGGTGTGTGCTGACAGAAACCACTACCGGCAATTATGGATGAAAACTT 420  
Oy 584 CGGAGACCGGTGTGTGCTGACAGAAACCACTACCGGCAATTATGGATGAAAACTT 643  
Db 421 TTCCAGTGTCTCAATTCAGACCTCTGCTCAATGGGACGCTGACCTCTCCCTGCGAGAG 480  
Oy 644 TTCCAGTGTCTCAATTCAGACCTCTGCTCAATGGGACGCTGACCTCTCTCTGCGAGAG 703  
Db 481 AAACAGAACACCTGTGACACTG 503  
Oy 704 AAACAGAACACCTGTGACACTG 726

RESULT 7  
ID US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.  
xx xxxxxx  
xx 01-JAN-1900  
xx Sequence 1, Application US/08050319B.  
xx Sequence 1, Application US/08050319B.  
xx Patent No. 5633145  
xx GENERAL INFORMATION:  
xx APPLICANT: M.Feldmann, P.W. Gray,  
xx TITLE OF INVENTION: Modified human TNFalpha (Tumor  
xx NUMBER OF SEQUENCES: 57  
xx CORRESPONDENCE ADDRESS:  
xx ADDRESS: Reed & Robbins  
xx STREET: 635 Bryant Street  
xx CITY: Palo Alto  
xx STATE: California  
xx COUNTRY: USA  
xx ZIP: 94301  
xx COMPUTER READABLE FORM:  
xx MEDIUM TYPE: Floppy disk  
xx COMPUTER: IBM PC compatible  
xx OPERATING SYSTEM: PC-DOS/MS-DOS  
xx SOFTWARE: Patent Release #1.0, version #1.25  
xx CURRENT APPLICATION DATA:  
xx APPLICATION NUMBER: US/08/050,319B  
xx FILING DATE: 10-May-1993  
xx CLASSIFICATION: 435  
xx ATTORNEY/AGENT INFORMATION:  
xx NAME: Robbins, Roberta L.  
xx REGISTRATION NUMBER: 33,208  
xx REFERENCE/DOCKET NUMBER: 5150-0030  
xx TELECOMMUNICATION INFORMATION:  
xx TELEPHONE: (415) 617-8999  
xx TELEFAX: (415) 327-3231  
xx INFORMATION FOR SEQ ID NO: 1:  
xx SEQUENCE CHARACTERISTICS:  
xx LENGTH: 501 base pairs  
xx TYPE: nucleic acid  
xx STRANDEDNESS: double  
xx TOPOLOGY: linear  
xx MOLECULE TYPE: DNA (genomic)  
xx FEATURE:  
xx NAME/KEY: CDS  
xx LOCATION: 1..501  
xx Sequence 501 BP; 121 A; 137 C; 137 G; 106 T; 0 other;  
Query Match 32.5%; Score 373; DB 7; Length 501;  
Best Local Similarity 99.0%; Pred. No. 4,58e-291;  
Matches 377; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Db 121 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180  
Oy 344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 403  
Db 181 AAGTGCACAAAGAAACCTACTGTACATGACTGTCCAGGCGCGGAGGATACGAGAC 240  
Oy 404 AAGTGCACAAAGAAACCTACTGTACATGACTGTCCAGGCGCGGAGGATACGAGAC 463  
Db 241 TGCAGGAGTGTGAGAGCGGCTCTCACCCTTCAAGAAACCACTCAGACACTGCTC 300  
Oy 464 TGCAGGAGTGTGAGAGCGGCTCTCACCCTTCAAGAAACCACTCAGACACTGCTC 523  
Db 301 AGTGTCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTCTTCTTGACAGTGGAC 360  
Oy 524 AGTGTCTCCAAATGCCGAAGAAATGGTTCAGGTGAGATCTCTTCTTGACAGTGGAC 583

Db 361 CGGACACCGTGTGTGCTGCGAGAGAACCGCATTTATGGAGTGAACCTT 420  
| | | | |  
Qy 584 CGGACACCGTGTGTGCTGCGAGAGAACCGCATTTATGGAGTGAACCTT 643  
| | | | |  
Db 421 TTCAGTCTTCATATGAGAGCTCTGCTCAATGGAGCCGTCACCTCTCTCCAGAG 480  
| | | | |  
Qy 644 TTCAGTCTTCATATGAGAGCTCTGCTCAATGGAGCCGTCACCTCTCTCCAGAG 703  
| | | | |  
Db 481 AACAGAACCGTGTGCGACC 501  
| | | | |  
Qy 704 AACAGAACCGTGTGCGACC 724  
| | | | |  
RESULT 8  
ID US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.  
XX  
AC xxxxxx  
XX 01-JAN-1900  
XX  
DE Sequence 3, Application US/08050319B.  
CC Sequence 3, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PC-DOS/MS-DOS  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 372 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..372  
CC Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;  
Query Match 31.7%; Score 364; DB 7; Length 372;  
Best Local Similarity 98.9%; Pred. No. 2,74e-283;  
Matches 368; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Db 1 GTGTCTCCCAAGAAATATATCCACCGCTCAAAATTAATTCATTGCTGTACCAAGTGC 60  
| | | | |

Qy 350 GTGTCTCCCAAGAAATATATCCACCGCTCAAAATTAATTCATTGCTGTACCAAGTGC 409  
| | | | |  
Db 61 CACAAGAACCTTACTTGTACATAGACTGTCCAGCCCGGGGAGATPACGACTGCAGG 120  
| | | | |  
Qy 410 CACAAGAACCTTACTTGTACATAGACTGTCCAGCCCGGGGAGATPACGACTGCAGG 469  
| | | | |  
Db 121 GAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCTCAGTGC 180  
| | | | |  
Qy 470 GAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAAACACCTCAGACACTGCTCAGTGC 529  
| | | | |  
Db 181 TCCAATATGCCGAAAGAAATGGTTCAGGTGAGATCTCTTTCACACAGTGGACCGGGAC 240  
| | | | |  
Qy 530 TCCAATATGCCGAAAGAAATGGTTCAGGTGAGATCTCTTTCACACAGTGGACCGGGAC 589  
| | | | |  
Db 241 ACCGTGTGTGCTCAGAGAGAACCGAGTACCGGCATTATTGAGTGAACCTTTTCAG 300  
| | | | |  
Qy 590 ACCGTGTGTGCTCAGAGAGAACCGAGTACCGGCATTATTGAGTGAACCTTTTCAG 649  
| | | | |  
Db 301 TGCTTCATTGCAAGCTCTGCTTCATGAGACCGTGCACCTCTCTCCAGAGAGAAACAG 360  
| | | | |  
Qy 650 TGCTTCATTGCAAGCTCTGCTTCATGAGACCGTGCACCTCTCTCCAGAGAGAAACAG 709  
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Db 361 AACACCGTGTGC 372  
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Qy 710 AACACCGTGTGC 721  
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RESULT 9  
ID US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.  
XX  
AC xxxxxx  
XX 01-JAN-1900  
XX  
DE Sequence 49, Application US/08050319B.  
CC Sequence 49, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PC-DOS/MS-DOS  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 49:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 474 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double



CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..471  
SQ Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;  
Query Match 30.1%; Score 345; DB 7; Length 474;  
Best Local Similarity 98.3%; Pred. No. 6,94e-267;  
Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Db 118 AGAGAGTGTAGAGCGGCTCTTACCGCTTTCAGAAAACCACTCAGACACTGCTCAGC 177  
|||  
Qy 467 AGGAGTGTAGAGCGGCTCTTACCGCTTTCAGAAAACCACTCAGACACTGCTCAGC 526  
Db 178 TGTCTCAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGACAGTGGACCG 237  
|||  
Qy 527 TGTCTCAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGACAGTGGACCG 586  
Db 238 GACACCGTGTGGCTGACAGAGAAACCACTACCGCATTTATGGAGTGAACCTTTTC 297  
|||  
Qy 587 GACACCGTGTGGCTGACAGAGAAACCACTACCGCATTTATGGAGTGAACCTTTTC 646  
Db 298 CAGTGTCTCAATTCAGACCTCTGCTCAATGAGACCGTGTGACCTCTCTCCAGAGAAA 357  
|||  
Qy 647 CAGTGTCTCAATTCAGACCTCTGCTCAATGAGACCGTGTGACCTCTCTCTCAGAGAAA 706  
Db 358 CAGACACCGTGTGACACCTGCTCAATGAGAGTCTTCTTAAGAGAAAAGAGTGTCTCC 417  
|||  
Qy 707 CAGACACCGTGTGACACCTGCTCAATGAGAGTCTTCTTAAGAGAAAAGAGTGTCTCC 766  
Db 418 TGTAGTAACGTGAAGAAACCTGGAGTGCACGAAGTGTGCTTACCCAGATTAG 474  
|||  
Qy 767 TGTAGTAACGTGAAGAAACCTGGAGTGCACGAAGTGTGCTTACCCAGATTAG 823  
RESULT 10  
ID US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.  
XX xxxxxx  
XX 01-JAN-1900  
DE Sequence 5, Application US/08273411.  
XX  
CC Sequence 5, Application US/08273411  
CC Patent No. 5625124  
CC GENERAL INFORMATION:  
CC APPLICANT: Falk, Per  
CC APPLICANT: Gordon, Jeffrey I.  
CC TITLE OF INVENTION: Animal Model for Gastro-Intestinal  
CC NUMBER OF SEQUENCES: 10  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Patrea L. Pabst  
CC STREET: 1100 Peachtree Street, Suite 2800  
CC CITY: Atlanta  
CC STATE: Georgia  
CC COUNTRY: USA  
CC ZIP: 30309-4530  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/273,411  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Pabst, Patrea L.  
CC REGISTRATION NUMBER: 31,284

CC REFERENCE/DOCKET NUMBER: WU106  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (404) 815-6508  
CC TELEFAX: (404) 815-6555  
CC INFORMATION FOR SEQ ID NO: 5:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2771 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC ANTI-SENSE: NO  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Sweetser, et al.  
CC JOURNAL: Genes & Dev.  
CC VOLUME: 2  
CC PAGES: 1318-1332  
CC DATE: 1988  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 561 TO 629  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Seeburg, et al.  
CC JOURNAL: DNA  
CC VOLUME: 1  
CC PAGES: 239-249  
CC DATE: 1982  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 620 TO 2771  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Sweetser, et al.  
CC JOURNAL: J. Biol. Chem.  
CC VOLUME: 261  
CC PAGES: 5553-5561  
CC DATE: 1986  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 617  
CC SEQUENCE 2771 BP; 666 A; 718 C; 704 G; 683 T; 0 other;  
SQ  
Query Match 25.1%; Score 288; DB 7; Length 2771;  
Best Local Similarity 95.6%; Pred. No. 8.12e-218;  
Matches 323; Conservative 0; Mismatches 11; Indels 4; Gaps 3;  
Db 680 ATGGCTACAGGTAAAGCGCCCTTAAATCCCTTGGGACAAATGTGTCTAGGGAGAGG 729  
|||  
Qy 6 ATGGCTACAGGTAAAGCGCCCTTAAATCCCTTGGGACAAATGTGTCTAGGGAGAGG 65  
Db 740 CACGCACTGTAGATGGAGCGGGGACCTAACCTCAGTTGGGCTTCTGATG--AG 797  
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Qy 66 CACGCACTGTAGATGGAGCGGGGACCTAACCTCAGTTGGGCTTCTGATGATGAG 125  
Db 798 TATGCCATGTAAAGCCAGTATG-GCC-AATCTCAGAAAGCTCTGTGCTCTGGAGGAT 855  
|||  
Qy 126 TATGCCATGTAAAGCCAGTATGATTTGCCCAATCTCAGAAAGCTCTGTGCTCTGGAGGAT 185  
Db 856 GGAGAGGAAACAAACAAAGCTCTGGAGAGGAGAGTGTGCTGCTCTGCTCGCGC 915  
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Qy 186 GGAGAGGAAACAAACAAAGCTCTGGAGAGGAGAGTGTGCTGCTCTGCTGCGCGC 245  
Db 916 TCCCTGTGTGCGCTGTGTTCTCCCAAGGCTCCCGAGCTCTGCTCTGCTGCTTTG 975  
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Qy 246 TCCGTGTGTGCGCTGTGTTCTCCCAAGGCTCCCGAGCTCTGCTCTGCTGCTTTG 305  
Db 976 GCCTGTGTGCGCTGTGTTCTCCCAAGGCTCCCGAGCTCTGCTCTGCTGCTTTG 1013  
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Qy 306 GCCTGTGTGCGCTGTGTTCTCCCAAGGCTCCCGAGCTCTGCTCTGCTGCTTTG 343  
RESULT 11  
ID US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.  
XX xxxxxx  
XX 01-JAN-1900  
XX

DE Sequence 3, Application US/08343401A.  
XX  
CC Sequence 3, Application US/08343401A  
CC Patent No. 5661132  
CC GENERAL INFORMATION:  
CC APPLICANT: Swalin, William F  
CC APPLICANT: Swalin, Michael D  
CC APPLICANT: Eriksson, Elof  
CC APPLICANT: Andree, Christophe  
CC TITLE OF INVENTION: Improved Wound Healing  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Quarles & Brady  
CC STREET: PO Box 2113  
CC CITY: Madison  
CC STATE: WI  
CC COUNTRY: USA  
CC ZIP: 53701-2113  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/343,401A  
CC FILING DATE: 22-NOV-1994  
CC CLASSIFICATION: 514  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Seay, Nicholas J  
CC REGISTRATION NUMBER: 27,386  
CC REFERENCE/DOCKET NUMBER: 11-229-9103-9  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 608-251-5000  
CC TELEFAX: 608-251-9166  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 4283 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: circular  
CC MOLECULE TYPE: DNA (genomic)  
CC IMMEDIATE SOURCE:  
CC CLONE: pMR1630  
CC FEATURE:  
CC NAME/KEY: exon  
CC LOCATION: 713..721  
CC FEATURE:  
CC NAME/KEY: exon  
CC LOCATION: 981..1253  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: join(713..721, 981..1253)  
CC FEATURE:  
CC NAME/KEY: s1g\_deptide  
CC LOCATION: 713..1049  
CC SEQUENCE 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;  
SQ  
Query Match 25.0%; Score 287; DB 7; Length 4283;  
Best Local Similarity 93.2%; Pred. No. 5.86e-217;  
Matches 315; Conservative 0; Mismatches 22; Indels 1; Gaps 1;  
Db 713 ATGGCTACAGGTAAAGCCCTTAAATCCCTTTGG-CACAAATGTGTCTGAGGGAGAG 771  
Oy 6 ATGGCTACAGGTAAAGCCCTTAAATCCCTTTGG-CACAAATGTGTCTGAGGGAGAG 65  
Db 772 CAGCACCCTGTAGATGGAGCGGGGACCTAACCCCTGAGGCTTTGGGCTTCTGAATGTAG 831  
Oy 66 CAGCACCCTGTAGATGGAGCGGGGACCTAACCCCTGAGGCTTTGAATGTAG 125  
Db 832 TATGCCATCTAAGCCCAATATTTGGCCAAATCTCAGAAAGCTCTGAGCTCCCTGAGGAT 891  
Oy 126 TATGCCATCTAAGCCCAATATTTGGCCAAATCTCAGAAAGCTCTGAGCTCCCTGAGGAT 185

Db 892 GGAGAGAAAAAACAAGAGCTCTGAGCAGAGAGAGTGTGGCTCTGCTCCGAC 951  
Oy 186 GGAGAGAAAAAACAAGAGCTCTGAGCAGAGAGAGTGTGGCTCTGCTCCGAC 245  
Db 952 TCCCTCTGTGGCTCTGCTGTTTCTCCCAAGAGTCCCGGACGCTCCGCTGCTTTTG 1011  
Oy 246 TCCGCTGTGGCTCTGCTGTTTCTCCCAAGAGTCCCGGACGCTCCGCTGCTTTTG 305  
Db 1012 GCCTGCTGCTGCTGCTGCTGCTTCAAGAGGAGGAGTCC 1049  
Oy 306 GCCTGCTGCTGCTGCTGCTGCTTCAAGAGGAGGAGTCC 343  
RESULT 12  
ID US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.  
XX  
AC xxxxxx  
XX 01-JAN-1900  
XX  
XX Sequence 1, Application US/08445265A.  
XX  
CC Sequence 1, Application US/08445265A  
CC Patent No. 5697901  
CC GENERAL INFORMATION:  
CC APPLICANT: Eriksson, Elof  
CC TITLE OF INVENTION: GENE DELIVERY BY MICRONEEDLE INJECTION  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Quarles & Brady  
CC STREET: 1 South Plackney Street  
CC CITY: Madison  
CC STATE: WI  
CC COUNTRY: US  
CC ZIP: 53703  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/445,265A  
CC FILING DATE:  
CC CLASSIFICATION: 604  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Seay, Nicholas J  
CC REGISTRATION NUMBER: 27386  
CC REFERENCE/DOCKET NUMBER: 110229.91080  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 608-251-9166  
CC TELEFAX: 608-251-9166  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 4283 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: circular  
CC MOLECULE TYPE: other nucleic acid  
CC DESCRIPTION: /desc = "Plasmid DNA"  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: join(713..721, 981..1250)  
CC SEQUENCE 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;  
SQ  
Query Match 25.0%; Score 287; DB 7; Length 4283;  
Best Local Similarity 93.2%; Pred. No. 5.86e-217;  
Matches 315; Conservative 0; Mismatches 22; Indels 1; Gaps 1;  
Db 713 ATGGCTACAGGTAAAGCCCTTAAATCCCTTTGG-CACAAATGTGTCTGAGGGAGAG 771  
Oy 6 ATGGCTACAGGTAAAGCCCTTAAATCCCTTTGG-CACAAATGTGTCTGAGGGAGAG 65

Db 772 CACGACCTGTAGATGAGACGGGGGCACTACCTCAGGCTTGGGGTTCTGAATGTGAG 831  
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Qy 66 CACGACCTGTAGATGAGACGGGGGCACTACCTCAGGCTTGGGGTTCTGAATGTGAG 125  
832 TATGCCATCTAAAGCCAGTATTGGCCAACTCTCAAGAAAGCTCTGGCTCCCTGAGGAT 891  
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Qy 126 TAGGGCAATGTAAGCCAGCAATATTGGCCAACTCTCAAGAAAGCTCTGGCTCCCTGAGGAT 185  
892 GAGAGAGAAAAAACAACAGCTCTGTGAGAGAGAGAGAGTGTGGCTCTTGTCTCCGGC 951  
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Qy 186 GAGAGAGAAAAAACAACAGCTCTGTGAGAGAGAGAGAGTGTGGCTCTTGTCTCCGGC 245  
952 TCCCTGTGTGCTGCTGTGCTTCTCCCAAGAGCTCCCGAGAGCTCCCTGTCTGCTTTG 1011  
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Qy 246 TCCGTGTGTGCTGCTGTGCTTCTCCCAAGAGCTCCCGAGAGCTCCCTGTCTGCTTTG 305  
1012 GCCTGCTGTGCTGCTGCTGCTTCAAGAGGCGAGTGC 1049  
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Qy 306 GCCTGCTGTGCTGCTGCTGCTTCAAGAGGCGAGTGC 343

RESULT 13  
ID US-08-050-319B-53 STANDARD; DNA; 477 BP.

XX xxxxxx  
AC  
DT 01-JAN-1900  
XX  
DE Sequence 53, Application US/08050319B.  
XX  
CC Sequence 53, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M. Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbings  
CC STREET: 635 Bryant Street  
CC City: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbings, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 53:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 477 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..474  
CC Sequence 477 BP; 117 A; 122 C; 131 G; 107 T; 0 other;

Query Match 22.2%; Score 255; DB 7; Length 477;  
Best Local Similarity 98.9%; Pred. No. 1.56e-189;  
Matches 258; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Db 121 GATAGTGTGTGTCCTCCAGGAAATATATATCCACCCCAAAATATATGATTTGCTGTACC 180  
GATAGTGTGTGTCCTCCAGGAAATATATATCCACCCCAAAATATATGATTTGCTGTACC 403  
Qy 181 AAGTCCACAAGAAAGCACTATTGTACAAATGACTGTCCAGGCCCCGGGCGAGATACGAC 240  
404 AAGTCCACAAGAAAGCACTATTGTACAAATGACTGTCCAGGCCCCGGGCGAGATACGAC 463  
Db 241 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACCACTCAGACACTGCTTC 300  
464 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACCACTCAGACACTGCTTC 523  
Qy 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTCAAGTGTGAGTGTGCTTCTTGTGACAGTGTGAC 360  
524 AGCTGCTCCAAATGCCGAAAGAAATGGGTCAAGTGTGAGTGTGCTTCTTGTGACAGTGTGAC 583  
Db 361 CGGAGACCGGTGTGTACTGTC 381  
584 CGGAGACCGGTGTGTACTGTC 604  
Qy

RESULT 14  
ID US-08-050-319B-51 STANDARD; DNA; UNC; 462 BP.

XX xxxxxx  
AC  
DT 01-JAN-1900  
XX  
DE Sequence 51, Application US/08050319B.  
XX  
CC Sequence 51, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M. Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbings  
CC STREET: 635 Bryant Street  
CC City: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbings, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 51:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 462 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear



\*\*\*\*\*  
[W] [O] [R] [E] [H]  
\*\*\*\*\*  
(TM)

Release 3.0.5AA John F. Collins, Blocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

\*\*\*\*\*  
MSPRCH\_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:20:59 1998; Maspar time 4.78 Seconds

Tabular output not generated. 367.559 Million cell updates/sec

Title: >US-08-804-166-4

Description: (1-307) from US08804166.pap

Perfect Score: 2341

Sequence: 1 SRTSLALFGLCLPLMQEG.....PSLPSRLPSPDTPILPQ 307

Scoring table: PAM 150

Gap 11

Searched: 62627 seqs, 5720858 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-issued

1:PACK1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PC790

10:PC791 11:PC792 12:PC793 13:PC794 14:PC795 15:PC796

Statistics: Mean 30.606; Variance 140.802; scale 0.217

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1124	48.0	455	7	US-08-321-	Sequence 2, Applicatio	4.13e-91
2	1124	48.0	455	7	US-08-050-	Sequence 25, Applicati	4.13e-91
3	1115	47.6	199	7	US-08-050-	Sequence 48, Applicati	2.79e-90
4	1025	43.8	145	6	US-08-425-	Sequence 2, Applicatio	5.45e-82
5	1025	43.8	145	6	US-08-425-	Sequence 1, Applicatio	5.45e-82
6	1020	43.6	145	7	US-08-298-	Sequence 1, Applicatio	1.57e-81
7	995	42.5	145	6	US-08-425-	Sequence 10, Applicati	3.15e-79
8	995	42.5	167	7	US-08-050-	Sequence 57, Applicati	2.54e-79
9	966	42.5	167	7	US-08-050-	Sequence 2, Applicatio	6.07e-78
10	981	41.9	124	7	US-08-050-	Sequence 4, Applicatio	2.54e-78
11	800	34.2	157	7	US-08-050-	Sequence 50, Applicati	2.36e-61
12	740	31.6	114	6	US-08-425-	Sequence 9, Applicatio	2.47e-55
13	734	31.4	114	6	US-08-425-	Sequence 7, Applicatio	1.63e-53
14	714	30.5	117	6	US-08-425-	Sequence 11, Applicati	8.72e-51
15	684	29.2	114	6	US-08-425-	Sequence 8, Applicatio	3.76e-48
16	666	28.4	158	7	US-08-050-	Sequence 54, Applicati	8.62e-48
17	651	27.8	117	6	US-08-425-	Sequence 12, Applicati	2.38e-44
18	633	26.2	149	6	US-08-425-	Sequence 5, Applicatio	4.02e-32
19	477	20.4	153	7	US-08-050-	Sequence 52, Applicati	6.36e-20
20	399	14.5	41	7	US-08-050-	Sequence 36, Applicati	1.29e-18
21	324	13.8	40	7	US-08-050-	Sequence 26, Applicati	4.28e-18
22	318	13.6	43	7	US-08-050-	Sequence 31, Applicati	4.28e-18

RESULT	1	STANDARD;	PRT;	455 AA.
ID	US-08-321-668-2			
AC	xxxxxx			
XX	01-JAN-1900			
DT				
DE	Sequence 2, Application US/08321668.			
XX				
CC	Sequence 2, Application US/08321668			
CC	Patent No. 5665859			
CC	GENERAL INFORMATION:			
CC	APPLICANT: WALLACH, David			
CC	APPLICANT: BRAKEBUSCH, Cord			
CC	APPLICANT: VARELOMEV, Eugene			
CC	APPLICANT: BATKIN, Michael			
CC	TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF			
CC	NUMBER OF SEQUENCES: 42			
CC	CORRESPONDENCE ADDRESSES:			
CC	ADDRESSEE: BROWDY AND NEIMARK			
CC	STREET: 419 Seventh Street, N.W., Suite 300			
CC	CITY: Washington			
CC	STATE: D.C.			
CC	COUNTRY: USA			
CC	ZIP: 20004			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Patentin Release #1.0, Version #1.30			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/321,668			
CC	FILING DATE: 12-OCT-1994			
CC	CLASSIFICATION: 435			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: IL 107268			
CC	FILING DATE: 12-OCT-1993			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: BROWDY, Roger L.			
CC	REGISTRATION NUMBER: 25,618			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: 202-628-5197			
CC	TELEFAX: 202-737-3528			
CC	TELEX: 248633			

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CC      INFORMATION FOR SEQ ID NO: 2
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 455 amino acids
CC          TYPE: amino acid
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 455 AA; 50494 MW; 1048031 CN;
SQ
Query Match          48.0%; Score 1124; DB 7; Length 455;
Best Local Similarity 99.3%; Pred. No. 4,13e-91;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db      41 DSVCPQGYIHPQNNISICTCKHNGTLYLNDCCPQGDITDCRECSGSPFASENHLRHCL 100
      |||
QY      23 DSVCPQGYIHPQNNISICTCKHNGTLYLNDCCPQGDITDCRECSGSPFASENHLRHCL 82
Db      101 SCSCRCRMEGVEISCTVDPRDVCGCRKNQRYHYSSENTFOCFNCSLCINGTVHLSCE 160
      |||
QY      83 SCSCRCRMEGVEISCTVDPRDVCGCRKNQRYHYSSENTFOCFNCSLCINGTVHLSCE 142
Db      161 KONTVCTCHAGFLRENECVSCS 183
      |||
QY      143 KONTVCTCHAGFLRENECVSCA 165
RESULT
ID      2
XX      US-08-050-319B-25          STANDARD;          PRT;          455 AA.
XX      xxxxxx
XX      01-JAN-1900
DE      Sequence 25, Application US/08050319B.
XX      Sequence 25, Application US/08050319B
XX      Patent No. 5633145
CC      GENERAL INFORMATION:
CC      APPLICANT: M. Feldmann, P.W. Gray,
CC      APPLICANT: M.J.C. Turner, F.M. Brennan
CC      TITLE OF INVENTION: Modified human TNFalpha (Tumor
CC      TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC      NUMBER OF SEQUENCES: 57
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Reed & Robbins
CC      STREET: 635 Bryant Street
CC      CITY: Palo Alto
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94301
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/050,319B
CC      FILING DATE: 10-May-1993
CC      CLASSIFICATION: 435
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Robbins, Roberta L.
CC      REGISTRATION NUMBER: 33,208
CC      REFERENCE/DOCKET NUMBER: 5150-0030
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (415) 617-8999
CC      TELEFAX: (415) 327-3231
CC      INFORMATION FOR SEQ ID NO: 25:
CC      SEQUENCE CHARACTERISTICS:
CC          LENGTH: 455 amino acids
CC          TYPE: amino acid
CC          TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 455 AA; 50579 MW; 1048388 CN;

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DB	Query Match	48.0%	Score 1124	DB 7	Length 455
OY	Best Local Similarity	99.3%	Pred. No. 4.13e-91		
	Matches 142	Conservative 1	Mismatches 0	Indels 0	Gaps 0
Db	41 DSVCPGKTIHPNNNSICCTKCHNGTYLYNDCCPGPGDITDCRCESSGFTASENHLRHCL	100			
OY	23 DSVCPGKTIHPNNNSICCTKCHNGTYLYNDCCPGPGDITDCRCESSGFTASENHLRHCL	82			
Db	101 SCSKCRKEMGVLEISCTYVDRTDYCGCRKQRYRIYSENFLFCFNGSLCLNGTYHLSCE	160			
OY	83 SCSKCRKEMGVLEISCTYVDRTDYCGCRKQRYRIYSENFLFCFNGSLCLNGTYHLSCE	142			
Db	161 KQNTVCTCHAGFLRENECVCS 183				
OY	143 KQNTVCTCHAGFLRENECVCSA 165				
RESULT	3	STANDARD	PRT	199 AA.	
XX	US-08-050-319B-48				
AC	xxxxxx				
DT	01-JAN-1900				
XX	Sequence 48, Application US/08050319B.				
DE	Sequence 48, Application US/08050319B				
XX	Patent No. 5633145				
CC	GENERAL INFORMATION:				
CC	APPLICANT: M. Feldmann, P.W. Gray,				
CC	APPLICANT: M.J.C. Turner, F.M. Brennan				
CC	TITLE OF INVENTION: Modified human TNFalpha (Tumor				
CC	TITLE OF INVENTION: Necrosis Factor alpha) Receptor				
CC	NUMBER OF SEQUENCES: 57				
CC	CORRESPONDENCE ADDRESS:				
CC	ADDRESSEE: Reed & Robbins				
CC	STREET: 635 Bryant Street				
CC	CITY: Palo Alto				
CC	STATE: California				
CC	COUNTRY: USA				
CC	ZIP: 94301				
CC	COMPUTER READABLE FORM:				
CC	MEDIUM TYPE: Floppy disk				
CC	COMPUTER: IBM PC compatible				
CC	OPERATING SYSTEM: PC-DOS/MS-DOS				
CC	SOFTWARE: Patentin Release #1.0, version #1.25				
CC	CURRENT APPLICATION DATA:				
CC	APPLICATION NUMBER: US/08/050,319B				
CC	FILING DATE: 10-May-1993				
CC	CLASSIFICATION: 435				
CC	ATTORNEY/AGENT INFORMATION:				
CC	NAME: Robbins, Roberta L.				
CC	REGISTRATION NUMBER: 33,208				
CC	REFERENCE/DOCKET NUMBER: 5150-0030				
CC	TELECOMMUNICATION INFORMATION:				
CC	TELEPHONE: (415) 617-8999				
CC	TELEFAX: (415) 327-3231				
CC	INFORMATION FOR SEQ. ID NO. 48:				
CC	SEQUENCE CHARACTERISTICS:				
CC	LENGTH: 199 amino acids				
CC	TYPE: amino acid				
CC	TOPOLOGY: linear				
CC	MOLECULE TYPE: protein				
CC	SEQUENCE 199 AA; 22186 MM; 195553 CN;				
Db	Query Match	47.6%	Score 1115	DB 7	Length 199
OY	Best Local Similarity	98.6%	Pred. No. 2.79e-90		
	Matches 141	Conservative 1	Mismatches 1	Indels 0	Gaps 0
Db	41 DSVCPGKTIHPNNNSICCTKCHNGTYLYNDCCPGPGDITDCRCESSGFTASENHLRHCL	100			
OY	23 DSVCPGKTIHPNNNSICCTKCHNGTYLYNDCCPGPGDITDCRCESSGFTASENHLRHCL	82			

Qy	Db	Qy	Db
83	101	161	143
SCSCRKMGGVVEISSCVDYDTCGGRKNDYRYHWSENLFCQNCSTCLNGVYHLSQOE	SCSCRKMGGVVEISSCVDYDTCGGRKNDYRYHWSENLFCQNCSTCLNGVYHLSQOE	KONTVCTCHAGFLEPNECVSCS	KONTVCTCHAGFLEPNECVSCA
142	160	183	165
SCSCRKMGGVVEISSCVDYDTCGGRKNDYRYHWSENLFCQNCSTCLNGVYHLSQOE	SCSCRKMGGVVEISSCVDYDTCGGRKNDYRYHWSENLFCQNCSTCLNGVYHLSQOE	KONTVCTCHAGFLEPNECVSCS	KONTVCTCHAGFLEPNECVSCA

ID	RESULT	4	STANDARD:	PRT:	145	AA.
XX	US-08-425-673-2					
XX	xxxxxx					
XX	01-JAN-1900					
XX	Sequence 2, Application US/08425673.					
XX						
CC	Sequence 2, Application US/08425673					
CC	Patent No. 5508261					
CC	GENERAL INFORMATION:					
CC	APPLICANT: Moyle, William R.					
CC	APPLICANT: Campbell, Robert K.					
CC	TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having					
CC	TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and					
CC	TITLE OF INVENTION: Methods For Preparing and Using Same					
CC	NUMBER OF SEQUENCES: 12					
CC	CORRESPONDENCE ADDRESS:					
CC	ADDRESSEE: Richard R. Muccino					
CC	STREET: P.O. Box 1267					
CC	CITY: Princeton					
CC	STATE: New Jersey					
CC	COUNTRY: USA					
CC	ZIP: 08551					
CC	COMPUTER READABLE FORM:					
CC	MEDIUM TYPE: Floppy disk					
CC	COMPUTER: IBM PC compatible					
CC	OPERATING SYSTEM: PC-DOS/MS-DOS					
CC	SOFTWARE: Patentin Release #1.0, Version #1.25					
CC	CURRENT APPLICATION DATA:					
CC	APPLICATION NUMBER: US/08/425,673					
CC	FILING DATE:					
CC	CLASSIFICATION: 514					
CC	PRIOR APPLICATION DATA:					
CC	APPLICATION NUMBER: US 07/717,151					
CC	FILING DATE: 18-JUN-1991					
CC	ATTORNEY/AGENT INFORMATION:					
CC	NAME: Muccino, Richard R.					
CC	REGISTRATION NUMBER: 32,538					
CC	REFERENCE/DOCKET NUMBER: UMD 1.0-004					
CC	TELECOMMUNICATION INFORMATION:					
CC	TELEPHONE: (609) 466-3407					
CC	TELEFAX: (609) 466-2760					
CC	INFORMATION FOR SEQ ID NO: 2:					
CC	SEQUENCE CHARACTERISTICS:					
CC	LENGTH: 145 amino acids					
CC	TYPE: amino acid					
CC	TOPOLOGY: linear					
CC	MOLECULE TYPE: peptide					
CC	HYPOTHETICAL: NO					
CC	ANTI-SENSE: NO					
CC	SEQUENCE 145 AA: 15544 MW: 114662 CN:					
DB	Query Match	43.88;	Score 1025;	DB 6;	Length 145;	
DB	Best Local Similarity	99.38;	Pred. No. 5,45e-82;			
DB	Matches 138;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
DB	7	PCRPRINATLAVEKEGCPVCITVNTITACAGYCPMTRYLQGLVLPALPQVCNRYRDVRES	66			
DB	169	PCRPRINATLAVEKEGCPVCITVNTITACAGYCPMTRYLQGLVLPALPQVCNRYRDVRES	228			
DB	67	ILPLGPGRGVNPVSTAVVALSCOCALCRSTTDCGGPRDHPFLTCDPFRDSSSKAPP	126			

QY	229	IRLEGCGRGVNPPVSIYAVALSQCALCRKSTTDCGGKDHPLICDDPFDODSSSSNAPP	288
Db	127	SLPSPSRLLPSPDPIRLQ	145
QY	289	SLPSPSRLLPSPDPIRLQ	307

ID	US-08-425-673-1	STANDARD:	PRT:	145 AA.
XX	xxxxxx			
XX	01-JAN-1900			
XX	Sequence 1, Application US/08425673.			
DE				
CC	Sequence 1, Application US/08425673			
CC	Patent No. 5508261			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Moyle, William R.			
CC	APPLICANT: Campbell, Robert R.			
CC	TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having			
CC	TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and			
CC	TITLE OF INVENTION: Methods For Preparing and Using Same			
CC	NUMBER OF SEQUENCES: 12			
CC	CORRESPONDENCE ADDRESSES:			
CC	ADDRESSEE: Richard R. Muccino			
CC	STREET: P.O. Box 1267			
CC	CITY: Princeton			
CC	STATE: New Jersey			
CC	COUNTRY: USA			
CC	ZIP: 08551			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Patentin Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/425,673			
CC	FILING DATE:			
CC	CLASSIFICATION: 514			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US 07/717,151			
CC	FILING DATE: 18-JUN-1991			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Muccino, Richard R.			
CC	REGISTRATION NUMBER: 32,538			
CC	REFERENCE/DOCKET NUMBER: UMD 1.0-004			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (609) 466-3407			
CC	TELEFAX: (609) 466-2760			
CC	INFORMATION FOR SEQ ID NO: 1:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 145 amino acids			
CC	TYPE: amino acid			
CC	TOPOLOGY: linear			
CC	MOLECULE TYPE: peptide			
CC	HYPOTHETICAL: NO			
CC	ANTI-SENSE: NO			
CC	SEQUENCE 145 AA: 15544 MW: 114662 CN:			
DB	Query Match 43.88: Score 1025. DB 6: Length 145:			
DB	Best Local Similarity 99.38: Pred. No. 5.45e-82;			
DB	Matches 138: Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
DB	7 PRCRPNATLAVERECCPCVITVNTICAGYCEPTMRVLOGVLPALPOVCNTRDVPRES 66			
DB	169 PRCRPNATLAVERECCPCVITVNTICAGYCEPTMRVLOGVLPALPOVCNTRDVPRES 228			
DB	67 IRLPGCPREVNPVSYAVVALSCCALCRSTTTCGCGKDHPLTCDDDRFFDSSSSKAPP 126			
DB	229 IRLPGCPREVNPVSYAVVALSCCALCRSTTTCGCGKDHPLTCDDDRFFDSSSSKAPP 288			

Db 127 SLSPSRLLPGSPDTPILPQ 145  
|||||  
QY 289 SLSPSRLLPGSPDTPILPQ 307  
|||||

RESULT 6  
ID US-08-298-189B-1 STANDARD: PRT: 145 AA.  
AC xxxxxx  
DT 01-JAN-1900

Sequence 1, Application US/08298189B.  
Sequence 1, Application US/08298189B  
Patent No. 5674727  
GENERAL INFORMATION:  
APPLICANT: Dr. Laurence A. Cole and Dr. Andrew Kardana  
TITLE OF INVENTION: No. 5674727el Methods for Detecting Reproductive  
TITLE OF INVENTION: Cancers or Tumors and Assay Products  
TITLE OF INVENTION: Therefor  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. Laurence A. Cole, c/o Dept. of Obstetrics and  
STREET: 333 Cedar Street  
CITY: New Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06510

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Microsoft Word 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/298.189B  
FILING DATE: 08/31/94  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brian D. Voyce  
REGISTRATION NUMBER: 28,917  
REFERENCE/DOCKET NUMBER: DS11  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-638-3939 or 803-272-1471  
TELEFAX: 919-638-3939 or 803-272-1471  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: NO. 5674727 applicable  
TOPOLOGY: Unknown  
MOLECULE TYPE: subunit of hormone, specifically the  
MOLECULE TYPE: beta/subunit of hCG  
ORIGINAL SOURCE: human urine  
FEATURE:  
NAME/KEY: beta subunit of hCG that is nicked by GBNE  
LOCATION: hCG  
IDENTIFICATION METHOD: N-terminal sequence analysis  
PUBLICATION INFORMATION:  
AUTHORS: Keutmann et alia  
TITLE: "A Receptor-binding Region in Human  
JOURNAL: Proc Nat'l Acad Sci USA  
VOLUME: 84  
ISSUE: No. 5674727 applicable  
PAGES: 2038-2042  
DATE: 1987

SEQUENCE 145 AA; 15476 MW; 116769 CN;  
Query Match 43.6%; Score 1020; DB 7; Length 145;  
Best Local Similarity 98.6%; Pred. No. 1.57e-81;  
Matches 137; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 7 PRCRPNTLAVKEGCGVCITVNTTICAGYCPMTKRYLGVLPAIPVVCNTYRDVRES 66

QY 169 PRCRPNTLAVKEGCGVCITVNTTICAGYCPMTKRYLGVLPAIPVVCNTYRDVRES 228  
|||||

Db 67 IRLPGCPGVNPNVSYAVALSCCALCKKSTTDCGPRDHPDTPDPPFODSSSKAPP 126  
|||||

QY 229 IRLPGCPGVNPNVSYAVALSCCALCKKSTTDCGPRDHPDTPDPPFODSSSKAPP 288  
|||||

Db 127 SLSPSRLLPGSPDTPILPQ 145  
|||||  
QY 289 SLSPSRLLPGSPDTPILPQ 307  
|||||

RESULT 7  
ID US-08-425-673-10 STANDARD: PRT: 145 AA.  
AC xxxxxx  
DT 01-JAN-1900

Sequence 10, Application US/08425673.  
Sequence 10, Application US/08425673  
Patent No. 5508261  
GENERAL INFORMATION:  
APPLICANT: Moyle, William R.  
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
TITLE OF INVENTION: Methods for Preparing and Using Same  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard R. Muccino  
STREET: P.O. Box 1267  
CITY: Princeton  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08551

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425.673  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/717,151  
FILING DATE: 18-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Muccino, Richard R.  
REGISTRATION NUMBER: 32,538  
REFERENCE/DOCKET NUMBER: UMD 1.0-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 466-3407  
TELEFAX: (609) 466-2760  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO

SEQUENCE 145 AA; 15448 MW; 114931 CN;  
Query Match 42.5%; Score 995; DB 6; Length 145;  
Best Local Similarity 96.4%; Pred. No. 3.13e-79;  
Matches 134; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 7 PRCRPNTLAVKEGCGVCITVNTTICAGYCPMTKRYLGVLPAIPVVCNTYRDVRES 66  
|||||

QY 169 PRCRPNTLAVKEGCGVCITVNTTICAGYCPMTKRYLGVLPAIPVVCNTYRDVRES 228  
|||||



DB 67 IRLPGCPGVNVSVAVALSCCALCDSSTDCGPGPHPLTCDPDRFODSSSKAPP 126  
OY 229 IRLPGCPGVNVSVAVALSCCALCDSSTDCGPGPHPLTCDPDRFODSSSKAPP 288  
DB 127 SLSPSPRLPGPSDTPILPQ 145  
OY 289 SLSPSPRLPGPSDTPILPQ 307

RESULT 8  
ID US-08-050-319B-57 STANDARD: PRT: 167 AA.  
AC xxxxxx  
XX 01-JAN-1900  
DE Sequence 57, Application US/08050319B.  
XX Sequence 57, Application US/08050319B.  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Reed & Robblins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robblins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 57:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 167 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 167 AA: 18626 MW: 139513 CN;  
Query Match 42.5%; Score 996; DB 7; Length 167;  
Best Local Similarity 100.0%; Pred. No. 2.54e-79;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
ID US-08-050-319B-2 STANDARD: PRT: 167 AA.  
AC xxxxxx  
XX 01-JAN-1900  
DE Sequence 2, Application US/08050319B.  
XX Sequence 2, Application US/08050319B.  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Reed & Robblins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050.319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robblins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 167 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 167 AA: 18626 MW: 139513 CN;  
Query Match 42.5%; Score 996; DB 7; Length 167;  
Best Local Similarity 100.0%; Pred. No. 2.54e-79;  
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 41 DSVCPGKXIHPONNSICCTCKHGTLYLNDGPGQDTCRCESGSFTASENHLRHCL 100  
OY 23 DSVCPGKXIHPONNSICCTCKHGTLYLNDGPGQDTCRCESGSFTASENHLRHCL 82  
DB 101 SCSCKREKMGVEISSCTVDROTVCGCRKNQYRHYSSENLFQCFNCSLCLNGTVHLSCOE 160  
OY 83 SCSCKREKMGVEISSCTVDROTVCGCRKNQYRHYSSENLFQCFNCSLCLNGTVHLSCOE 142

DB 161 KONTVCT 167  
OY 143 KONTVCT 149

RESULT 10  
ID US-08-050-319B-4 STANDARD: PRT: 124 AA.  
AC xxxxxx  
XX 01-JAN-1900  
DT

XX Sequence 4, Application US/08050319B.  
DE  
XX Sequence 4, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbings  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbings, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 4:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 124 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 124 AA; 14047 MW; 75840 CN;  
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Query Match 41.9%; Score 981; DB 7; Length 124;  
Best Local Similarity 100.0%; Pred. No. 6.07e-78;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 VCPGKTIHPQNNSTCCCKHKGTYLNDGPGQDTDCRCESSGFTASENHLRHCLSC 60  
QY 25 VCPGKTIHPQNNSTCCCKHKGTYLNDGPGQDTDCRCESSGFTASENHLRHCLSC 84  
Db 61 SKCRKEMQVEISSCTVDRTVCGCRKNQRYHYSSENTFOCFNCSLCINGTYHLSQCKEQ 120  
QY 85 SKCRKEMQVEISSCTVDRTVCGCRKNQRYHYSSENTFOCFNCSLCINGTYHLSQCKEQ 144  
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RESULT 11  
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AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 50, Application US/08050319B.  
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CC Sequence 50, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan

CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbings  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbings, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 50:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 157 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 157 AA; 17570 MW; 122247 CN;  
SQ  
Query Match 34.2%; Score 800; DB 7; Length 157;  
Best Local Similarity 96.2%; Pred. No. 2.36e-61;  
Matches 102; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Db 36 DREKRECSGFTASENHLRHCLSCSKCRKEMQVEISSCTVDRTVCGCRKNQRYHYS 95  
QY 60 DTRCECSGFTASENHLRHCLSCSKCRKEMQVEISSCTVDRTVCGCRKNQRYHYS 119  
Db 96 ENLFOCFNCSLCINGTYHLSQCKEQNTVCTCHAGFFLRENCVCS 141  
QY 120 ENLFOCFNCSLCINGTYHLSQCKEQNTVCTCHAGFFLRENCVCS 165  
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ID US-08-425-673-9 STANDARD; PRT; 114 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 9, Application US/08425673.  
CC  
CC Sequence 9, Application US/08425673  
CC Patent No. 5508261  
CC GENERAL INFORMATION:  
CC APPLICANT: Moyle, William R.  
CC APPLICANT: Campbell, Robert K.  
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
CC TITLE OF INVENTION: Methods for Preparing and Using Same  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Richard R. Muccino  
CC STREET: P.O. Box 1267  
CC CITY: Princeton  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 08551  
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/425,673  
CC FILING DATE:  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/717,151  
CC FILING DATE: 18-JUN-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Muccino, Richard R.  
CC REGISTRATION NUMBER: 32,538  
CC REFERENCE/DOCKET NUMBER: DMD 1.0-004  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (609) 466-3407  
CC TELEFAX: (609) 466-2760  
CC INFORMATION FOR SEQ ID NO: 9:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 114 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
SQ SEQUENCE 114 AA; 12250 MW; 68564 CN;  
  
Query Match 31.6%; Score 740; DB 6; Length 114;  
Best Local Similarity 93.3%; Pred. No. 7.01e-56;  
Matches 97; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
  
Db 7 PRCPINATLAVEKEGCPVCITVNTICAGYCPMTVRVLOGVLPALPQVVCNRYDFEES 66  
169 PRCPINATLAVEKEGCPVCITVNTICAGYCPMTVRVLOGVLPALPQVVCNRYDFEES 228  
QY 67 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTC 110  
QY 229 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTC 272  
  
RESULT 13  
ID US-08-425-673-7 STANDARD; PRT: 114 AA.  
XX xxxxxx  
DT 01-JAN-1900  
DE Sequence 7, Application US/08425673.  
XX  
CC Sequence 7, Application US/08425673  
CC Patent No. 5508261  
CC GENERAL INFORMATION:  
CC APPLICANT: Moyle, William R.  
CC APPLICANT: Campbell, Robert K.  
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
CC TITLE OF INVENTION: Methods For Preparing and Using Same  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Richard R. Muccino  
CC STREET: P.O. Box 1267  
CC CITY: Princeton  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 08551  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/425,673

CC FILING DATE:  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/717,151  
CC FILING DATE: 18-JUN-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Muccino, Richard R.  
CC REGISTRATION NUMBER: 32,538  
CC REFERENCE/DOCKET NUMBER: DMD 1.0-004  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (609) 466-3407  
CC TELEFAX: (609) 466-2760  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 114 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
SQ SEQUENCE 114 AA; 12401 MW; 67071 CN;  
  
Query Match 31.4%; Score 734; DB 6; Length 114;  
Best Local Similarity 91.7%; Pred. No. 2.47e-55;  
Matches 99; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
Db 7 PRCPINATLAVEKEGCPVCITVNTICAGYCPMTVRVLOGVLPALPQVVCNRYDFEES 66  
169 PRCPINATLAVEKEGCPVCITVNTICAGYCPMTVRVLOGVLPALPQVVCNRYDFEES 228  
QY 67 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTC 114  
QY 229 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDCGGPKDHPPLTC 276  
  
RESULT 14  
ID US-08-425-673-11 STANDARD; PRT: 117 AA.  
XX xxxxxx  
DT 01-JAN-1900  
DE Sequence 11, Application US/08425673.  
XX  
CC Sequence 11, Application US/08425673  
CC Patent No. 5508261  
CC GENERAL INFORMATION:  
CC APPLICANT: Moyle, William R.  
CC APPLICANT: Campbell, Robert K.  
CC TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
CC TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
CC TITLE OF INVENTION: Methods For Preparing and Using Same  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Richard R. Muccino  
CC STREET: P.O. Box 1267  
CC CITY: Princeton  
CC STATE: New Jersey  
CC COUNTRY: USA  
CC ZIP: 08551  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/425,673  
CC FILING DATE:  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/717,151  
CC FILING DATE: 18-JUN-1991  
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Muccino, Richard R.  
CC REGISTRATION NUMBER: 32,538  
CC REFERENCE/DOCKET NUMBER: UMD 1.0-004  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (609) 466-3407  
CC TELEFAX: (609) 466-2760  
CC INFORMATION FOR SEQ ID NO: 11:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 117 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC HYPOTHEICAL: NO  
CC ANTI-SENSE: NO  
SQ SEQUENCE 117 AA; 12890 MW; 72412 CN;  
  
Query Match 30.5%; Score 714; DB 6; Length 117;  
Best Local Similarity 98.9%; Pred. No. 1.63e-53;  
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Db 7 PROCRINATLAVEKGCPCVCTIVNTTICAGCPTMTRYLGVLPAIPQVVCNRYDRVRES 66  
OY 169 PROCRINATLAVEKGCPCVCTIVNTTICAGCPTMTRYLGVLPAIPQVVCNRYDRVRES 228  
DB 67 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDC 100  
OY 229 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDC 262  
  
RESULT 15  
ID US-08-425-673-8 STANDARD; PRT; 114 AA.  
AC xxxxxx  
XX 01-JAN-1900  
DE Sequence 8, Application US/08425673.  
XX Sequence 8, Application US/08425673  
XX Patent No. 5508261  
XX GENERAL INFORMATION:  
XX APPLICANT: Moyie, William R.  
XX TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having  
XX TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and  
XX TITLE OF INVENTION: Methods for Preparing and Using Same  
XX NUMBER OF SEQUENCES: 12  
XX CORRESPONDENCE ADDRESS:  
XX ADDRESSEE: Richard R. Muccino  
XX STREET: P.O. Box 1267  
XX CITY: Princeton  
XX STATE: New Jersey  
XX COUNTRY: USA  
XX ZIP: 08551  
XX COMPUTER READABLE FORM:  
XX MEDIUM TYPE: Floppy disk  
XX COMPUTER: IBM PC compatible  
XX OPERATING SYSTEM: PC-DOS/MS-DOS  
XX SOFTWARE: PatentIn Release #1.0, Version #1.25  
XX CURRENT APPLICATION DATA:  
XX APPLICATION NUMBER: US/08/425,673  
XX FILING DATE:  
XX CLASSIFICATION: 514  
XX PRIOR APPLICATION DATA:  
XX APPLICATION NUMBER: US 07/717,151  
XX FILING DATE: 18-JUN-1991  
XX ATTORNEY/AGENT INFORMATION:  
XX NAME: Muccino, Richard R.  
XX REGISTRATION NUMBER: 32,538  
XX REFERENCE/DOCKET NUMBER: UMD 1.0-004  
XX TELECOMMUNICATION INFORMATION:  
XX TELEPHONE: (609) 466-3407  
XX TELEFAX: (609) 466-2760

CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 114 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: peptide  
CC HYPOTHEICAL: NO  
CC ANTI-SENSE: NO  
SQ SEQUENCE 114 AA; 12242 MW; 69571 CN;  
  
Query Match 29.2%; Score 684; DB 6; Length 114;  
Best Local Similarity 94.7%; Pred. No. 8.72e-51;  
Matches 89; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
Db 7 PROCRINATLAVEKGCPCVCTIVNTTICAGCPTMTRYLGVLPAIPQVVCNRYDRVRES 66  
OY 169 PROCRINATLAVEKGCPCVCTIVNTTICAGCPTMTRYLGVLPAIPQVVCNRYDRVRES 228  
DB 67 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDC 100  
OY 229 IRLPGCPRGVNPVSYAVALSQCQALCRSTTDC 262  
  
Search completed: Wed May 6 08:21:12 1998  
Job time : 13 secs.

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Mpsrch_un n.a. - n.a. database search, using Smith-Waterman algorithm

Run on:      Wed May 6 10:28:56 1998;  MasPar time 67.26 Seconds
              941.976 Million cell updates/sec

Tabular output not generated.

Title:
Description:  >US-08-804-166-3
               (1-1202) from US08804166.seq
Perfect Score: 1202

N.A. Sequence:
Comp:         1 CTCGAGANGGCTACAGGTA.....CCCGATCTCTCCCAATTA 1202
               GAGCTTACCGATGTCATT.....GGGGCTAGGAGGGTGTATT

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Nmatch STD : Dbase 0; Query 0

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Post-processing: Minimum Match 0%
                  Listing first 45 summaries
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-Issued  
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:PC190  
10:PC191 11:PC192 12:PC193 13:PC194 14:PC195 15:PC196

**Pred.** No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	424	35.3	2062	7	US-08-021-	Sequence 24, Applicati	0.00e+00
2	424	35.3	2175	7	US-08-021-	Sequence 1, Applicatio	0.00e+00
3	424	35.3	6889	6	US-08-286-	Sequence 2, Applicatio	0.00e+00
4	424	35.3	6889	14	PCT-US55-0	Sequence 4, Applicatio	0.00e+00
5	420	34.9	600	7	US-08-050-	Sequence 4, Applicatio	0.00e+00
6	381	31.7	504	7	US-08-050-	Sequence 56, Applicati	6.08e-27
7	379	31.5	501	7	US-08-050-	Sequence 1, Applicatio	2.43e-27
8	370	30.8	372	7	US-08-050-	Sequence 3, Applicatio	3.96e-16
9	302	25.0	2771	7	US-08-073-	Sequence 5, Applicatio	8.84e-21
10	301	25.0	474	7	US-08-050-	Sequence 49, Applicati	3.47e-21
11	301	25.0	4283	7	US-08-343-	Sequence 1, Applicatio	5.54e-21
12	301	25.0	4283	7	US-08-445-	Sequence 3, Applicatio	5.54e-21
13	255	21.2	477	7	US-08-050-	Sequence 1, Applicatio	5.54e-21
14	169	14.1	462	7	US-08-050-	Sequence 53, Applicati	2.07e-17
15	103	8.6	138	5	US-08-086-	Sequence 51, Applicati	1.03e-10
16	99	8.2	138	5	US-08-086-	Sequence 2, Applicatio	5.77e-57
17	88	7.3	7218	7	US-08-232-	Sequence 1, Applicatio	5.92e-54
18	69	5.7	534	6	US-08-187-	Sequence 14, Applicati	9.89e-46
19	69	5.7	654	6	US-08-187-	Sequence 3, Applicatio	8.57e-32
						Sequence 1, Applicatio	8.57e-32

## ALIGNMENTS

AC XXXXXXX

DT 01-JAN-1900

DE Sequence 24, Application US/08050319B

CC Sequence 24, Application US/08050319B

CC GENERAL INFORMATION:

CC APPLICANT: M.J.C. Turner, F.M Brennan  
CC WITH AN INTERVIEW: 04/04/2014

CC	TITLE OF INVENTION: Necrosis Factor alpha) Receptor
CC	NUMBER OF SENTENCES: 57

CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Beed & Bohhine

STREET: 635 Bryant Street  
CITY: Palo Alto

CC STATE: CALIF  
CC COUNTRY: USA

CC ZIP: 94501  
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk  
CC COMPUTER: IBM PC compatible

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CC SOFTWARE: PatentIn Release #1.0, version #1.25
CC OFFENDING SYSTEM: FC-DOS/MS-DOS
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APPLICATION NUMBER: US/08/050,319E

CC CLASSIFICATION: 435

CC NAME: Robbins, Roberta L.  
CC  
CC

CC REFERENCE/DOCKET NUMBER: 5150-0030

CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231

CC INFORMATION FOR SEQ ID NO: 24:  
CC SEQUENCE CHARACTERISTICS:

[illegible]

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CC      ZIP: 20004
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.30
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/321,668
CC      FILING DATE: 12-OCT-1994
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: IL 107268
CC      FILING DATE: 12-OCT-1993
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: BROWDY, ROGER L.
CC      REGISTRATION NUMBER: 25,618
CC      REFERENCE/DOCKET NUMBER: WALLACH-13
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 202-628-5197
CC      TELEFAX: 202-737-3528
CC      TELEX: 248633
CC      INFORMATION FOR SEQ ID NO: 1:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 2175 base pairs
CC      TYPE: nucleic acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: cDNA
CC      FEATURE:
CC      NAME/KEY: CDS
CC      LOCATION: 256..1620
CC      Sequence 2175 BP; 474 A; 641 C; 604 G; 456 T; 0 other;
SQ
Query Match 35.3%; Score 424; DB 7; Length 2175;
Matches 423; Conservatve 99.8%; Pred. No. 0.00e+00; Mismatches 1; Indels 0; Gaps 0
Db 376 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATATATGATTTGCTGTACC 435
Qy 345 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATATATGATTTGCTGTACC 404
Db 436 AAGTGCACAAAGAACCTACTGTACATGACTGTCCAGGCCCGGGGACAGATACGGAC 495
Qy 405 AAGTGCACAAAGAACCTACTGTACATGACTGTCCAGGCCCGGGGACAGATACGGAC 464
Db 496 TGCAGGGAGTGTGAGAGGGGCTCCTTCACCCCTTCAGAAAACCACTCAGACATGCTC 555
Qy 465 TGCAGGGAGTGTGAGAGGGGCTCCTTCACCCCTTCAGAAAACCACTCAGACATGCTC 524
Db 556 AGCTGCTCCAATATGCCGAAGAAAGAAATGGATGAGATCTCTTTTGACAGTGGAC 615
Qy 525 AGCTGCTCCAATATGCCGAAGAAAGAAATGGATGAGATCTCTTTTGACAGTGGAC 584
Db 616 CGGGACACCGTGTGTGCTGCAGGAAGAACCACTACCGGGCATTTATGGAGTGAACCTT 675
Qy 585 CGGGACACCGTGTGTGCTGCAGGAAGAACCACTACCGGGCATTTATGGAGTGAACCTT 644
Db 676 TTCCAGTCTCTCAATATGAGGCTCTGCTCTCAATGGAGACCGTGCACCTCTCTGCGACGAG 735
Qy 645 TTCCAGTCTCTCAATATGAGGCTCTGCTCTCAATGGAGACCGTGCACCTCTCTGCGACGAG 704
Db 736 AAACGACACACCGTGTGACCTGCGATGCGATGCTTTCTTTCAAGAGAAAAGAGTGTGTC 795
Qy 705 AAACGACACACCGTGTGACCTGCGATGCGATGCTTTCTTTCAAGAGAAAAGAGTGTGTC 764
Db 796 TCCTGT 801
Qy 765 TCCTGT 770

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XX AC xxxxxx  
XX DT 01-JAN-1900  
DE Sequence 2, Application US/08286740.  
XX Sequence 2, Application US/08286740  
CC Patent No. 5561053  
CC GENERAL INFORMATION:  
CC APPLICANT: Crowley, Craig W.  
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING  
CC TITLE OF INVENTION: HOST CELLS  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Genentech, Inc.  
CC STREET: 460 Point San Bruno Blvd  
CC CITY: South San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94080  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: patin (Genentech)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/286,740  
CC FILING DATE: 05-AUG-1994  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lee, Wendy M.  
CC REGISTRATION NUMBER:  
CC REFERENCE/DOCKET NUMBER: 798  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-1994  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6889 bases  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC Sequence 6889 BP; 1826 C; 1681 G; 1653 T; 0 other;  
SQ  
Query Match 35.3%; Score 424; DB 6; Length 6889;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
DB 1725 GATAGTGTGTGTCCTCCCAAGAAATATATATCCACCTCAAAATATTGATTTGCTGTACC 1784  
OY 345 GATAGTGTGTGTCCTCCCAAGAAATATATATCCACCTCAAAATATTGATTTGCTGTACC 404  
DB 1785 AAGTCCACAAAGAAAGAACTACTGTACATGACTGTCCAGGCCGGGGGAGATACGGAC 1844  
OY 405 AAGTCCACAAAGAAAGAACTACTGTACATGACTGTCCAGGCCGGGGGAGATACGGAC 464  
DB 1845 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC 1904  
OY 465 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC 524  
DB 1905 AGCTGCTCCAAATGCCGAAGAAATGGGTGAGTGGAGATCTCTCTTCCAGATGGAC 1964  
OY 525 AGCTGCTCCAAATGCCGAAGAAATGGGTGAGTGGAGATCTCTCTTCCAGATGGAC 584  
DB 1965 CGGAGACCGGTGTGTGCTGTCAGAGAAACCACTACCGGATTTATTTGAGTGAACCTT 2024  
OY 585 CGGAGACCGGTGTGTGCTGTCAGAGAAACCACTACCGGATTTATTTGAGTGAACCTT 644

DB 2025 TTCACGTCTTCATTCAGACCTCTGCTCAATGGAGCCGTGCACCTCTCTCCAGAG 2084  
OY 645 TTCACGTCTTCATTCAGACCTCTGCTCAATGGAGCCGTGCACCTCTCTCCAGAG 704  
DB 2085 AACAGACACCGGTGTGACCTGTCATGAGGTTTCTTTCTAAGAGAAAAGAGTGTGC 2144  
OY 705 AACAGACACCGGTGTGACCTGTCATGAGGTTTCTTTCTAAGAGAAAAGAGTGTGC 764  
DB 2145 TCCTGT 2150  
OY 765 TCCTGT 770  
RESULT 4  
ID PCT-US95-09576-2 STANDARD; DNA; UNC; 6889 BP.  
XX AC xxxxxx  
XX DT 01-JAN-1900  
DE Sequence 2, Application PC/TUS9509576.  
XX Sequence 2, Application PC/TUS9509576  
CC GENERAL INFORMATION:  
CC APPLICANT: GENENTECH, INC.  
CC TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING  
CC TITLE OF INVENTION: HOST CELLS  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Genentech, Inc.  
CC STREET: 460 Point San Bruno Blvd  
CC CITY: South San Francisco  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94080  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: patin (Genentech)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/09576  
CC FILING DATE:  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/286740  
CC FILING DATE: 05-AUG-1994  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lee, Wendy M.  
CC REGISTRATION NUMBER: 00,000  
CC REFERENCE/DOCKET NUMBER: 798PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-1994  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 6889 bases  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC Sequence 6889 BP; 1729 A; 1826 C; 1681 G; 1653 T; 0 other;  
SQ  
Query Match 35.3%; Score 424; DB 14; Length 6889;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
DB 1725 GATAGTGTGTGTCCTCCCAAGAAATATATATCCACCTCAAAATATTGATTTGCTGTACC 1784  
OY 345 GATAGTGTGTGTCCTCCCAAGAAATATATATCCACCTCAAAATATTGATTTGCTGTACC 404  
DB 1785 AAGTCCACAAAGAAAGAACTACTGTACATGACTGTCCAGGCCGGGGGAGATACGGAC 1844

|||||  
QY 405 AAGGCCAAGAGGACCTACTTGTACATGCTCCAGCCCGGGCAGGATACGGAC 464  
DB 1845 TGCAGGAGTGTGAGAGGGCTCTTCCAGCCTTCAGAAAACCACTCAGACTGCCTC 1904  
QY 465 TGCAGGAGTGTGAGAGGGCTCTTCCAGCCTTCAGAAAACCACTCAGACTGCCTC 524  
DB 1905 AGCTGCTCAAAATGCCGAAAGAAATGGGTGAGTGCAGATCTCTTTCAGACAGTGCAC 1964  
QY 525 AGCTGCTCAAAATGCCGAAAGAAATGGGTGAGTGCAGATCTCTTTCAGACAGTGCAC 584  
DB 1965 CGGACACCCGTGTGTGCTGAGAGAAAGACAGTACCGGCACTTATTTGAGAGTGAACCTT 2024  
QY 585 CGGACACCCGTGTGTGCTGAGAGAAAGACAGTACCGGCACTTATTTGAGAGTGAACCTT 644  
DB 2025 TTCCAGTCTCAATTCGACGCTCTGCCTCAATGGAGACCGTGCACCTCTCCGACAGAG 2084  
QY 645 TTCCAGTCTCAATTCGACGCTCTGCCTCAATGGAGACCGTGCACCTCTCCGACAGAG 704  
DB 2085 AAACGAAACACCGTGTGACACTGCATGACAGTTCTTTCTTAAGAGAAACGAGTGTGTC 2144  
QY 705 AAACGAAACACCGTGTGACACTGCATGACAGTTCTTTCTTAAGAGAAACGAGTGTGTC 764  
DB 2145 TCCCTGT 2150  
QY 765 TCCCTGT 770

RESULT 5  
ID US-08-050-319B-47 STANDARD; DNA; UNC; 600 BP.

XXXXXX  
AC 01-JAN-1900  
DE Sequence 47, Application US/08050319B.  
XX Sequence 47, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robblins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: IBM PC compatible  
CC SOFTWARE: PC-DOS/MS-DOS  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robblins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC TELEPHONE: (415) 617-8999  
CC TELECOMMUNICATION INFORMATION:  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 47:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 600 base pairs  
CC TYPE: nucleic acid

CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..597  
SQ Sequence 600 BP; 148 A; 157 C; 162 G; 133 T; 0 other;  
Query Match 34.9%; Score 420; DB 7; Length 600;  
Best Local Similarity 99.3%; Pred. No. 0.00e+00;  
Matches 423; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 121 GATAGTGTGTGCCACAGGAAATATATCCACCCTCAAAATAATGATTTGCTGTAC 180  
QY 345 GATAGTGTGTGCCACAGGAAATATATCCACCCTCAAAATAATGATTTGCTGTAC 404  
DB 181 AAGTCCCAAGAGAACCTACTTGTACATGACTGTGCAAGCCCGGGGAGATACGGAC 240  
QY 405 AAGTCCCAAGAGAACCTACTTGTACATGACTGTGCAAGCCCGGGGAGATACGGAC 464  
DB 241 TGCAGGAGTGTGAGAGGGGCTCTTCACGCTTCAGAAAACCACTCAGACTGCCTC 300  
QY 465 TGCAGGAGTGTGAGAGGGGCTCTTCACGCTTCAGAAAACCACTCAGACTGCCTC 524  
DB 301 AGCTGCTCAAAATGCCGAAAGAAATGGGTGAGTGCATCTCTTTCGACAGTGCAC 360  
QY 525 AGCTGCTCAAAATGCCGAAAGAAATGGGTGAGTGCATCTCTTTCGACAGTGCAC 584  
DB 361 CGGACACCCGTGTGTGCTGAGAGAAAGACAGTACCGGCACTTATTTGAGTGAACCTT 420  
QY 585 CGGACACCCGTGTGTGCTGAGAGAAAGACAGTACCGGCACTTATTTGAGTGAACCTT 644  
DB 421 TTCCAGTCTCAATTCGACGCTCTGCCTCAATGGAGACCGTGCACCTCTCCGACAGAG 480  
QY 645 TTCCAGTCTCAATTCGACGCTCTGCCTCAATGGAGACCGTGCACCTCTCCGACAGAG 704  
DB 481 AAACGAAACACCGTGTGACACTGCATGACAGTTCTTTCTTAAGAGAAACGAGTGTGTC 540  
QY 705 AAACGAAACACCGTGTGACACTGCATGACAGTTCTTTCTTAAGAGAAACGAGTGTGTC 764  
DB 541 TCCCTGT 546  
QY 765 TCCCTGT 770

RESULT 6  
ID US-08-050-319B-56 STANDARD; DNA; UNC; 504 BP.

XXXXXX  
AC 01-JAN-1900  
DE Sequence 56, Application US/08050319B.  
XX Sequence 56, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M.Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robblins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible



CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,3198  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 56:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 504 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..501  
CC Sequence 504 BP, 122 A, 137 C, 138 G, 107 T, 0 other;  
SQ  
  
Query Match 31.7%; Score 381; DB 7; Length 504;  
Best Local Similarity 99.7%; Pred. No. 6,06e-276;  
Matches 382; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Db 121 GATAGTGTGTCCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 180  
|||  
Qy 345 GATAGTGTGTGTCCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 404  
|||  
Db 181 AAGTGCCACAAGAACTTACTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 240  
|||  
Qy 405 AAGTGCCACAAGAACTTACTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 464  
|||  
Db 241 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAAGAAAACCACTAGACACTGCTC 300  
|||  
Qy 465 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAAGAAAACCACTAGACACTGCTC 524  
|||  
Db 301 AGCTGCTCCAATGCGGAAGAAATGGGTGAGTGAATCTCTTGCACAGTGGAC 360  
|||  
Qy 525 AGCTGCTCCAATGCGGAAGAAATGGGTGAGTGAATCTCTTGCACAGTGGAC 584  
|||  
Db 585 CGGACACCGTGTGTGCTGCGAAGAACAGTACCGGCATTATTGGAGTGAACCTT 644  
|||  
Qy 421 TTCCAGTCTTCAATTCGACGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 480  
|||  
Qy 645 TTCCAGTCTTCAATTCGACGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 704  
|||  
Db 481 AAACGAAACCGGTGTGCACCTG 503  
|||  
Qy 705 AAACGAAACCGGTGTGCACCTG 727  
|||  
  
RESULT 7  
ID US-08-050-319B-1 STANDARD; DNA; UNC; 501 BP.  
  
XX xxxxxx  
XX 01-JAN-1900  
XX  
XX  
XX Sequence 1, Application US/08050319B.  
CC Sequence 1, Application US/08050319B  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M Brennan

CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUCLEOTIDE SEQUENCE: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,3198  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 501 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..501  
CC Sequence 501 BP, 121 A, 137 C, 137 G, 106 T, 0 other;  
SQ  
  
Query Match 31.5%; Score 379; DB 7; Length 501;  
Best Local Similarity 99.7%; Pred. No. 2,43e-274;  
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Db 121 GATAGTGTGTCCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 180  
|||  
Qy 345 GATAGTGTGTGTCCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 404  
|||  
Db 181 AAGTGCCACAAGAACTTACTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 240  
|||  
Qy 405 AAGTGCCACAAGAACTTACTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 464  
|||  
Db 241 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAAGAAAACCACTAGACACTGCTC 300  
|||  
Qy 465 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAAGAAAACCACTAGACACTGCTC 524  
|||  
Db 301 AGCTGCTCCAATGCGGAAGAAATGGGTGAGTGAATCTCTTGCACAGTGGAC 360  
|||  
Qy 525 AGCTGCTCCAATGCGGAAGAAATGGGTGAGTGAATCTCTTGCACAGTGGAC 584  
|||  
Db 585 CGGACACCGTGTGTGCTGCGAAGAACAGTACCGGCATTATTGGAGTGAACCTT 644  
|||  
Qy 421 TTCCAGTCTTCAATTCGACGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 480  
|||  
Qy 645 TTCCAGTCTTCAATTCGACGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 704  
|||  
Db 481 AAACGAAACCGGTGTGCACCTG 501  
|||  
Qy 705 AAACGAAACCGGTGTGCACCTG 725  
|||  
  
RESULT 8  
ID US-08-050-319B-3 STANDARD; DNA; UNC; 372 BP.

XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 3, Application US/08050319B.  
XX  
CC Sequence 3, Application US/08050319B.  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M.Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Reed & Robblins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robblins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 372 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..372  
CC Sequence 372 BP; 98 A; 102 C; 95 G; 77 T; 0 other;  
SQ  
Query Match 30.8%; Score 370; DB 7; Length 372;  
Best Local Similarity 99.7%; Pred. No. 3,966-267;  
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 GTGTGTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACCAAGTGC 60  
GTT  
QY 351 GTGTGTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACCAAGTGC 410  
GTT  
Db 61 CACAAAGGAACCTACTTGTGCATGACTGTCCAGGCCGGGGCAGATACGAGTGCAGG 120  
TT  
QY 411 CACAAAGGAACCTACTTGTGCATGACTGTCCAGGCCGGGGCAGATACGAGTGCAGG 470  
TT  
Db 121 GAGTGTGAGAGGGCTCTTCCACCGCTTCAGAAACCACTCAGACCTCCCTCAGTGC 180  
TT  
QY 471 GAGTGTGAGAGGGCTCTTCCACCGCTTCAGAAACCACTCAGACCTCCCTCAGTGC 530  
TT  
Db 181 TCCAAATGCCGAAGGAATGGGTGAGTGGAGATCTCTTTGCAAGTGGACCGGGAC 240  
TT  
QY 531 TCCAAATGCCGAAGGAATGGGTGAGTGGAGATCTCTTTGCAAGTGGACCGGGAC 590  
TT  
Db 241 ACCGTGTGTGCTGCAGGAAGAACCACTACCGCATTTATGAGTGAACCTTTTCAG 300  
TT

QY 591 ACCGTGTGTGCTGCAGGAAGAACCACTACCGCATTTATGAGTGAACCTTTTCAG 650  
TT  
Db 301 TGCTCAATTGACAGCCTCTGCTCATGAGACCGTGCACCTCTCTGCGAGGAACAG 360  
TT  
QY 651 TGCTCAATTGACAGCCTCTGCTCATGAGACCGTGCACCTCTCTGCGAGGAACAG 710  
TT  
Db 361 AACACCGTGTGC 372  
TT  
QY 711 AACACCGTGTGC 722  
TT  
RESULT 9  
ID US-08-273-411-5 STANDARD; DNA; UNC; 2771 BP.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 5, Application US/08273411.  
XX  
CC Sequence 5, Application US/08273411.  
CC Patent No. 5625124  
CC GENERAL INFORMATION:  
CC APPLICANT: Falk, Per  
CC APPLICANT: Gordon, Jeffrey I.  
CC TITLE OF INVENTION: Animal Model for Gastro-Intestinal  
CC NUMBER OF SEQUENCES: 10  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Patrea L. Pabst  
CC STREET: 1100 Peachtree Street, Suite 2800  
CC CITY: Atlanta  
CC STATE: Georgia  
CC COUNTRY: USA  
CC ZIP: 30309-4530  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/273,411  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Pabst, Patrea L.  
CC REGISTRATION NUMBER: 31,284  
CC REFERENCE/DOCKET NUMBER: WU106  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (404) 815-6508  
CC TELEFAX: (404) 815-6555  
CC INFORMATION FOR SEQ ID NO: 5:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2771 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Sweetser, et al.  
CC JOURNAL: Genes & Dev.  
CC VOLUME: 2  
CC PAGES: 1318-1332  
CC DATE: 1988  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 561 TO 629  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Seeburg, et al.  
CC JOURNAL: DNA  
CC VOLUME: 1  
CC PAGES: 239-249

CC DATE: 1982  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 620 TO 2771  
CC PUBLICATION INFORMATION:  
CC AUTHORS: Sweetser, et al.  
CC JOURNAL: J. Biol. Chem.  
CC VOLUME: 261  
CC PAGES: 5553-5561  
CC DATE: 1986  
CC RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 617  
CC Sequence 2771 BP: 666 A; 718 C; 704 G; 683 T; 0 other;  
SQ  
Query Match 25.1%; Score 302; DB 7; Length 2771;  
Best Local Similarity 97.6%; Pred. No. 8.84e-213;  
Matches 330; Conservative 0; Mismatches 4; Indels 4; Gaps 2;  
DB 680 ATGGCTACAGGTAAGGCGCCCTAAATCCCTTTGGCAGCAATGTCTGTGAGGGAGAG 739  
OY 7 ATGGCTACAGGTAAGGCGCCCTAAATCCCTTTGGCAGCAATGTCTGTGAGGGAGAG 66  
DB 740 CAGCGACCTGTAGATGGAGGGGGGACCTAACCCCTGAGTTGGGCTTGAATG--AG 797  
OY 67 TAGCGACCTGTAGATGGAGGGGGGACCTAACCCCTGAGTTGGGCTTGAATGTAG 126  
DB 798 TATCGCATGTAGAGCCAGTAT--GGCAGATCTCAGAAAGCTCGCTCCCTGAGAGAT 855  
OY 127 TATCGCATGTAGAGCCAGTATTTGGCAGATGTCAAAAGCTCTGCTCCCTGAGAGAT 186  
DB 856 GAGAGAGAAAAACAACAGCTCTCTGAGCAGGAGAGAGTGTCTGCTCTCTCCGCG 915  
OY 187 GAGAGAGAAAAACAACAGCTCTCTGAGCAGGAGAGAGTGTCTGCTCTCTCCGCG 246  
DB 916 TCCCTGTGTGCTCTGCT 975  
OY 247 TCCCTGTGTGCTCTGCT 306  
DB 976 GCCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 1013  
OY 307 GCCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 344  
RESULT 10  
ID US-08-050-319B-49 STANDARD; DNA; UNC; 474 BP.  
XX xxxxxx  
AC 01-JAN-1900  
DT  
XX  
DE Sequence 49, Application US/08050319B.  
XX  
CC Sequence 49, Application US/08050319B.  
CC Patent No. 5633145  
CC GENERAL INFORMATION:  
CC APPLICANT: M. Feldmann, P.W. Gray,  
CC APPLICANT: M.J.C. Turner, F.M. Brennan  
CC TITLE OF INVENTION: Modified human TNFalpha (Tumor  
CC TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
CC NUMBER OF SEQUENCES: 57  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Reed & Robbins  
CC STREET: 635 Bryant Street  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94301  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/050,319B  
CC FILING DATE: 10-May-1993

CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Robbins, Roberta L.  
CC REGISTRATION NUMBER: 33,208  
CC REFERENCE/DOCKET NUMBER: 5150-0030  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 617-8999  
CC TELEFAX: (415) 327-3231  
CC INFORMATION FOR SEQ ID NO: 49:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 474 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: CDNA to mRNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 1..471  
SQ Sequence 474 BP; 110 A; 126 C; 132 G; 106 T; 0 other;  
Query Match 25.0%; Score 300; DB 7; Length 474;  
Best Local Similarity 97.5%; Pred. No. 3.47e-211;  
Matches 308; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
DB 105 GAGACAGGAGAGAGAGAGTGTGAGAGCGGCTCTCACCCTTCAGAAACCACTCAG 164  
OY 455 GGATACGAGCTCAGAGGAGTGTGAGAGCGGCTCTCACCCTTCAGAAACCACTCAG 514  
DB 165 ACACCTGCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTCTTG 224  
OY 515 ACACCTGCTCAGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTCTTG 574  
DB 225 CACAGTGAACCGGAGACCGTGTGTGCTGTCAGAGAAACAGTACCGCATTTATGGAG 284  
OY 575 CACAGTGAACCGGAGACCGTGTGTGCTGTCAGAGAAACAGTACCGCATTTATGGAG 634  
DB 285 TGAAACCTTTTCAGTGTGTTCAATGTCAGCGCTGCTCAATGGAGCGTCACTCTC 344  
OY 635 TGAAACCTTTTCAGTGTGTTCAATGTCAGCGCTGCTCAATGGAGCGTCACTCTC 694  
DB 345 CTGCGAGAGAAACAGAACCGGTGTGTCACCTGTCAGAGGTTCTTTCTAAGAGAAA 404  
OY 695 CTGCGAGAGAAACAGAACCGGTGTGTCACCTGTCAGAGGTTCTTTCTAAGAGAAA 754  
DB 405 CGAGTGTGTCTCTGT 420  
OY 755 CGAGTGTGTCTCTGT 770  
RESULT 11  
ID US-08-343-401A-3 STANDARD; DNA; UNC; 4283 BP.  
XX xxxxxx  
AC 01-JAN-1900  
DT  
XX  
DE Sequence 3, Application US/08343401A.  
XX  
CC Sequence 3, Application US/08343401A.  
CC Patent No. 5661132  
CC GENERAL INFORMATION:  
CC APPLICANT: Swain, William F  
CC APPLICANT: Macklin, Michael D  
CC APPLICANT: Eriksson, Eiof  
CC APPLICANT: Andree, Christophe  
CC TITLE OF INVENTION: Improved Wound Healing  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESSES:  
CC ADDRESSEE: Quarles & Brady  
CC STREET: PO Box 2113  
CC CITY: Madison  
CC STATE: WI

CC COUNTRY: USA  
CC ZIP: 53701-2113  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/343,401A  
CC FILING DATE: 22-NOV-1994  
CC CLASSIFICATION: 514  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Seay, Nicholas J  
CC REGISTRATION NUMBER: 27,386  
CC REFERENCE/DOCKET NUMBER: 11-229-9103-9  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 608-251-5000  
CC TELEFAX: 608-251-9166  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 4283 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: circular  
CC MOLECULE TYPE: DNA (genomic)  
CC IMMEDIATE SOURCE:  
CC CLONE: PMRG1630  
CC FEATURE:  
CC NAME/KEY: exon  
CC LOCATION: 713..721  
CC FEATURE:  
CC NAME/KEY: exon  
CC LOCATION: 981..1253  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: join(713..721, 981..1253)  
CC NAME/KEY: sig\_peptide  
CC LOCATION: 713..1049  
CC SEQUENCE: 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;  
SQ Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;  
  
Query Match 25.0%; Score 301; DB 7; Length 4283;  
Best Local Similarity 95.3%; Pred. No. 5.54e-212;  
Matches 322; Conservative 0; Mismatches 15; Indels 1; Gaps 1;  
  
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QY 7 ATGCTACAGTAAAGCGCCCTAAATCCCTTGGCGCACATGTCTCTGAGGGAGAG 66  
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Db 772 CAGCGACCTAGATGGAGCGGGGCACTAACCTCAGAGTTGGGCTTGAATGTAG 831  
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QY 67 TAGGACCTAGATAGGAGCGGGGCACTAACCTCAGAGTTGGGCTTGAATGTAG 126  
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Db 832 TATGCCATCTAAAGCCCGATTTGGCCATCTCAGAAAGCTCCTGCTCCCTGGAGAT 891  
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QY 127 TATGCCATCTAAAGCCCGATTTGGCCATCTCAGAAAGCTCCTGCTCCCTGGAGAT 186  
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Db 892 GGAGAGAAAAAACAAGAGCTCCTGGAGCAGGAGAGTGTGGCTCTTCTCCGGC 951  
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QY 187 GGAGAGAAAAAACAAGAGCTCCTGGAGCAGGAGAGTGTGGCTCTTCTCCGGC 246  
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QY 247 TCCCTCTGTGCTGTGTTCTCCCAAGGCTCCCGAGCTCCCTGCTCTGAGTTTG 306  
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Db 1012 GCCTGTCTGCTGCTGCTGCTTCAAGAGGCGATGCC 1049  
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QY 307 GCCTGTCTGCTGCTGCTGCTTCAAGAGGCGATGCC 344  
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ID US-08-445-265A-1 STANDARD; DNA; UNC; 4283 BP.

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AC xxxxxx  
XX 01-JAN-1900  
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XX  
DE Sequence 1, Application US/08445265A.  
XX  
CC Sequence 1, Application US/08445265A.  
CC Patent No. 5697901  
CC GENERAL INFORMATION:  
CC APPLICANT: Eriksen, Elof  
CC TITLE OF INVENTION: GENE DELIVERY BY MICRONEEDLE INJECTION  
CC NUMBER OF SEQUENCES: 4  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Quarles & Brady  
CC STREET: 1 South Pinckney Street  
CC CITY: Madison  
CC STATE: WI  
CC COUNTRY: US  
CC ZIP: 53703  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/445,265A  
CC FILING DATE:  
CC CLASSIFICATION: 604  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Seay, Nicholas J  
CC REGISTRATION NUMBER: 27386  
CC REFERENCE/DOCKET NUMBER: 110229,91080  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 608-251-5000  
CC TELEFAX: 608-251-9166  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 4283 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: circular  
CC MOLECULE TYPE: other nucleic acid  
CC DESCRIPTION: /desc = "plasmid DNA"  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: join(713..721, 981..1250)  
CC SEQUENCE: 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;  
SQ Sequence 4283 BP; 1023 A; 1095 C; 1114 G; 1051 T; 0 other;  
  
Query Match 25.0%; Score 301; DB 7; Length 4283;  
Best Local Similarity 95.3%; Pred. No. 5.54e-212;  
Matches 322; Conservative 0; Mismatches 15; Indels 1; Gaps 1;  
  
Db 713 ATGCTACAGTAAAGCGCCCTAAATCCCTTGG-CACAAATGTCTCTGAGGGAGAG 771  
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QY 7 ATGCTACAGTAAAGCGCCCTAAATCCCTTGGCGCACATGTCTCTGAGGGAGAG 66  
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Db 772 CAGCGACCTAGATGGAGCGGGGCACTAACCTCAGAGTTGGGCTTGAATGTAG 831  
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QY 67 TAGGACCTAGATAGGAGCGGGGCACTAACCTCAGAGTTGGGCTTGAATGTAG 126  
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Db 832 TATGCCATCTAAAGCCCGATTTGGCCATCTCAGAAAGCTCCTGCTCCCTGGAGAT 891  
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QY 127 TATGCCATCTAAAGCCCGATTTGGCCATCTCAGAAAGCTCCTGCTCCCTGGAGAT 186  
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Db 892 GGAGAGAAAAAACAAGAGCTCCTGGAGCAGGAGAGTGTGGCTCTTCTCCGGC 951  
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QY 187 GGAGAGAAAAAACAAGAGCTCCTGGAGCAGGAGAGTGTGGCTCTTCTCCGGC 246  
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Db 952 TCCCTCTGTGCTGTGTTCTCCCAAGGCTCCCGAGCTCCCTGCTCTGAGTTTG 1011  
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QY 247 TCCCTCTGTGCTGTGTTCTCCCAAGGCTCCCGAGCTCCCTGCTCTGAGTTTG 306  
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QY 662 CAGCCTGCTCAATGGAGACCGTCTCTCGCAGGAGAAACAGACCGGTGTG 721  
DB 360 CACCTGCCATCAGGTTCTTCTTAAGAGAAAACAGATGTCTCTGT 408  
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QY 722 CACCTGCCATCAGGTTCTTCTTAAGAGAAAACAGATGTCTCTGT 770

RESULT 15  
ID US-08-086-915-2 STANDARD; DNA; UNC; 138 BP.

XX  
AC xxxxxx

DT 01-JAN-1900

DE Sequence 2, Application US/08086915.

CC Sequence 2, Application US/08086915

CC Patent No. 544167

CC GENERAL INFORMATION:

CC APPLICANT: Pettersson, Kim SI

CC TITLE OF INVENTION: Variant Lutetizing Hormone Encoding DNA

CC NUMBER OF SEQUENCES: 17

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Adduci, Mastriani, Schumberg & Schill

CC STREET: 1140 Connecticut Avenue, N.W., Suite 250

CC CITY: Washington

CC STATE: D.C.

CC COUNTRY: U.S.A.

CC ZIP: 20036

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/086,915

CC FILING DATE: 07-JUL-1993

CC CLASSIFICATION: 536

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Kubovcik, Ronald J.

CC REGISTRATION NUMBER: 25,401

CC REFERENCE/DOCKET NUMBER: 15873005

CC TELEPHONE: 202-467-2006

CC TELEFAX: 202-467-2006

CC INFORMATION FOR SEQ ID NO: 2:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 138 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: double

CC TOPOLOGY: linear

CC MOLECULE TYPE: DNA (genomic)

CC HYPOTHETICAL: NO

CC ANTI-SENSE: NO

CC ORIGINAL SOURCE:

CC ORGANISM: Homo sapiens

CC DEVELOPMENTAL STAGE: Adult

CC Sequence 138 BP; 24 A; 51 C; 42 G; 21 T; 0 other;

Query Match 8.6%; Score 103; DB 5; Length 138;

Best Local Similarity 99.0%; Pred. No. 5,77e-57;

Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 34 CCACGGTCCACCCCATCATGCTGCTGTGAGAGAGAGGCTGCCCCGTGTC 93

QY 783 CCACGGTCCGCGCCCATCAATGCCACCTGGCTGTGAGAGAGGCTGCCCCGTGTC 842

DB 94 ATCACCGTCAACACCAACCATCTGTGCGGCTACTGCCCCACCATG 138

QY 843 ATCACCGTCAACACCAACCATCTGTGCGGCTACTGCCCCACCATG 887

Search completed: Wed May 6 10:31:18 1998  
Job time : 142 secs.



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QY 464 TCGAGGAGGTGAGAGCGGCTCTTCCACCGCTTCAGAAAAACACCTCGACACTGCTC 523
DB 181 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGTCTCTTCTGACAGTGGAC 240
QY 524 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGTCTCTTCTGACAGTGGAC 583
DB 241 CGGGACACCGTGTGTGGCTGTCAGAGAAACCACTACCGGCAATTATTGGATGAAACCTT 300
QY 584 CGGGACACCGTGTGTGGCTGTCAGAGAAACCACTACCGGCAATTATTGGATGAAACCTT 643
DB 301 TTCAGTGTCTCAATTGACAGCCTTCCCTCAATGGAGACCGTGCACCTCTCTCCAGAG 360
QY 644 TTCAGTGTCTCAATTGACAGCCTTCCCTCAATGGAGACCGTGCACCTCTCTCCAGAG 703
DB 361 AAACAGAACACCGTGTGACACCTGTCATGACAGTGTCTTCTTAAGAGAAAAAGAGTGTG 420
QY 704 AAACAGAACACCGTGTGACACCTGTCATGACAGTGTCTTCTTAAGAGAAAAAGAGTGTG 763
DB 421 TCCTGT 426
QY 764 TCCTGT 769

RESULT 2 A21525 510 bp DNA PAT 26-JUL-1994
LOCUS
DEFINITION oligonucleotide probe.
ACCESSION A21525
NID 9583574
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 510)
AUTHORS
JOURNAL Patent: GB 2246569-A 4 05-FEB-1992;
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BASE COUNT 136 a 132 c 133 g 109 t
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Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 454 TCCTGT 459
QY 764 TCCTGT 769

RESULT 3 A20257 600 bp DNA PAT 20-SEP-1995
LOCUS
DEFINITION Synthetic nucleotide sequence of plasmid p-TNFrecl.
ACCESSION A20257
NID 91247896
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 600)
AUTHORS
JOURNAL MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR
FEATURES
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            1..600
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BASE COUNT 148 a 157 c 162 g 133 t
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Query Match 40.4%; Score 424; DB 25; Length 600;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 404 AAGTGCACAAAGAAACCTACTTGTACATGACTGTCCAGGCCCGGGGCGAGATACGGAC 463
DB 241 TCGAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACCACTGACACTGCTC 300
QY 464 TCGAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACCACTGACACTGCTC 523
DB 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGTCTCTTTCGACAGTGGAC 360
QY 524 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGTCTCTTTCGACAGTGGAC 583
DB 361 CGGGACACCGTGTGTGGCTGTCAGAGAAACCACTACCGGCAATTATTGGATGAAACCTT 420
QY 584 CGGGACACCGTGTGTGGCTGTCAGAGAAACCACTACCGGCAATTATTGGATGAAACCTT 643
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QY 644 TTCAGTGTCTCAATTGACAGCCTTCCCTCAATGGAGACCGTGCACCTCTCTCCAGAG 703
DB 481 AAACAGAACACCGTGTGACACCTGTCATGACAGTGTCTTCTTAAGAGAAAAAGAGTGTG 540
QY 704 AAACAGAACACCGTGTGACACCTGTCATGACAGTGTCTTCTTAAGAGAAAAAGAGTGTG 763
DB 541 TCCTGT 546
QY 764 TCCTGT 769

RESULT 4 A29103 1331 bp DNA PAT 03-JUL-1995
LOCUS
DEFINITION H.sepiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION A29103
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NID 91247517  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1331)  
 AUTHORS Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratowa, C.  
 TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
 JOURNAL Patent: EP 0393438-A 53 24-OCT-1990;  
 BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

FEATURES  
 source Location/Qualifiers  
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BASE COUNT 298 a 407 c 343 g 283 t  
 ORIGIN

Query Match 40.4%; Score 424; DB 25; Length 1331;  
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
 Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 333 GATAGTGTGTGTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 392  
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 Db 393 AAGTGCACAAAGAAACCTACTTGTACATGACTGTCCAGGCGCGGGGCGAGATACGGAC 452  
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 Qy 404 AAGTGCACAAAGAAACCTACTTGTACATGACTGTCCAGGCGCGGGGCGAGATACGGAC 463  
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 Db 453 TCCAGGAGTGTGAGAGCGGCTCTCCACCGCTTCAGAAAACCACTCAGACACTGCTC 512  
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 Db 573 CGGGACACCGT 632  
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 Qy 584 CGGGACACCGT 643  
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 Db 633 TTCCAGTGTCTCAATTCAGACCTCTGCTCAATGGGACGCTGACCTCTCTGCCAGGAG 692  
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 Qy 644 TTCCAGTGTCTCAATTCAGACCTCTGCTCAATGGGACGCTGACCTCTCTGCCAGGAG 703  
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 Db 693 AAACAGACACCGT 752  
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 Qy 704 AAACAGACACCGT 763  
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 Db 753 TCCTGT 758  
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 Qy 764 TCCTGT 769

RESULT 5  
 LOCUS A29098 1368 bp DNA PAT 03-JUL-1995  
 DEFINITION Synthetic DNA for TNF-receptor from patent EP0393438.  
 ACCESSION NID A29098  
 KEYWORDS 91248892  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 1368)  
 AUTHORS Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratowa, C.  
 TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
 JOURNAL Patent: EP 0393438-A 48 24-OCT-1990;  
 BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H  
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 source Location/Qualifiers  
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source /db\_xref="taxon:32644"  
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BASE COUNT 293 a 424 c 375 g 276 t  
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Query Match 40.4%; Score 424; DB 25; Length 1368;  
 Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
 Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180  
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 Qy 344 GATAGTGTGTGTCCCAAGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 403  
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 Db 181 AAGTGCACAAAGAAACCTACTTGTACATGACTGTCCAGGCGCGGGGCGAGATACGGAC 240  
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 Qy 404 AAGTGCACAAAGAAACCTACTTGTACATGACTGTCCAGGCGCGGGGCGAGATACGGAC 463  
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 Db 241 TCCAGGAGTGTGAGAGCGGCTCTCCACCGCTTCAGAAAACCACTCAGACACTGCTC 300  
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 Db 361 CGGGACACCGT 420  
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 Qy 584 CGGGACACCGT 643  
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 Db 481 AAACAGACACCGT 540  
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 Qy 704 AAACAGACACCGT 763  
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 Db 541 TCCTGT 546  
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 Qy 764 TCCTGT 769

RESULT 6  
 LOCUS HUMTNFRP 2050 bp mRNA PRI 11-OCT-1991  
 DEFINITION Human tumor necrosis factor receptor(TNF) mRNA, complete cds.  
 ACCESSION M60275 M37764  
 NID 9339759  
 KEYWORDS TNF receptor; transmembrane receptor; tumor necrosis factor receptor.  
 SOURCE Human placenta, cDNA to mRNA.  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 2050)  
 AUTHORS Gray, P.W., Barrett, K.J., Chantray, D., Turner, M. and Feldman, M.  
 TITLE Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)  
 MEDLINE 91017509  
 COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-AUG-1990.

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 CDS 155..1516

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BASE COUNT								
ORIGIN								

Query Match	40.48;	Score 424;	DB 27;	Length 2050;
Best Local Similarity	99.88;	Pred. No. 0.00e+00;		
Matches 425;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Db	275	GATATGTGTGCCCCCAAGAAAAATATATCCACCTCAAAATATATGGATTTGGCTGAC	3394
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Db	335	AAATGCCAACAAGAACCTACTTGTACATGACTGTCCAGGCCGGGGAGATACGAC	3948
Oy	404	AAATGCCAACAAGAACCTACTTGTACATGACTGTCCAGGCCGGGGAGATACGAC	4638
Db	395	TGCAGGGAGTGTGAAGGGGCTCCCTACCGCTTCAGAAAAACACCTCAGACACTGGCTC	4538
Oy	464	TGCAGGGAGTGTGAAGGGGCTCCCTACCGCTTCAGAAAAACACCTCAGACACTGGCTC	5238
Db	455	AGCTCTCCAAATGCGAAGAAAGAAATGGGTAGGTGAGATCTCTTTGGCAGTGGAC	5148
Oy	524	AGCTCTCCAAATGCGAAGAAAGAAATGGGTAGGTGAGATCTCTTTGGCAGTGGAC	5838
Db	515	CGGGACACCGGTGTGTGGCTGCAGAGAAACCAATACCGGACTTTATTGGATGAAACCTT	5748
Oy	584	CGGGACACCGGTGTGTGGCTGCAGAGAAACCAATACCGGACTTTATTGGATGAAACCTT	6438
Db	575	TTTCAGTCTCTCAATTGCAAGCCTCGCCTCAATGGAGACCGGACCTCTCTGCGAGAG	6348
Oy	644	TTTCAGTCTCTCAATTGCAAGCCTCTGCTCAATGGAGACCGGACCTCTCTGCGAGAG	7038
Db	635	AAACGAACACCGTGTGCACCTGCGCATGCAAGTTCTTTAAGAGAAAAAGATGTGC	6948
Oy	704	AAACGAACACCGTGTGCACCTGCGCATGCAAGTTCTTTAAGAGAAAAAGATGTGC	7638
Db	695	TTCTGT 700	
Oy	764	TTCTGT 769	

RESULT	7	143805	2062 bp	DNA	PAT	10-JUL-1997
LOCUS						
DEFINITION		Sequence 24 from patent US 5633145.				
ACCESSION		I43805				
NID		G2468903				
KEYWORDS		.				
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		Unclassified.				
AUTHORS		1 (bases 1 to 2062)				
TITLE		Feldman,M., Gray,P.W., Turner,M.J.C. and Brennan,F.M.				
JOURNAL		TMF alpha. receptor-derived binding protein				
FEATURES		Patent: US 5633145-A 24 27-MAY-1997;				
		Location/Qualifiers				
source		1..2062				
		/organism="unknown"				

BASE COUNT	429 a	617 c	573 g	443 t
ORIGIN				

Query Match	40.48;	Score 424;	DB 25;	Length 2062;
Best Local Similarity	99.88;	Pred. No. 0.00e+00;		
Matches	425;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

Db	275	GATTAATGTTGTGCCCAAGAAAATATATCCACCCCTAAAATAATTGATTTGCTGTACC	334
Qy	344	GATATGTGTGTCCCAAGAAAAATATATCCACCCCTAAAATAATTGATTTGCTGTACC	403
Db	335	AAATGCCAACAAAGAACTACTTGTACATATGCTCCAGGCCCGGGGAGATACGGAC	394
Qy	404	AAATGCCAACAAAGAACTACTTGTACATATGCTCCAGGCCCGGGGAGATACGGAC	463
Db	395	TGCAGGGAGTGTGAGAGGGGTCTCTTCAACGGCTTCAAAAAACCACTCAACACTGGCTC	455
Qy	464	TGCAGGGAGTGTGAGAGGGGTCTCTTCAACGGCTTCAAAAAACCACTCAACACTGGCTC	523
Db	455	AGCTCTCTCAAAATGCCGAAGAAGAAATGGGTGAGGTGAGATCTTTTGTGCACAGTGGAC	514
Qy	524	AGCTCTCTCAAAATGCCGAAGAAGAAATGGGTGAGGTGAGATCTTTTGTGCACAGTGGAC	583
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Qy	584	CGGGACACCGTGTGTGGCTGCAGAGAAACCATGATCCGGCATTTATGGAGTGAACCTT	643
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Qy	644	TTCAGATGCTTCAATTTGACAGCTCTGACCTCAATGGAGACCGGCACCTCTCTCTGCCAGAG	703
Db	635	AAACGAACACCGTGTGCACCTGCCATCAGCAGTTCTTTCTAAGAGAAAAAGATGTGTCTC	694
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Qy	764	TCTCT 769	

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DEFINITION	TNF alpha gene.				
ACCESSION	A21522				
NTID	g579599				
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
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	Vertebrata; Eutheraia; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 2062)				
AUTHORS	Patent: GB 2246565-A 1 05-FEB-1992;				
JOURNAL	Location/Qualifiers				
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BASE COUNT 429 a 617 c 573 g 443 t  
ORIGIN

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Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCCAATATATGATTTGCTGAC 403  
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QY 764 TCCTGT 769

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LOCUS HUMTNER 2087 bp mRNA PRI 10-NOV-1993  
DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION M33294  
NID 9339744  
KEYWORDS cell surface receptor; tumor necrosis factor receptor.  
SOURCE Human placenta, cDNA to mRNA.  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 2087)  
Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Wong, G.H.,  
Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Kohr, W.J. and  
Goeddel, D.V.  
TITLE Molecular cloning and expression of a receptor for human tumor  
necrosis factor  
JOURNAL Cell 61, 361-370 (1990)  
MEDLINE 90235285  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
by T. Schall, 26-MAR-1990.  
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ORIGIN

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QY 704 AACAGAACACCGTGTGACCTGTCATGACAGTTTCTTTTAAGAGAAAAAGAGTGTG 763  
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Db 722 TCCTGT 727  
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QY 764 TCCTGT 769

RESULT 10  
LOCUS HUMTNERB 2111 bp mRNA PRI 14-NOV-1990  
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION M58286  
NID 9339753  
KEYWORDS tumor necrosis factor receptor.  
SOURCE Human cell line HL60, cDNA to mRNA.  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 2111)  
Loetscher, H., Pan, Y.-C.E., Lahm, H.-W., Gentz, R., Brockhaus, M.,  
Tabuchi, H. and Lesslauer, W.  
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis  
factor receptor  
JOURNAL Cell 61, 351-359 (1990)  
MEDLINE 90235284  
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187..273  
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CDS sig\_peptide  
187..273  
/product="tumor necrosis factor receptor"



**AUTHORS** Himmeler, A., Maurer-Fogy, I., Kroenke, M., Scherlich, P.,  
Pfeizenmaier, K., Lantz, M., Olsson, I., Hauptmann, R., Stratowa, C. and  
Adolf, G. R.

**TITLE** Molecular cloning and expression of human and rat tumor necrosis  
factor receptor chain (p60) and its soluble derivative, tumor  
necrosis factor-binding protein

**JOURNAL** DNA Cell Biol. 9, 705-715 (1990)

**MEDLINE** 91090841

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294..1571

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Best Local Similarity 99.8% Pred. No. 0.00e+00;

Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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464 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTCAGAAACCACTCAGACATGCTC

507 AGCTGCTCAAAATGCCAAGAAAGAAATGGTCCAGTGGAGATCTCTTGGACAGTGGAC

524 AGCTGCTCAAAATGCCAAGAAAGAAATGGTCCAGTGGAGATCTCTTGGACAGTGGAC

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644 TTCCAGTGTTCATTTGACAGCTCTGCTCAATGGAGACCGTGTCTCTCTGACAGAG

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764 TCCTGT 769

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**LOCUS** HSTNFR1A 2161 bp RNA PRI 18-JAN-1993

**DEFINITION** H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.

**ACCESSION** X55313

**KEYWORDS** 937223

**SOURCE** TNF-R gene; tumor necrosis factor receptor 1.

**ORGANISM** human.

**REFERENCE** Homo sapiens

**AUTHORS** Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

**TITLE** Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 2161)

Nophar, Y., Kemper, O., Brakbusch, C., Englemann, H., Zwan, R.,

Aderka, D., Holtmann, H. and Wallach, D.

Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA

for the type I TNF-R, cloned using amino acid sequence data of its

soluble form, encodes both the cell surface and a soluble form of

the receptor

EMBO J. 9 (10), 3269-3278 (1990)

9106021

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KONTVCTCHAGFFLRNEECVSCNCKRSLECTRLCPQLEENVKGTSDSGTVLLPVI

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Db 796 TCCTGT 801  
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DEFINITION Sequence 1 from Patent EP0657536.  
ACCESSION A43873  
NID 92299022  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2175)  
AUTHORS Wallach,D., Brachebusch,C., Varfolomeev,E. and Batkin,M.  
TITLE Processes capable of shedding the soluble TNF-receptor and TNF-R derived peptides and antibodies against the proteases inhibiting the shedding  
Patent: EP 0657536-A 1 14-JUN-1995;  
YEDA RES & DEV (IL)  
Other publication ZA 9407962 951121  
Other publication JP 7194376 950801  
Other publication AU 7574294 950504  
Other publication CA 2133872 950413.  
JOURNAL Location/Qualifiers

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ORIGIN

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Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 796 TCCTGT 801  
Oy 764 TCCTGT 769

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DEFINITION Sequence 1 from patent US 5665859.  
ACCESSION I64751  
NID 92481645  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2175)  
AUTHORS Wallach,D., Brachebusch,C., Varfolomeev,E. and Batkin,M.  
TITLE Molecules influencing the shedding of the TNF receptor, their preparation and their use  
Patent: US 5665859-A 1 09-SEP-1997;  
JOURNAL Location/Qualifiers

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BASE COUNT 474 a 641 c 604 g 456 t  
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Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      764  TCCTGT 769
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 Job time : 1085 secs.

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IL-1R-linker-TNF-R-linker-TNF-R or  
 CC TNF-R-linker-TNF-R  
 CC The linker may comprise 5-100 amino acids selected from Gly, Asp,  
 CC Ser, Thr and Ala. These linkers separate the individual moieties  
 CC by such a distance that each component of the fusion protein is  
 CC capable of folding into the secondary or tertiary structure required  
 CC for its biological activity. These fusion proteins may be used in  
 CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
 CC particularly in conditions in which both TNF and IL-1 play a causative  
 CC role. They may be used to treat cachexia, rheumatoid arthritis,  
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
 CC cerebral malaria, allograft and xenograft rejection in graft versus  
 CC host disease, sepsis, septic shock, inflammation, allergies and  
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 Db 481 aaacagaaacacggtgtgcacctgtcactgacaggttcttcttaagagaaacagagtg 540  
 OY |||||||  
 OY 704 AAACAGAAACACCGTGTGACACTGTCATGCAAGTTCCTTCTTAAGAGAAACGAGTGTGC 763  
 Db 541 tctctgt 546  
 OY |||||||  
 OY 764 TCCTGT 769  
 RESULT 4  
 ID 024440; standard; DNA; 2062 BP.  
 AC 024440;  
 DT 05-NOV-1992 (first entry)  
 DE Encodes TNF-alpha 55KD receptor.  
 KW tumour necrosis factor alpha; extracellular binding domain;  
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
 KW malaria; viral meningitis; graft versus host disease;  
 KW autoimmune disease; rheumatoid arthritis.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 156..1517  
 FT /tag- a  
 FT /product- human TNF-alpha  
 FT mat\_peptide 1265..1267  
 FT /tag- b  
 FT /note- "3"  
 FT mat\_peptide 1265..1267  
 FT /tag- c  
 FT /codon- seq: "TGG", aa: Thr

FT mat\_peptide 1258..1260  
 FT /tag- d  
 FT /codon- Seq "AAG", aa: Leu  
 FT mat\_peptide 1433..1435  
 FT /tag- e  
 FT /codon- Seq: "GAC", aa: Asn  
 FT sig\_peptide 156..274  
 FT /tag- f  
 PN MO9207076-R.  
 PD 30-APR-1992.  
 PF 18-OCT-1991; G01826.  
 PR 18-OCT-1990; GB-022648.  
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.  
 PI Brennan FM, Feldmann M, Gray PW, Turner MJC;  
 DI WPT: 92-167156/20.  
 DR P-PSDB; R24000  
 PT New polypeptide capable of binding human TNF alpha - comprises  
 PT first three cysteine-rich subdomains of TNF alpha receptor for  
 PT treating autoimmune disease, septic shock, HIV etc.  
 PS Claim 4; Fig 1; 43pp; English.  
 CC This sequence encodes human TNF-alpha 55KD receptor. A placenta cDNA  
 CC library in pGL3 was screened with probe Q29236. Ten hybridising clones  
 CC were plaque purified and cDNA size determined by PAGE against an  
 CC Eco RI digested phage DNA. The inserts of two cDNA clones were then  
 CC sequenced. The coding region of the majority of the human TNF-alpha  
 CC 55KD receptor was isolated as an EcoRI fragment encoding 374 amino  
 CC acids, and cloned into a mammalian cell expression vector, resulting  
 CC in pTNFR. A derivative of the TNF-alpha receptor was produced by  
 CC engineering a termination codon just prior to the transmembrane  
 CC domain. PCR with primers Q29237,8 generated a 300bp  
 CC restriction fragment which was cloned into pTNFR, giving pTNFRcd.  
 CC DNA sequencing confirmed this contained the designed DNA sequence.  
 CC The TNF-alpha receptor expression plasmids were then transfected  
 CC into monkey COS-7 cells.  
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
 SO Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T;  
 Query Match 40.4%; Score 424; DB 4; Length 2062;  
 Best Local Similarity 99.8%; Pred. No. 2,42e-296;  
 Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 275 gatagtggtgtgtcccaagaaatatatccaccccaaaatcgaattgctgtacc 334  
 OY |||||||  
 OY 344 GATAGTGTGTGCCCAAGAAATATATCCACCCCAAAATATTCATTGCTGTACC 403  
 Db 335 aagtgccaaagaaacactactgttacaatgaactgtcagggccgggagagatacgaac 394  
 OY |||||||  
 OY 404 AAGTGCCAAAGAAAGAACCTTACTTGTACATGACTGTCCAGGCCGGGCGAGATACGAGAC 463  
 Db 395 tgcaggagtggtgagagcggtctctcaccgcttcagaaacacacactcagacactgctc 454  
 OY |||||||  
 OY 464 TCGAGGAGTGTGAGAGCGGCTCTCACCCTTCAGAAACACACTCAGACACTGCTC 523  
 Db 455 agctgtccaaatgccaagaaatggttcaggtgagatcttcttcgacagtgagac 514  
 OY |||||||  
 OY 524 AACTGTCTCAAAATGCGGAAGGAATGGGTGCAAGTGTGCAATCTTTCGACAGTGGAC 583  
 Db 515 cgggagacacggtgtgtcgtcagagaaacagttaccgcatattgtgagtaaaacctt 574  
 OY |||||||  
 OY 584 CGGAGACCGGTGTGTGCTGCAGAGAAACAGTACCGGCAATATTGAGTGAAGAAACCTT 643  
 Db 575 ttcagtgcttcaatgtcagcctctcctcaatgtagcagcttcctcctcagagag 634  
 OY |||||||  
 OY 644 TTCAGTGTCTCAATGTGACAGCCTCTCCTCAATGAGACCGTGCACCTCTCTCCAGGAG 703  
 Db 635 aaacagaaacacggtgtgcacctgtcactgacaggttcttcttaagagaaacagagtg 694  
 OY |||||||  
 OY 704 AAACAGAAACACCGTGTGACACTGTCATGCAAGTTCCTTCTTAAGAGAAACGAGTGTGC 763  
 Db 695 tctctgt 700  
 OY |||||||  
 OY 764 TCCTGT 769

```
RESULT 5
ID Q20973 standard; DNA; 2062 BP.
AC Q20973;
DC 11-MAY-1992 (first entry)
DE TNF-alpha binding protein gene.
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;
extracellular domain.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 155..1522
FT /tag- a 155..274
FT sig_peptide 155..274
FT /tag- b 275..1522
FT mat_peptide 275..1522
FT /tag- c 473..532
FT misc_feature 473..532
FT /tag- d
FT /note- "homologous to probe Q20974"
FT misc_feature 242..751
FT /tag- e
FT /note- "encodes the extracellular domain of human
FT TNF alpha receptor"
FT GN 88246569-A.
PD 05-FEB-1992.
PD 15-JUN-1990; 013410.
PR 15-JUN-1990; GB-013410.
PA (CHAR-) CHARING CROSS SUNLE.
PI Feldman M, Gray P, Turner M, Brennan F;
DR WPI: 92-043613/06.
DR P-PSDB: R20787.
PT New tumour necrosis factor alpha binding protein and polypeptide
PT - useful in treating cachexia, sepsis and auto immune diseases
PS e.g. rheumatoid arthritis
PS Disclosure: Fig 1; 25pp; English.
CC The sequence is that of DNA encoding tumour necrosis factor alpha
CC binding protein which was obtd. from a human placental cDNA library
CC in lambda gtl1 using a probe (Q20974). The DNA also encodes the
CC extracellular domain of human TNF alpha receptor and as such it is
CC useful for treating diseases where TNF alpha is involved as a
CC causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC specifically rheumatoid arthritis. See also Q20974.
CC Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;
SQ

Query Match 40.4%; Score 424; DB 3; Length 2062;
Best Local Similarity 99.8%; Pred. No. 2,42e-296;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 275 gatagtggtgtccccaagaagaatataccaccctcaaatattcgattgctgtacc 334
QY |||||||
QY 344 GATAGTGGTGTGCCCAAGAAATATATCCACCCTCAAAATATTCATTGCTGTACC 403
Db 335 aagtgcccaaaagaaacactactgtgacatgactgtccaggcccgaggcaagatcggac 394
QY |||||||
QY 404 AAGTGCCCAAAAGAAACCTACTGTACATGACGTCCAGGCCCGGGCAGAGATCGGAC 463
Db 395 tgcaggagtggtgaaagcggctccttcacacgcttcagaaaaaacactcagaacatgctc 454
QY |||||||
QY 464 TGCAGGAGGTGTGAGAGAGGGCTCCTTCACCGCTTGAAGAAACACCTAGACACGCTC 523
Db 455 agctgtcccaaatgcggaaggaatgggtcagggtgagatctcttcctgacagtgagac 514
QY |||||||
QY 524 AGCTGCTCCAATGCGGAAGGAATGGGTGAGATGTCCTTCTTGACACATGGAC 583
Db 515 cgggaacacggtgtgtgtggtgcaggaagaacacgtaccggtcattatgtgaatgaacctt 574
QY |||||||
QY 584 CGGGACACCGTGTGTGCTGAGAGAAACAGTACCGGCATTATGGAGTGAAGAAACCTT 643
Db 575 ttccagtgctccaattgacagcctcgtcctcaatggagacggtgacacctctcctgacaggag 634
QY |||||||
QY 644 TTCCAGTGCTTCAATTGACAGCTCTGCTCAATGGAGACCGTGTGACACCTCTCTGCGAAGAG 703
Db 635 aaacagaacacggtgtgacacctgcacgtgttctcttaagaagaacagatgtgtc 694
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QY 704 AAACAGAACCCGTGTGACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGATGTGTC 763
Db 695 tccgtgt 700
QY 764 TCCGTGT 769

RESULT 6
ID Q10883 standard; cDNA; 2088 BP.
AC Q10883;
DC 13-MAY-1991 (first entry)
DE 30kD TNF inhibitor precursor gene in lambda-gtl0-7ctnfp.
KW Tumour necrosis factor; inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 171..1536
FT /tag- a
FT A09058976-A.
PD 24-JAN-1991.
PD 16-JUL-1990; 058976.
PR 18-JUL-1989; US-381080.
PR 11-DEC-1989; US-450329.
PR 07-FEB-1990; US-479661.
PA (SYNE-) SYNERGEN INC.
DR WPI: 91-073847/11.
DR P-PSDB: R10986.
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
PS Disclosure: Fig 21; 142pp; English.
CC The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC which the sequence was obtd. was isolated from a cDNA library
CC prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
CC gene can be inserted into expression vectors for prep'n. of TNF
CC inhibitor for use in the treatment of inflammatory and degenerative
CC diseases.
CC See also Q10878, Q10884 and Q10907.
CC Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T;
SQ

Query Match 40.4%; Score 424; DB 2; Length 2088;
Best Local Similarity 99.8%; Pred. No. 2,42e-296;
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 289 gatagtggtgtccccaagaagaatataccaccctcaaatattcgattgctgtacc 348
QY |||||||
QY 344 GATAGTGGTGTGCCCAAGAAATATATCCACCCTCAAAATATTCATTGCTGTACC 403
Db 349 aagtgcccaaaagaaacactactgtgacatgactgtccaggcccgaggcaagatcggac 408
QY |||||||
QY 404 AAGTGCCCAAAAGAAACCTACTGTACATGACGTCCAGGCCCGGGCAGAGATCGGAC 463
Db 409 tgcaggagtggtgaaagcggctccttcacacgcttcagaaaaaacactcagaacatgctc 468
QY |||||||
QY 464 TGCAGGAGGTGTGAGAGAGGGCTCCTTCACCGCTTCAGAAACACCTCAGACATGGCTC 523
Db 469 agctgtcccaaatgcggaaggaatgggtcagggtgagatctcttcctgacagtgagac 528
QY |||||||
QY 524 AGCTGCTCCAATGCGGAAGGAATGGGTGAGATGTCCTTCTTGACACATGGAC 583
Db 529 cgggaacacggtgtgtgtggtgcaggaagaacacgtaccggtcattatgtgaatgaacctt 588
QY |||||||
QY 584 CGGGACACCGTGTGTGCTGAGAGAAACAGTACCGGCATTATGGAGTGAAGAAACCTT 643
Db 589 ttccagtgctccaattgacagcctcgtcctcaatggagacggtgacacctctcctgacaggag 648
QY |||||||
QY 644 TTCCAGTGCTTCAATTGACAGCTCTGCTCAATGGAGACCGTGTGACACCTCTCTGCGAAGAG 703
Db 649 aaacagaacacggtgtgacacctgcacgtgttctcttaagaagaacagatgtgtc 708
QY |||||||
QY 704 AAACAGAACCCGTGTGACACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGATGTGTC 763
Db 709 tccgtgt 714
|||||
```

QY 764 TCCTGT 769

RESULT 7

ID Q10955 standard; cDNA; 2111 BP.

AC Q10955;

DT 24-MAY-1991 (first entry)

DE Encodes human 55kD TNF-binding protein.

KW Tumour Necrosis Factor; binding proteins; septic shock;

KW autoimmune glomerulonephritis; lymphokine; cytokine.

FH Location/Qualifiers

FT sig\_peptide 187..273

FT /tag= a

FT mat\_peptide 274..1551

FT /tag= b

FT /product= 55kD TNF-BP

PN EP-417563-A.

PD 20-MAR-1991.

PE 31-AUG-1990; 116707.

PF 12-SEP-1989; CH-003319.

PR 08-MAR-1990; CH-000746.

PR 20-APR-1990; CH-001347.

PA (HOEF) HOFFMANN-LA ROCHE AG.

PI Brochhaus W, Dembic Z, Gentz R, Lesslauer W, Lotscher H;

PI Schlaeger EJ;

DR WPI: 91-081851/12.

DR P-PSDB; R11082.

PT Insoluble tumour necrosis factor binding proteins - and DNA

PT encoding them, useful in pharmaceutical prods. and for antibody

PT prodn.

PS Claim 4: Fig 1: 26pp; German.

CC Partial amino acid sequences were determined for the 55 and 75kD

CC TNF-BPs (see R11072-R11081) and oligonucleotide primers were

CC synthesized based on these partial sequences. The primers were used

CC to produce a cDNA fragment for use as a probe to screen a human

CC placental cDNA bank constructed in lambda gill. Positive clones were

CC identified and sequenced. DNA constructs comprising the TNF-BP coding

CC sequence may also contain a fragment encoding a human Ig domain.

CC Recombinant constructs are used to transform cells to confer

CC improved TNF-binding properties.

CC See also Q10956.

SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;

Query Match 40.4%; Score 424; DB 2; Length 2111;

Best Local Similarity 99.8%; Pred. No. 2,42e-296;

Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 307 gatagtggtgtcccaagaagaataatataccaccctcaaaataatcgattgtgtacc 366  
|||||  
QY 344 GATAGTGTGTGTCCCAAGAAATATATCCACCTCAAAATATTCATTGCTGTACC 403  
|||||  
Db 367 aagtgcacaaagaacctactgttacaatgactgtccagggccggggagacagac 426  
|||||  
QY 404 AAGTGCACAAAGAACCTACTTGTACAAATGATGTCAGGCCGGGGAGATACGGAC 463  
|||||  
Db 427 tgcagggagtggtgagcggctcttcacggcttcagaaaaaacacccccaagactgctc 486  
|||||  
QY 464 TGCAGGGAGTGTGAGACGGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCTC 523  
|||||  
Db 487 agctgtcccaaatgacgaagaagaatggtcaggttgagatctcttcttgagagtgagac 546  
|||||  
QY 524 AGCTGCTCCAAATCCCAAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACACAGTGAC 583  
|||||  
Db 547 cggagacacgtgtgtgctcaggaagaacacagacagacacacacacacacacacacac 606  
|||||  
QY 584 CGGACACCGTGTGTGCTGACAGAAACAGTACCGGATTAFTGAGAAACCTT 643  
|||||  
Db 607 ttccagtgcttcaatttgacgctctgctcgaatggagacgtgacacacacacacacacacac 666  
|||||  
QY 644 TTCAGTGTCAATTCAGACCTCTGCTCAATGGAGACCGTCTCTCTGACAGAG 703  
|||||  
Db 667 aaacagaacacacgtgtgac 726  
|||||

QY 704 AACAGAACACCGTGTGACCTGTCATGACGTTTCTTCTAAGAGAAAAGAGTGTGC 763

Db 727 tcctgt 732

QY 764 TCCTGT 769

RESULT 8

ID Q06285 standard; DNA; 2141 BP.

AC Q06285;

DT 29-JAN-1991 (first entry)

DE Human Tumour Necrosis Factor-Receptor cDNA Insert.

KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

KW lambdaTNF-R2; ratTNF-R8; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 213..1577

FT /tag= a

FT /label=huTNF-R

PN EP-393438-A.

PD 24-OCT-1990.

PE 06-APR-1990; 106624.

PF 21-APR-1989; DE-913101.

PR 21-JUN-1989; DE-920282.

PA (BOEH) BOEHRINGER INGELHEIMINT.

PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;

DR WPI: 90-321987/43.

DR P-PSDB; R07451.

PT DNA encoding TNF binding protein and TNF-receptor - used in

PT tumour treatment and to understand mechanism to TNF action

PS disclosure: Fig 91(1-2): 51pp; German.

CC ratTNF-R8 (Q06284) was used to screen the HS913T cDNA library.

CC lambdaTNF-R2 encodes the complete human TNF-R2 and was used to

CC construct a plasmid (pADTNF-R) expressing the product the same way

CC as pADTNF-BP (see Q06282).

CC See also Q06282-Q06285.

SQ Sequence 2141 BP; 455 A; 633 C; 593 G; 460 T;

Query Match 40.4%; Score 424; DB 1; Length 2141;

Best Local Similarity 99.8%; Pred. No. 2,42e-296;

Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 333 gatagtggtgtcccaagaagaataatataccaccctcaaaataatcgattgtgtacc 392  
|||||  
QY 344 GATAGTGTGTGTCCCAAGAAATATATCCACCTCAAAATATTCATTGCTGTACC 403  
|||||  
Db 393 aagtgcacaaagaacctactgttacaatgactgtccagggccggggagacagac 452  
|||||  
QY 404 AAGTGCACAAAGAACCTACTTGTACAAATGATGTCAGGCCGGGGAGATACGGAC 463  
|||||  
Db 453 tgcagggagtggtgagcggctcttcacggcttcagaaaaaacacccccaagactgctc 512  
|||||  
QY 464 TGCAGGGAGTGTGAGACGGCTCTTCACCGCTTCAGAAAACCACTCAGACACTGCTC 523  
|||||  
Db 513 agctgtcccaaatgacgaagaagaatggtcaggttgagatctcttcttcacagtgagac 572  
|||||  
QY 524 AGCTGCTCCAAATGCCCAAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGAC 583  
|||||  
Db 573 cggagacacgtgtgtgctcaggaagaagaacagtaacggagataatggatgtaaaacct 632  
|||||  
QY 584 CGGACACCGTGTGTGCTGACAGAAACAGTACCGGATTAFTGAGAAACCTT 643  
|||||  
Db 633 ttccagtgcttcaatttgacgctctgctcgaatggagacgtgacacacacacacacacacac 692  
|||||  
QY 644 TTCAGTGTCAATTCAGACCTCTGCTCAATGGAGACCGTCTCTCTGACAGAG 703  
|||||  
Db 693 aaacagaacacacgtgtgac 752  
|||||  
QY 704 AACAGAACACCGTGTGACCTGTCATGACGTTTCTTCTAAGAGAAAAGAGTGTGC 763  
|||||  
Db 753 tcctgt 758  
|||||  
QY 764 TCCTGT 769



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QY 584 CCGGACACCGTGTGTGCTCAGAGAACACAGTACCGCATTTATGAGTGAACCTT 643
DB 2025 ttccagtgtcctaattcagcagcctctcgaatgagcagctgcacctctcgcagag 2084
QY 644 TTCCAGTGTCTTAATTCACACCTCTGCTCAATGGACGCTGACCTCTCTGCAAGAG 703
DB 2085 aaacagacacgctgtgcacctgcacatgcaggttctcttaagagaaacagagtgctc 2144
QY 704 AAACAGAACACCGTGTGACCTGCGCATGCAAGTCTTCTTAAGAGAAAAGAGTGTCTC 763
DB 2145 tcctgt 2150
QY 764 TCCTGT 769

RESULT 11
ID Q50870 standard; DNA; 2170 BP.
AC Q50870;
DT 13-MAY-1994 (first entry)
DE p55 Tumour necrosis factor receptor coding sequence.
KW TNF: tumour necrosis factor; receptor; disease; autoimmunity;
KM rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 256..1623
FT /tag- a
FT /product- p55 Tumour necrosis factor receptor.
FT EP-568925-A.
FT 10-NOV-1993.
FT 29-APR-1993; 106981.
FT 03-MAY-1992; IL-101769.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT Brakedusch C, Wallach D;
FT MPI; 93-353057/45.
FT P-PSDB; R42197.
PT Modulating activity of tumour necrosis factor receptor - using
PT peptides), antibodies, etc. which interact with critical regions
PT of receptor or effector protein, for controlling auto-immune
PT disease, septic shock, etc.
PS Claim 2; Figure 1; 17pp; English.
CC Modification of the tumour necrosis factor receptor by mutation or
CC deletion modulates signal transduction and/or cleavage effected by
CC the receptor. This modulation of activity can also be achieved by
CC using effector proteins which interact with the TNF receptor.
CC Molecules which interact with the TNF receptor or the effector
CC proteins can be used to treat or prevent diseases associated with
CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC rejection; graft vs. host disease or septic shock. They can also
CC be used to treat overdoes of exogenous TNF.
SQ Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T;

Query Match 40.2%; Score 422; DB 9; Length 2170;
Best Local Similarity 99.5%; Pred. No. 8.37e-295;
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 584 CCGGACACCGTGTGTGCTCAGAGAACACAGTACCGCATTTATGAGTGAACCTT 643
DB 676 ttccagtgtcctaattcagcagcctctcgaatgagcagctgcacctctcgcagag 735
QY 644 TTCCAGTGTCTTAATTCACACCTCTGCTCAATGGACGCTGACCTCTCTGCAAGAG 703
DB 736 aaacagacacgctgtgcacctgcacatgcaggttctcttaagagaaacagagtgctc 795
QY 704 AAACAGAACACCGTGTGACCTGCGCATGCAAGTCTTCTTAAAGAGAAAAGAGTGTCTC 763
DB 796 tcctgt 801
QY 764 TCCTGT 769

RESULT 12
ID Q12215 standard; DNA; 2176 BP.
AC Q12215;
DT 12-SEP-1991 (first entry)
DE Type I TNF receptor.
KW Tumour Necrosis factor; TNF; binding protein; TBP-I; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT terminator 244..246
FT /tag- a
FT /note- "in-frame termination codon"
FT CDS 256..1620
FT /tag- a
FT /product- type I TNF receptor
FT sig_peptide 256..318
FT /tag- b
FT mat_peptide 319..1620
FT /tag- c
FT misc_RNA 319..864
FT /tag- d
FT /label- soluble domain
FT /note- "may be 2 codons shorter or a few codons
FT longer"
FT misc_feature 376..414
FT /tag- e
FT /note- "TBP-I derived sequence"
FT misc_feature 583..627
FT /tag- f
FT /note- "TBP-I derived sequence"
FT misc_feature 850..858
FT /tag- g
FT /note- "TBP-I derived sequence"
FT misc_RNA 889..957
FT /tag- h
FT /label- transmembrane domain
FT repeat_unit 385..504
FT /tag- i
FT /number- 1
FT repeat_unit 505..633
FT /tag- j
FT /number- 2
FT repeat_unit 634..756
FT /tag- k
FT /number- 3
FT repeat_unit 757..858
FT /tag- l
FT /number- 4
FT poly_signal 2145..2150
FT /tag- m
FT EP-433900-A.
FT 26-JUN-1991.
FT 13-DEC-1980; 124133.
FT 13-DEC-1989; IL-092697.
FT 12-JUL-1990; IL-095064.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT Wallach D, Nopnar Y, Kemper O, Engelmann H, Brakedusch C;
FT Aderka D;
```

DR WPI: 91-186774/26.  
DR P-PSDB: R12550.  
PT Recombinant tumour necrosis factor binding protein I - prep'd. by  
PT transfecting eukaryotic cells with vector contg. deoxyribonucleic  
PT acid encoding human type I TNF receptor or soluble domain  
PS Discloure: Fig 1(D): 10pp; English.  
CC The Tumour Necrosis Factor Binding Protein I is the soluble form of  
CC type I TNF-receptor and constitutes a fragment of the cell surface  
CC form of this receptor, corresp. to its extracellular domain.  
CC There is no characteristic poly(A) addition signal near the 3' end  
CC of the cDNA. The sequence ACTMAA (tag m) may serve as an  
CC alternative to this signal, but with low efficiency.  
CC See also 012212-15.  
SQ Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T;  
  
Query Match 40.3%; Score 422; DB 2; Length 2176;  
Best Local Similarity 99.5%; Pred. No. 8.37e-295;  
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
DB 376 gatagtgtgtgtccccaaggaataatattccacccctcaataattgattgacgtacc 435  
|||  
OY 344 GATAGTGTGTGTCCCAAGGAATAATATCCACCCCTCAATAATTCATTGTCTGTACC 403  
|||  
DB 436 aagtgccacaagaagaaacctactgttacaatgtactcagggccggggagagatacggac 495  
|||  
OY 404 AAGTGCCACAAAGGAACCTACTTGTACATGACTGTCCAGGCCGGGCGAGATACGAGAC 463  
|||  
DB 496 tgcaggagagtgtagaagcggctccctcaccgcttcagaagaacacccctcagacactgcctc 555  
|||  
OY 464 TCGAGGAGATGTGAGAGCGGCTCCTTCACCGGTTCAGAAAACCACTCAGACACTGCCCTC 523  
|||  
DB 556 agctgtcccaaatgcccgaagaagaatggttcagggtgagatctctcttcagacagtggac 615  
|||  
OY 524 ACTGTCTCCAAATGCGGAAGGAAGGCGTCAAGTGTGAGATCTCTTCTTGCAAGTGAGAC 583  
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DB 616 cgggacacacgtgtgtgtgtgcaggaagaacacgtaccgcatattgaggtgtaaaacctt 675  
|||  
OY 584 CGGACACCGTGTGTGTGCTGTCCAGGAAGAACAGTACCGGCATTATTGGATGAAAACTTT 643  
|||  
DB 676 ttccagtgcttaaatgtcagcctctcgtcccaatgagacggttcacacctccctgcagagag 735  
|||  
OY 644 TTCAGTGTCTTAATGTGACGCGCTCTCCCTCAATGGGACCGTGCACTCTCTGCCAGGAG 703  
|||  
DB 736 aaacagaaacacggtgtgcacctgcagcatcagagttcttcttaagagaagaagaagtgtgc 795  
|||  
OY 704 AAACAGAAACACCGTGTGCACTGTCCATGCAAGTTCTTCTTAAGAGAAAAAGAGTGTGC 763  
|||  
DB 796 tccgtgt 801  
|||  
OY 764 TCCTGT 769  
  
RESULT 13  
ID 024445 standard; DNA: 504 BP.  
AC 024445:  
DT 05-NOV-1992 (first entry)  
DE Encodes truncated TNF-alpha 55kd receptor (165 amino acids).  
KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
PN WO9207076-A.  
PD 30-APR-1992.  
PF 18-OCT-1991: G01826.  
PR 18-OCT-1990: GB-022648.  
PA (CHAR.) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;  
DR WPI: 92-167156/20.  
DR P-PSDB: R24084.  
PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for  
PT treating autoimmune disease, septic shock, HIV etc.

PS Example: Fig 11: 43pp; English.  
CC This sequence encodes the designed TNF-alpha 55kd receptor  
CC derivative, as present in pdeletay. This construct was generated by  
CC cloning of the BglII/HindIII digested product of a PCR using  
CC primers 5A and 4D into BglII/HindIII 5'-delta-tac. This introduced  
CC a termination codon after amino acid 167, to yield pdeletay.  
CC This derivative lacks the membrane proximal 4th subdomain, yet  
CC retains the ability to bind TNF-alpha with high affinity  
CC (10power8 - 10power9 Mpower-1) The deriv. can be used in the  
CC regulation of TNF-alpha mediated responses by binding and  
CC sequestering human TNF-alpha e.g. in the treatment of pulmonary  
CC diseases, septic shock, HIV infection, malaria, viral meningitis,  
CC graft versus host disease and autoimmune diseases, sep. Rheumatoid  
CC arthritis. The deriv. is given at 10-100ug/dose.  
CC See also 024440-51, R24000, R24080-84, R27585, Q29236-8  
SQ Sequence 504 BP; 122 A; 137 C; 138 G; 107 T;  
  
Query Match 36.3%; Score 381; DB 4; Length 504;  
Best Local Similarity 99.7%; Pred. No. 2.76e-263;  
Matches 382; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
DB 121 gatagtgtgtgtccccaaggaataatattccacccctcaataattgattgacgtacc 180  
|||  
OY 344 GATAGTGTGTGTCCCAAGGAATAATATCCACCCCTCAATAATTCATTGTCTGTACC 403  
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DB 181 aagtgccacaagaagaaacctactgttacaatgtactcagggccggggagagatacggac 240  
|||  
OY 404 AAGTGCCACAAAGGAACCTACTTGTACATGACTGTCCAGGCCGGGCGAGATACGAGAC 463  
|||  
DB 241 tgcaggagagtgtagaagcggctccctcaccgcttcagaagaacacccctcagacactgcctc 300  
|||  
OY 464 TCGAGGAGATGTGAGAGCGGCTCCTTCACCGGTTCAGAAAACCACTCAGACACTGCCCTC 523  
|||  
DB 301 agctgtcccaaatgcccgaagaagaatggttcagggtgagatctctcttcagacagtggac 360  
|||  
OY 524 ACTGTCTCCAAATGCGGAAGGAATGGGTCAAGTGTGAGATCTCTTCTTGCAATGGAC 583  
|||  
DB 361 cgggacacacgtgtgtgtgtgcaggaagaacacgtaccgcatattgaggtgtaaaacctt 420  
|||  
OY 584 CGGACACCGTGTGTGTGCTGTCCAGGAAGAACAGTACCGGCATTATTGGATGAAAACTTT 643  
|||  
DB 421 ttccagtgcttaaatgtcagcctctcgtcccaatgagacggttcacacctccctgcagagag 480  
|||  
OY 644 TTCAGTGTCTTAATGTGACGCGCTCTCCCTCAATGGGACCGTGCACTCTCTGCCAGGAG 703  
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DB 481 aaacagaaacacggtgtgcacctgc 503  
|||  
OY 704 AAACAGAAACACCGTGTGCACTGT 726  
  
RESULT 14  
ID 024442 standard; DNA: 474 BP.  
AC 024442:  
DT 05-NOV-1992 (first entry)  
DE Encodes truncated TNF-alpha 55kd receptor (155 amino acids).  
KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
PN WO9207076-A.  
PD 30-APR-1992.  
PF 18-OCT-1991: G01826.  
PR 18-OCT-1990: GB-022648.  
PA (CHAR.) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;  
DR WPI: 92-167156/20.  
DR P-PSDB: R24081.  
PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for  
PT treating autoimmune disease, septic shock, HIV etc.  
PS Example: Fig 8: 43pp; English.  
CC This sequence encodes the designed TNF-alpha 55kd receptor





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\*\*\*\*\*  
 WIRE (TM)  
 \*\*\*\*\*

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 Distribution rights by Oxford Molecular Ltd

\*\*\*\*\*  
 MPerch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 12:38:32 1998; Maspar time 969.27 Seconds

Tabular output not generated. 1315.719 Million cell updates/sec

Title: >US-08-804-166-1

Description: (1-1049) from US08804166.seq

Perfect Score: 1049

N.A. Sequence: 1 TCACATGCTACAGGTAG.....TTATTCACCAATCTTAG 1049

Comp: AGGTGACCGATGTCATTC.....AATATAGTGTAGATTC

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

embl-est  
 1:em-est1 2:em-est2 3:em-est3 4:em-est4 5:em-est5  
 6:em-est6 7:em-est8 8:em-gss 9:em-est13  
 genbank-est  
 10:gb-est1 11:gb-est2 12:gb-est3 13:gb-est4 14:gb-est5  
 15:gb-est6 16:gb-est7 17:gb-est8 18:gb-est9 19:gb-est10  
 20:gb-est11 21:gb-est12 22:gb-est13 23:gb-est14 24:gb-est15  
 25:gb-est16 26:gb-est17 27:gb-est18 28:gb-est19 29:gb-est20

Statistics: Mean 11.127; Variance 1.959; scale 5.680

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	258	24.6	373	23	HUM505B08B	0.00e+00
2	258	24.6	379	23	C18240	0.00e+00
3	258	24.6	392	11	R76249	0.00e+00
4	258	24.6	464	23	C17209	0.00e+00
5	258	24.6	467	11	R71429	0.00e+00
6	257	24.5	423	12	H00861	0.00e+00
7	256	24.4	433	11	R23843	0.00e+00
8	256	24.4	452	12	H00781	0.00e+00
9	254	24.2	478	23	C17142	0.00e+00
10	251	23.9	330	23	C18403	0.00e+00
11	250	23.8	458	11	R77385	0.00e+00
12	248	23.6	482	12	H03289	0.00e+00
13	245	23.4	336	23	HUM530G10B	0.00e+00

14	236	22.5	519	23	C18044	Human placenta cDNA 5'	0.00e+00
15	234	22.3	429	31	AA79136	z146h1.s1 Soares feta	0.00e+00
16	232	22.1	423	23	C17966	Human placenta cDNA 5'	0.00e+00
17	229	21.8	471	12	H47149	Yp73607.r1 Homo sapien	0.00e+00
18	227	21.6	403	11	R65664	Y116809.r1 Homo sapien	0.00e+00
19	227	21.6	430	12	H00795	Yj30702.r1 Homo sapien	0.00e+00
20	226	21.5	386	17	W86567	Yh26c09.r1 Homo sapien	0.00e+00
21	226	21.5	439	12	H01069	Yh26c09.r1 Homo sapien	0.00e+00
22	222	21.1	513	23	AA411787	zwe62b09.r1 Soares tota	0.00e+00
23	221	20.9	336	11	R79875	Y185407.r1 Homo sapien	0.00e+00
24	219	20.9	468	11	R23095	Yh19505.r1 Homo sapien	0.00e+00
25	216	20.6	365	23	HUM505C02B	Human placenta cDNA 5'	0.00e+00
26	216	20.6	526	16	H94810	Y211C05.r1 Soares feta	0.00e+00
27	215	20.5	527	31	AA77267	Z196B03.s1 Soares feta	0.00e+00
28	214	20.4	294	10	T48916	Y070C06.r1 Homo sapien	0.00e+00
29	214	20.4	348	11	R33236	Yh48410.r1 Homo sapien	0.00e+00
30	213	20.3	429	13	H77743	Yh23T09.r1 Homo sapien	0.00e+00
31	212	20.2	478	31	AA778170	Z145C10.s1 Soares feta	0.00e+00
32	210	20.0	420	10	T49525	Y076F03.r1 Homo sapien	0.00e+00
33	205	19.5	291	23	HUM511F08B	Human placenta cDNA 5'	0.00e+00
34	203	19.4	365	11	R23453	Yh39B02.r1 Homo sapien	0.00e+00
35	203	19.4	393	11	R33285	Yh81D04.r1 Homo sapien	0.00e+00
36	203	19.4	465	29	AA704477	Y211D06.s1 Soares feta	0.00e+00
37	202	19.3	261	23	HUM525D05B	Human placenta cDNA 5'	0.00e+00
38	201	19.2	438	14	N57230	Yw65E07.r1 Homo sapien	0.00e+00
39	197	18.8	465	14	W01919	Z335C04.r1 Soares feta	0.00e+00
40	196	18.7	479	11	R68866	Y437D02.r1 Homo sapien	0.00e+00
41	195	18.6	347	11	R34458	Yh85B04.r1 Homo sapien	0.00e+00
42	194	18.5	450	12	H04324	Yj20912.s1 Homo sapien	0.00e+00
43	194	18.5	450	29	AA677403	Z162G07.s1 Soares feta	0.00e+00
44	192	18.3	344	11	R27121	Yh52h07.r1 Homo sapien	0.00e+00
45	188	17.9	267	13	N40676	Yw79B10.r1 Homo sapien	0.00e+00

## ALIGNMENTS

RESULT	LOCUS	1	HUM505B08B	373 bp	MRNA	EST	21-MAY-1996
DEFINITION							
ACCESSION							
NID							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							
1 (bases 1 to 373)							
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shlomiyah,H., Takeuchi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.							
Unpublished (004)							
Unpublished (1995)							
2 (bases 1 to 373)							
Fujiwara,T.							
Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd, Japan (Tel:0886-65-2888, Fax:0886-37-1035)							
Submitted (30-May-1995) to DDBJ by:							
Tsutomu Fujiwara							
Otsuka GEN Research Institute							
Otsuka Pharmaceutical Co., Ltd							
463-10 Kagasuno Kawachi-cho							
Tokushima, Tokushima							
771-01							
Japan							
Phone: 0886-65-2888							

Fax : 0886-37-1035.

FEATURES  
 source Location/Qualifiers  
 1. 373  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Clontech human placenta polyA+ mRNA (#5518)"

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 Best Local Similarity 99.2%; Pred. No. 0.00e+00;  
 Matches 260; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 47 TTGCCCCAGATCAGCAGCTACAGAGAAACCCATCTTCCAGCGGGTCCCAACTACT 106  
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 QY 787 TTGCCAGATCAGCAGCTACAGAGAAACCCATCTTCCAGCGGGTCCCAACTACT 846  
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 DB 107 TCAGTGCATGGGCTGCTGCTCTAGAGCATATCCCATCTCAAGTCCCAAGAAC 166  
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 QY 847 TCAGTGCATGGGCTGCTGCTCTAGAGCATATCCCATCTCAAGTCCCAAGAAC 906  
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 DB 167 GATGTGGTCCAAAGAACGTCACCTCAGAGTCACCTGCTGTAGTAATCATATTA 226  
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 QY 907 GATGTGGTCCAAAGAACGTCACCTCAGAGTCACCTGCTGTAGTAATCATATTA 966  
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 DB 227 CAGGTCACAGTAATGGGGGTTTCAAACTGAGAACACACAGCGGCTGCCACTGAGTAC 286  
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 QY 967 CAGGTCACAGTAATGGGGGTTTCAAACTGAGAACACACAGCGGCTGCCACTGAGTAC 1026  
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 DB 287 TTGTATTATCACAATCTTAA 308  
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 QY 1027 TTGTATTATCACAATCTTAA 1048  
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RESULT 2  
 LOCUS C18240 379 bp mRNA EST 09-SEP-1996

DEFINITION Human placenta cDNA 5'-end GEN:559D08.  
 ACCESSION C18240  
 NID 91579842  
 KEYWORDS EST; EST(expressed sequence tag); Human placenta.  
 SOURCE Homo sapiens placenta cDNA to mRNA, clone:559D08.  
 ORGANISM Homo sapiens  
 Eukaryotes; Mitocondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae;  
 Homo.

REFERENCE  
 AUTHORS 1 (sites)  
 Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,  
 Kyushiki,H., Nageita,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,  
 Shinomiya,H., Suzuki,M., Takachi,A., Takeda,S., Watanabe,T.,  
 Maekawa,H., Nakamura,Y. and Takahashi,E.  
 Otsuka cDNA project  
 Unpublished (1996)  
 2 (bases 1 to 379)

REFERENCE  
 AUTHORS Fujiwara,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu  
 Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical  
 Co., Ltd. 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,  
 Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)

FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="559D08"  
 /tissue\_type="placenta"

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 Matches 259; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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 QY 787 TTGCCAGATGACAGCTACAGAGAAACCCATCTTCTCCAGCGGGTCCCAACTACT 846  
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 DB 127 TCAGTGCATGGGCTGCTGCTCTAGAGCATATCCCATCTCAAGTCCCAAGAAC 186  
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 QY 847 TCAGTGCATGGGCTGCTGCTCTAGAGCATATCCCATCTCAAGTCCCAAGAAC 906  
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 QY 907 GATGTGGTCCAAAGAACGTCACCTCAGAGTCACCTGCTGTAGTAATCATATTA 966  
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 QY 967 CAGGTCACAGTAATGGGGGTTTCAAACTGAGAACACACAGCGGCTGCCACTGAGTAC 1026  
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 DB 307 TTGTATTATCACAATCTTAA 328  
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 QY 1027 TTGTATTATCACAATCTTAA 1048  
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RESULT 3  
 LOCUS R76249 392 bp mRNA EST 06-JUN-1995

DEFINITION y172b05.r1 Homo sapiens cDNA clone 144753 3' similar to gb.v00518  
 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.  
 ACCESSION R76249  
 NID 9850931  
 KEYWORDS EST.  
 SOURCE human clone-144753 library-Soares placenta NB2HP vector-pT773D  
 (Pharmacia) with a modified polylinker host-DH10B (ampicillin  
 resistant) primer-Promega -2iml3i Rsite1-Not I Rsite2-Eco RI female  
 placenta obtained at birth (full term). 1st strand cDNA was primed  
 with a Not I - oligo(dT) primer [5'  
 AACTGAGAAATTCGGCGCCGACGAGATTTTCTTTTCTTTT 3'], double-stranded  
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the modified pT773  
 vector. Library went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens  
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Chonmata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
 AUTHORS 1 (bases 1 to 392)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hiltman,M., Kucaba,T., Le,M., Lennom,G., Marra,M.,  
 Parsons,D., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.  
 The WashU-Merck EST Project  
 Unpublished (1995)

TITLE  
 JOURNAL  
 COMMENT Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 High quality sequence stops: 328  
 Source: IMAGE Consortium, LBNL.  
 This clone is available royalty-free through LBNL; contact the  
 IMAGE Consortium (info@imgc.lbnl.gov) for further information.

FEATURES  
 source Location/Qualifiers  
 1. 392  
 /organism="Homo sapiens"  
 /clone="144753"

BASE COUNT 100 a 90 c 89 g 112 t 1 others  
 ORIGIN

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 Best Local Similarity 99.2%; Pred. No. 0.00e+00;

Matches 260; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 35 TTGCCCAAGATGACGCTACAGAGAAACCCATCTTCTCCAGCCGGGTGCCCAATACT 94  
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Oy 787 TTGCCCAAGATGACGCTACAGAGAAACCCATCTTCTCCAGCCGGGTGCCCAATACT 846  
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Db 95 TCAGTGCATGGGCTGCTCTCTCTAGAGCATATCCCATCTCACTAAGGTCCAGAGAC 154  
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Oy 847 TCAGTGCATGGGCTGCTCTCTCTAGAGCATATCCCATCTCACTAAGGTCCAGAGAC 906  
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Db 155 GATGTGGTCCAAAGAACGTCACCTCAGAGTCCATCTGCTGTAGCTAAATCATATATA 214  
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Oy 907 GATGTGGTCCAAAGAACGTCACCTCAGAGTCCATCTGCTGTAGCTAAATCATATATA 966  
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Db 215 CAGGTCACATATAGGGGGGTTTAAAGTGGAGAACACACGGCGTCCACTGCAGTAC 274  
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Oy 967 CAGGTCACATATAGGGGGGTTTAAAGTGGAGAACACACGGCGTCCACTGCAGTAC 1026  
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Db 275 TTGTATATATCACAATCTTAA 296  
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Oy 1027 TTGTATATATCACAATCTTAA 1048  
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RESULT 4 C17209 464 bp mRNA EST 04-SEP-1996

LOCUS

DEFINITION Human placenta cDNA 5'-end GENE:541F08.

ACCESSION C17209

NID g1571916

KEYWORDS EST:(expressed sequence tag); Human placenta.  
Homo sapiens placenta cDNA to mRNA, clone:541F08.

SOURCE Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;  
Homo.

REFERENCE 1 (sites)  
Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,  
Kiyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,  
Shinomura,H., Suzuki,M., Takachi,A., Takeda,S., Watanabe,T.,  
Maekawa,H., Nakamura,Y. and Takahashi,E.  
Otsuka cDNA project  
Unpublished (1996)  
2 (bases 1 to 464)  
Fujiwara,T.  
Direct Submission  
Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu  
Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical  
Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,  
Japan (Tel: +81-886-65-2888, Fax: +81-886-37-1035)

FEATURES  
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/tissue\_type="placenta"

BASE COUNT 114 a 117 c 95 g 138 t

ORIGIN

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Best Local Similarity 99.2%; Pred. No. 0.00e+00;  
Matches 260; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 219 CAGGTCACAGTAATGGGGGGTTTCAAGTGAGAACACACGGCGTCCACTGCAGTAC 278  
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Oy 967 CAGGTCACAGTCATGGGGGGTTTCAAGTGAGAACACACGGCGTCCACTGCAGTAC 1026  
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Db 279 TTGTATATATCACAATCTTAA 300  
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Oy 1027 TTGTATATATCACAATCTTAA 1048  
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RESULT 5  
LOCUS R71429 467 bp mRNA EST 01-JUN-1995

DEFINITION Y151003.f1 Homo sapiens cDNA clone 142757 5' similar to gb:V00518  
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.

ACCESSION R71429

NID g844946

KEYWORDS EST.  
human clone-142757 library-soares placenta Nb2HP vector-pT7p3D  
(Pharmacia) with a modified polylinker host-DH10B (ampicillin  
resistant) primer-M13p1 Rsite1-Not I Rsite2-Eco RI female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - oligo(dT) primer (5'  
ACTGAGAGATATCGCGCGCGAGAGATTTTTTTTTTTTTTTT 3'), double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT773  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bernaldo.

ORGANISM Homo sapiens  
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 467)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maize,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)

REFERENCE 1 (bases 1 to 467)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maize,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Source  
1..467  
/organism="Homo sapiens"  
/clone="142757"

BASE COUNT 113 a 114 c 98 g 139 t 3 others

ORIGIN

Query Match 24.6%; Score 258; DB 11; Length 467;  
Best Local Similarity 99.2%; Pred. No. 0.00e+00;  
Matches 260; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

|||||  
QY 907 GATGTGGTCCAAAAGAACGTCACCTCAGACTCGCTGCTACTTAATCATATTA 966  
Db 230 CAGGTCACAGTAATGGGGGTTTCAAAGTGAGACACACGCGGCGCCAGTAC 289  
QY 967 CAGGTCACAGTACTGGGGGTTTCAAAGTGAGACACACGCGGCGCCAGTAC 1026  
Db 290 TTGTTATTATCACAATCTTAA 311  
QY 1027 TTGTTATTATCACAATCTTAA 1048  
RESULT 6 H00861 423 bp mRNA EST 19-JUN-1995  
LOCUS  
DEFINITION Y131H01.r1 Homo sapiens cDNA clone 150385 5' similar to gb:V00518  
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.  
ACCESSION H00861  
NID 9863794  
KEYWORDS EST.  
SOURCE human clone-150385 library-Soares placenta NB2HP vector-pT773D  
(Pharmacia) with a modified polylinker host-DH10B (ampicillin  
resistant) primer-M13p1 Rsite1-Not I Rsite2-Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - 01390(GT) primer [5',  
AACTGGAAGATTCGCGCGCGCGGAGATTTTCTTTTCTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT73  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.  
ORGANISM Homo sapiens  
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chondata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 423)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence stops: 344  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source 1..423  
/organism="Homo sapiens"  
/clone="150385"  
BASE COUNT 109 a 95 c 95 g 119 t 5 others  
ORIGIN  
Query Match 24.5%; Score 257; DB 12; Length 423;  
Best Local Similarity 98.9%; Pred. No. 0.00e+00;  
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Db 18 TTGCCAGAAATGACGCTACAGAAACCAATCTTCTCCAGCGGGGTGCCCAATACT 77  
QY 787 TTGCCAGAAATGACGCTACAGAAACCAATCTTCTCCAGCGGGGTGCCCAATACT 846  
Db 78 TCAGTGCATGGGCTGCTCTCTAGAGCATATCCACTCACTAAGGTCCAAAGAAC 137  
QY 847 TCAGTGCATGGGCTGCTCTCTAGAGCATATCCACTCACTAAGGTCCAAAGAAC 906

Db 138 GATGTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGTGTACTTAATCATATTA 197  
QY 907 GATGTGGTCCAAAAGAACGTCACCTCAGAGTCCACTTGTGTACTTAATCATATTA 966  
Db 198 CAGGTCACAGTAATGGGGGTTTCAAAGTGAGACACACGCGGCGCCAGTAC 257  
QY 967 CAGGTCACAGTACTGGGGGTTTCAAAGTGAGACACACGCGGCGCCAGTAC 1026  
Db 258 TTGTTATTATCACAATCTTAA 279  
QY 1027 TTGTTATTATCACAATCTTAA 1048  
RESULT 7 R23843 433 bp mRNA EST 20-APR-1995  
LOCUS  
DEFINITION YH48C04.r1 Homo sapiens cDNA clone 132966 5' similar to gb:V00518  
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.  
ACCESSION R23843  
NID 9778731  
KEYWORDS EST.  
SOURCE human clone-132966 library-Soares placenta NB2HP vector-pT773D  
(Pharmacia) with a modified polylinker host-DH10B (ampicillin  
resistant) primer-M13p1 Rsite1-Not I Rsite2-Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - 01390(GT) primer [5',  
AACTGGAAGATTCGCGCGCGCGGAGATTTTCTTTTCTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT73  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo.  
ORGANISM Homo sapiens  
Eukaryote; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 433)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence stops: 334  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source 1..433  
/organism="Homo sapiens"  
/clone="132966"  
BASE COUNT 111 a 104 c 90 g 127 t 1 others  
ORIGIN  
Query Match 24.4%; Score 256; DB 11; Length 433;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 261; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Db 2 CAGATTCGCAAGATGACGCTACAGAAACCAATCTTCTCCAGCGGGGTGCCCA 61  
QY 783 CAGTTCCAGAAATGACGCTACAGAAACCAATCTTCTCCAGCGGGGTGCCCA 842  
Db 62 TACTTCAGTGCATGGGCTGCTCTCTAGAGCATATCCACTCACTAAGGTCCAA 121  
QY 843 TACTTCAGTGCATGGGCTGCTCTCTAGAGCATATCCACTCACTAAGGTCCAA 902

DB	122	AGACATATGTGGTCCAAAAGAACGTCACCTGAGATCCACTTGCCTGTAGCTAAATCAT	181
QY	903	AGACATATGTGGTCCAAAAGAACGTCACCTGAGATCCACTTGCCTGTAGCTAAATCAT	962
DB	182	ATACAGGGTCCACGTAATGGGGGGTTCCAAAGTGAGAGACACACAGCGCTGCCACTCA	241
QY	963	ATAACAGGGTCCACGTAATGGGGGGTTCCAAAGTGAGAGACACACAGCGGGTGCCTCA	1022
DB	242	GTACTTGTATTATATCAAAATCTTAA	267
QY	1023	GTACTTGTATTATATCAAAATCTTAA	1048
RESULT	8		
LOCUS	H00781	452 bp	mRNA EST 19-JUN-1995
DEFINITION	y330d01.r1 Homo sapiens cDNA clone 150241 5' similar to gb:v00518		
ACCESSION	GLTCO3PROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN); .		
NID	H00781		
KEYWORDS	98637714		
SOURCE	EST.		
	human clone-150241 library-Soares placenta NB3HP vector-pT773D		
	(Pharmacia) with a modified polylinker host-BH108 (ampicillin		
	resistant) primer-M13P1 Rsite1-Not I Rsite2-Eco RI Female placenta		
	obtained at birth (full term). 1st strand cDNA was primed with a		
	Not I - oligo(dT) primer 15',		
	AATGCAAGATTCGGCGCCGACGAGATTTTTTTTTTTTTTTT 3'), double-stranded		
	cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not		
	I and cloned into the Not I and Eco RI sites of the modified pT773		
	vector. Library went through one round of normalization. Library		
	constructed by Bento Soares and M.Fatima Bonaldo.		
ORGANISM	Homo sapiens		
	Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;		
	Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;		
	Sarcopterygii; Chonamata; Tetrapoda; Amniota; Mammalia; Theria;		
	Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 452)		
REFERENCE	Hillier,L., Clark,N., Dubnue,T., Elliston,K., Hawkins,M.,		
AUTHORS	Holman,M., Hiltman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,		
	Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,		
	Tevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and		
	Wilson,R.		
TITLE	The Mashu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK		
	Mashu-Merck EST Project		
	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: est@watson.wustl.edu		
	High quality sequence stops: 322		
	Source: IMAGE Consortium, LNLN		
	This clone is available royalty-free through LNLN; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
FEATURES	Location/Qualifiers		
source	1..452		
	/organism="Homo sapiens"		
	/clone="150241"		
BASE COUNT	107 a	104 c	103 g 133 t 5 others
ORIGIN			
Query Match	24.4%	Score 256:	DB 12: Length 452;
Best Local Similarity	99.2%	Pred. No. 0.00e+00;	
Matches 258:	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
DB	44	TTGCCAGAAATCAGGCTACAGAGAAACCCATTTCTTCCAGCGGGGTCGCCAATACT	103
QY	787	TTGCCAGAAATCAGGCTACAGAGAAACCCATTTCTTCCAGCGGGGTCGCCAATACT	846
DB	104	TCAGTGCATGGCGCTGCTTCTTCAAGACCAATCCCACTCCATNAAGTCCAGAGAGAC	163

QY	847	TCAGTGCATGGGCTGCTCTCTCTAGAGCATATCCCACTCCACTCAAGTCCAGAAAGAC	906
Db	164	GATGTGGTCCAAAAGAAAGTCACCTCAGAGTCACCTGCTGTGTAGCTAAATCATATAA	223
QY	907	GATGTGGTCCAAAAGAAAGTCACCTCAGAGTCACCTGCTGTGTAGCTAAATCATATAA	966
Db	224	CAGGTGCACACTAATGGGGGTTTCAAGTGGAGAACACACGGCGTCCACTGCAGTAC	283
QY	967	CAGGTGCACACTCAAGGGGGTTTCAAGTGGAGAACACACGGGGTCCACTGCAGTAC	1026
Db	284	TTGTATATATCACAAAATCTT 303	
QY	1027	TTGTATATATCACAAAATCTT 1046	
RESULT	9		
LOCUS	C17142	478 bp	mRNA EST 04-SEP-1996
DEFINITION	Human placenta cDNA 5'-end GEM-539604.		
ACCESSION	C17142		
NID	g1571849		
KEYWORDS	EST; EST (expressed sequence tag); Human placenta.		
SOURCE	Homo sapiens placenta cDNA to mRNA, clone:539604.		
ORGANISM	Homo sapiens		
	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1. (sites)		
AUTHORS	Fujiwara, T., Hirano, H., Hishigaki, H., Horie, M., Kawai, A., Kuga, Y., Kyushiki, H., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Suzuki, M., Takaiichi, A., Takeda, S., Watanabe, T., MaeKawa, H., Nakamura, Y. and Takahashi, E.		
TITLE	Otsuka cDNA project		
JOURNAL	Unpublished (1996)		
REFERENCE	2 (bases 1 to 478)		
AUTHORS	Fujiwara, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawanchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)		
FEATURES	Location/Qualifiers		
source	1. .478		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="539604"		
	/tissue-type="placenta"		
BASE COUNT	125 a 113 c 96 g 144 t		
ORIGIN			
Query Match	24.2%; Score 254; DB 23; Length 478;		
Best Local Similarity	99.2%; Pred. No. 0.00e+00;		
Matches 256; Conservative	0; Mismatches 2; Indels 0; Gaps 0;		
Db	1	CCAGATGCACGCTACAGAGAAAACCATCTTCTCCACGCGGGTGGCCCATACTTCAG	60
QY	791	CCAGATGCACGCTACAGAGAAAACCATCTTCTCCACGCGGGTGGCCCATACTTCAG	850
Db	61	TGCATGGGCTGCTGCTTCTCTAGACATATCCCACTCACTAAGTCCAAAGACGATG	120
QY	851	TGCATGGGCTGCTGCTTCTCTAGACATATCCCACTCACTAAGTCCAAAGACGATG	910
Db	121	TTGGTCCAAAAGAAAGTCACCTCAGAGTCACCTGCTGTAGCTAAATCATATAACAG	180
QY	911	TTGGTCCAAAAGAAAGTCACCTCAGAGTCACCTGCTGTAGCTAAATCATATAACAG	970
Db	181	GTCACAGTAATGGGGGTTTCAAGTGGAGAACACACGCGGTGCCACTGCAGTACTGT	240
QY	971	GTCACAGTATGGGGGTTTCAAGTGGAGAACACACGCGGTGCCACTGCAGTACTGT	1030
Db	241	TATATCACAAAATCTTAA 258	

QY 1031 TATTATCAAAATCTTAA 1048

RESULT 10 C18403 330 bp mRNA EST 09-SEP-1996

LOCUS

DEFINITION Human placenta cDNA 5'-end GEN=561H02.

ACCESSION C18403

KEYWORDS EST; EST(expressed sequence tag); Human placenta.

SOURCE Homo sapiens placenta cDNA to mRNA, clone:561H02.

ORGANISM Homo sapiens

Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (sites)

AUTHORS Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shimohira,H., Suzuki,M., Takachi,A., Takeda,S., Watanabe,T., Maekawa,H., Nakamura,Y. and Takahashi,E.

TITLE Otsuka cDNA project

JOURNAL Unpublished (1996)

REFERENCE 2 (bases 1 to 330)

AUTHORS Fujiwara,T.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)

FEATURES

source

1..330

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="561H02"

/tissue-type="placenta"

BASE COUNT 82 a 87 c 73 g 88 t

ORIGIN

Query Match 23.9%; Score 251; DB 23; Length 330;

Best Local Similarity 98.9%; Pred. No. 0.00e+00;

Matches 259; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Db 67 TTGCCAAGATGACGCTACAGAAACCATTCTTCTCCAGCGGGTCCCAATCTACT 126

QY 787 TTGCCAAGATGACGCTACAGAAACCATTCTTCTCCAGCGGGTCCCAATCTACT 846

Db 127 TCAGTCATGGGGTGTCTCTCTAGAGCATATCCCACTCCACTAAGTCCCAAGAAC 186

QY 847 TCAGTCATGGGGTGTCTCTCTAGAGCATATCCCACTCCACTAAGTCCCAAGAAC 906

Db 187 GATGTTGTCACAAAGACGTCACTCAGATGCTGCTGTAGTAATCATATATA 246

QY 907 GATGTTGTCACAAAGACGTCACTCAGATGCTGCTGTAGTAATCATATATA 966

Db 247 CAGGTCACAGTAATGGGGGTTTCAAGTGAGA-CCACAGCGCGTGCACATGACATG 305

QY 967 CAGGTCACAGTAATGGGGGTTTCAAGTGAGA-CCACAGCGCGTGCACATGACATG 1026

Db 306 TTGTTATTATCAAAATCTTAA 327

QY 1027 TTGTTATTATCAAAATCTTAA 1048

RESULT 11

LOCUS R77385 458 bp mRNA EST 06-JUN-1995

DEFINITION Y175d11.r1 Homo sapiens cDNA clone 145077 5' similar to gb:V00518 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.

ACCESSION R77385

KEYWORDS EST.

SOURCE human clone=145077 library=Soares placenta Nb2HP vector=PT73D (Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer-M13R1 Ralte1-Not I Ralte2-Eco RI female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGAGAGATCCGCGCGGAGGAGATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bernaldo.

ORGANISM Homo sapiens

Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 458)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marre,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisan,E., Waterson,K., Williamson,A., Woldmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 393

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

FEATURES

source

1..458

/organism="Homo sapiens"

/clone="145077"

BASE COUNT 119 a 109 c 97 g 133 t

ORIGIN

Query Match 23.8%; Score 250; DB 11; Length 458;

Best Local Similarity 99.2%; Pred. No. 0.00e+00;

Matches 252; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 16 AATGCGCTACAGAAACCATTCTTCTCCAGCGGGTCCCAATCTTCACTGCA 75

QY 795 AATGCGCTACAGAAACCATTCTTCTCCAGCGGGTCCCAATCTTCACTGCA 854

Db 76 TGGCTGCTGCTTCTCTAGACATATCCCACTCCACTAAGTCCCAAGAGATGTTGG 135

QY 855 TGGCTGCTGCTTCTCTAGACATATCCCACTCCACTAAGTCCCAAGAGATGTTGG 914

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QY 915 TCCAAAAGAGCTCACTCAGAGTCACTTGTGTAGTAATCATATTAACAGGGTCA 974

Db 196 CAGTATGGGGGTTTCAAGTGAGAACACACAGCGCGTGCACATGCACTACTGTTATT 255

QY 975 CAGTATGGGGGTTTCAAGTGAGAACACACAGCGCGTGCACATGCACTACTGTTATT 1034

Db 256 ATCACAATCTTAA 269

QY 1035 ATCACAATCTTAA 1048

RESULT 12

LOCUS H03289 482 bp mRNA EST 20-JUN-1995

DEFINITION Y144h10.r1 Homo sapiens cDNA clone 151651 5' similar to gb:V00518 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.

ACCESSION H03289

KEYWORDS EST.



SOURCE human clone-151651 library-Soares Placenta NB2HP vector-pT73D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13RPI Rsite1-Not I Rsite2-Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - 0190(OT) primer [5].

REFERENCE 1 (bases 1 to 482)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Eliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The Washu-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK  
Washu-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 301  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

FEATURES  
source  
1. 482  
Location/Qualifiers  
/organism="Homo sapiens"  
/clone="151651"

BASE COUNT 111 a 106 c 118 g 142 t 5 others

ORIGIN

Query Match 23.6%; Score 248; DB 12; Length 482;  
Best Local Similarity 98.9%; Pred. No. 0.00e+00;  
Matches 261; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Db 51 TTGCCCAAGATGACGCTACAGAGAAACCCATTCTTCCAGCGGGGTGCCCAATACT 110  
|||||  
Qy 787 TTGCCCAAGATGACGCTACAGAGAAACCCATTCTTCCAGCGGGGTGCCCAATACT 846  
|||||

Db 111 TCAGTCATGGGCTGCTCTTCTAGAGCATATCCACTCCACTAAGTCCAAAGAAC 170  
|||||  
Qy 847 TCAGTCATGGGCTGCTCTTCTAGAGCATATCCACTCCACTAAGTCCAAAGAAC 906  
|||||

Db 171 GATGTTGTCCTCAAAAGAACGCTCAGAGTCCACTTGCCTGCTACTAATATATTA 230  
|||||  
Qy 907 GATGTTGTCCTCAAAAGAACGCTCAGAGTCCACTTGCCTGCTACTAATATATTA 966  
|||||

Db 231 CAGGTCACAGTATGGGGGTTTCAAGTGGAGAACACACGCGGCTGCCTGAGT 290  
|||||  
Qy 967 CAGGTCACAGTATGGGGGTTTCAAGTGGAGAACACACGCGGCTGCCTGAGT 1024  
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Db 291 ACTTGTATTATCACAATCTTAA 314  
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Qy 1025 ACTTGTATTATCACAATCTTAA 1048  
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RESULT 13  
LOCUS HOM530G10B 336 bp mRNA EST 13-DEC-1995

DEFINITION Human placenta cDNA 5'-end GEN-530G10.

ACCESSION D79076

NID 91180949

KEYWORDS EST; EST(expressed sequence tag); Human placenta.

SOURCE Homo sapiens placenta cDNA to mRNA, clone\_1lb:human placenta polyA+.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 336)

AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takachi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maezawa,H., Shin,S. and Nakamura,Y.

TITLE Large-scale sequencing project at Otsuka GEN Research Institute

JOURNAL Unpublished (1995)

REFERENCE 2 (bases 1 to 336)

AUTHORS Fujiwara,T.

TITLE Direct Submission

JOURNAL Submitted (07-NOV-1995) to the DDBJ/EMBL/Genbank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan

COMMENT Submitted (7-NOV-1995) to DDBJ by:  
Tsutomu Fujiwara  
Otsuka GEN Research Institute  
Otsuka Pharmaceutical CO., Ltd  
463-10 Kagasuno Kawauchi-cho  
Tokushima, Tokushima  
771-01  
Japan  
Phone:0886-65-2888  
Fax :0886-37-1035.

FEATURES  
source  
1. 336  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="human placenta polyA+"  
/issue\_type="placenta"

BASE COUNT 76 a 89 c 78 g 93 t

ORIGIN

Query Match 23.4%; Score 245; DB 23; Length 336;  
Best Local Similarity 98.0%; Pred. No. 0.00e+00;  
Matches 250; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 47 TTGCCCAAGATGACGCTACAGAGAAACCCATTCTTCCAGCGGGGTGCCCAATACT 106  
|||||  
Qy 787 TTGCCCAAGATGACGCTACAGAGAAACCCATTCTTCCAGCGGGGTGCCCAATACT 846  
|||||

Db 107 TCAGTCATGGGCTGCTCTTCTAGAGCATATCCACTCCACTAAGTCCAAAGAAC 166  
|||||  
Qy 847 TCAGTCATGGGCTGCTCTTCTAGAGCATATCCACTCCACTAAGTCCAAAGAAC 906  
|||||

Db 167 GATGTTGTCCTCAAAAGAACGCTCAGAGTCCACTTGTGCTAGTACTAATATATTA 226  
|||||  
Qy 907 GATGTTGTCCTCAAAAGAACGCTCAGAGTCCACTTGTGCTAGTACTAATATATTA 966  
|||||

Db 227 CAGGTCACAGTATGGGGGTTTCAATAGTGGGACCCACACGCGTGCCTGCTGAGT 286  
|||||  
Qy 967 CAGGTCACAGTATGGGGGTTTCAATAGTGGGACCCACACGCGTGCCTGCTGAGT 1026  
|||||

Db 287 TTGTATTATCACA 301  
|||||  
Qy 1027 TTGTATTATCACA 1041  
|||||

RESULT 14  
LOCUS C18044 519 bp mRNA EST 09-SEP-1996

DEFINITION Human placenta cDNA 5'-end GEN-556F06.

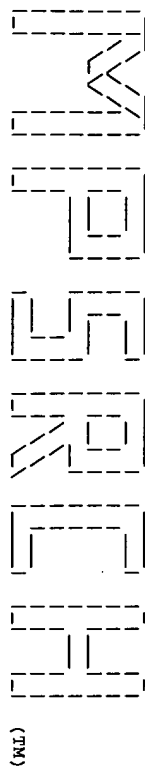
ACCESSION C18044

NID 91579646

KEYWORDS EST; EST(expressed sequence tag); Human placenta.

SOURCE Homo sapiens placenta cDNA to mRNA, clone:556F06.





(TM)

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\*\*\*\*\*  
MSPrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed May 6 08:50:59 1998; MasPar time 8.51 Seconds  
Tabular output not generated. 449,440 Million cell updates/sec

Title: >US-08-804-166-2  
Description: (1-256) from US08804166.pep  
Perfect Score: 1994  
Sequence: 1 SRTSLILAFGLCLPMLQEG.....GFKVENHTGCHSTCYVHKS 256

Scoring table: PAM 150  
Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

a-geneseq31  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26

Statistics: Mean 31.442; Variance 119.617; scale 0.263

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1994	100.0	256	26	W33357	TBP(20-161)/hCG-alpha	1.90e-207
2	1667	83.6	285	26	W33359	TBP(20-190)/hCG-alpha	1.11e-170
3	1321	66.2	307	26	W33358	TBP(20-161)/hCG-beta	6.46e-132
4	1291	64.7	336	26	W33360	TBP(20-190)/hCG-beta	1.46e-128
5	1124	56.4	161	5	R27496	Native 30 kD TNF inh1	6.19e-110
6	1124	56.4	199	4	R24080	Truncated TNF-alpha 5	6.19e-110
7	1124	56.4	309	13	R70108	TNF-R-GBPH fusion pro	6.19e-110
8	1124	56.4	371	2	R07449	Tumour Necrosis Facto	6.19e-110
9	1124	56.4	451	13	R70107	TNF-R-GBP 130 fusion	6.19e-110
10	1124	56.4	455	8	R42059	Lambda derived TNF-R.	6.19e-110
11	1124	56.4	455	2	R10986	30kD TNF inhibitor pr	6.19e-110
12	1124	56.4	455	4	R20787	TNF-alpha binding pro	6.19e-110
13	1124	56.4	455	14	R75084	p55 TNF-R.	6.19e-110
14	1124	56.4	455	2	R07451	Human Tumour Necrosis	6.19e-110
15	1124	56.4	455	2	R11082	Human 55kD TNF-bindin	6.19e-110
16	1124	56.4	455	4	R24000	TNF-alpha 55kD recept	6.19e-110
17	1124	56.4	547	13	R70104	TNF-R-GBPH fusion pro	6.19e-110
18	1124	56.4	884	13	R70109	TNF-R-GBP 130 fusion	6.19e-110
19	1124	56.4	900	13	R70103	TNF-R-GBP 130 fusion	6.19e-110

20	1124	56.4	1245	13	R70106	TNF-R-Pl. vivax Duffy	6.19e-110
21	1124	56.4	1604	13	R70105	TNF-R-EBA 175 fusion	6.19e-110
22	1118	56.1	433	8	R51032	Mutant p55 tumour nec	2.88e-109
23	1118	56.1	443	8	R51033	Mutant p55 tumour nec	2.88e-109
24	1118	56.1	455	8	R51034	Mutant p55 tumour nec	2.88e-109
25	1118	56.1	455	8	R42197	p55 Tumour necrosis f	2.88e-109
26	1110	55.7	455	3	R12550	Type I TNF receptor	2.24e-108
27	996	49.9	168	4	R24084	Truncated TNF-alpha 5	1.06e-95
28	800	40.1	158	4	R24081	Truncated TNF-alpha 5	5.13e-74
29	788	39.5	461	2	R07450	Rat Tumour Necrosis F	1.08e-72
30	672	33.7	96	3	R15182	hCG/DCG alpha subunit	5.96e-60
31	667	33.5	92	1	P92146	Beta subunit of urina	2.10e-59
32	667	33.5	96	3	R15195	hCG alpha subunit mut	2.10e-59
33	667	33.5	116	26	W31665	Secreted protein huma	2.10e-59
34	667	33.5	116	2	R10095	Engineered human alph	2.10e-59
35	667	33.5	116	19	R99417	Dimeric glycoprotein	2.10e-59
36	667	33.5	222	15	R86268	Partially deglycosyla	2.10e-59
37	667	33.5	222	15	R86256	Single chain gonadotr	2.10e-59
38	667	33.5	226	15	R86255	Single chain gonadotr	2.10e-59
39	667	33.5	229	15	R86250	Single chain gonadotr	2.10e-59
40	667	33.5	234	15	R86254	Single chain gonadotr	2.10e-59
41	667	33.5	234	15	R86249	Single chain gonadotr	2.10e-59
42	667	33.5	234	15	R86248	Single chain gonadotr	2.10e-59
43	667	33.5	237	15	R86253	Single chain gonadotr	2.10e-59
44	667	33.5	237	15	R86251	Single chain gonadotr	2.10e-59
45	667	33.5	265	15	R86247	Single chain gonadotr	2.10e-59

## ALIGNMENTS

RESULT 1  
ID W33357 standard; Protein: 256 AA.

AC W33357;  
DE 19-MAR-1998 (first entry)  
DT TBP(20-161)/hCG-alpha fusion protein.  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW alpha subunit; hCG-alpha.

OS Homo sapiens.  
PN WO9730161-A1.  
PD 21-AUG-1997.  
PF 20-FEB-1997; U02315.  
PR 20-FEB-1996; US-011936.  
PA (ISITF) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell KR, Chappel SC, Jameson BA;  
PI WPI: 97-425036/39.

DR N-PSDB: T94007.  
DR Hydr dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PS hormone, especially FSH, for inducing follicular maturation  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotropin-alpha subunit  
CC (hCG-alpha) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
SQ number of injections needed.  
Sequence 256 AA.

Query Match 100.0%; Score 1994; DB 26; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.90e-207;  
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	ststlllafgllclpvlpgsadsvcpgqkyihpqnmslckckhkytlyndcpqpgd	60
Qy	1	SRTSLILAFGLCLPMLQEGSADSVCPQKYLHPQNNISICRKHGTYLNDCCPQGD	60
Db	61	tdreecssffasenhhlhclscskcrkemqgvelastvdrdcvgrgkrqyrhwse	120

QY 61 TDCEGSGSTASENHLRLCSCKREKQVEISSCTVDRDTCGCRNORRYHWE 120  
Db 121 nlfqfncslngtlvhsceqkntvctchagffirencvscagapgcpectlqenp 180  
QY 121 NLFQFNCSLNGTLVHSCQEKONTVCTCHAGFFIRENCEVSCAGAPGCPECTLOPNP 180  
Db 181 ffgapgaplqcmccfrrayptlrskktmvgkntvscavakynrvvmgfkfv 240  
QY 181 FFQAPGAPLQCMCCFRRAYPTLRSKKTMVGNVTSESTCVAKSYNRTVVMGFKFV 240  
Db 241 enhtgchscvtyhks 256  
QY 241 ENHTGCHSCVTYHKS 256

RESULT 2  
ID W33359 standard; Protein; 285 AA.  
AC W33359;  
DE 19-MAR-1998 (first entry)  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW alpha subunit; hCG-alpha.  
OS Homo sapiens.  
PN MO9730161-A1.  
PD 21-AUG-1997.  
PF 20-FEB-1997; U02315.  
PR 20-FEB-1996; US-011936.  
PI (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chappe SC, Jameson BA;  
DR WPI: 97-425036/39.  
DR N-PSDB: T94021.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PT hormone, especially FSH, for inducing follicular maturation  
PS Example; Pages 37-38; 60pp; English.  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotropin-alpha subunit  
CC (hCG-alpha) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.  
SQ Sequence 285 AA;

Query Match 83.6%; Score 1667; DB 26; Length 285;  
Best Local Similarity 89.1%; Pred. No. 1,11e-170;  
Matches 234; Conservative 2; Mismatches 0; Indels 29; Gaps 1;

Db 1 srtlllaifglclpwlqgsadsvcpqgkylhpqnsicctckhkylyndcpqpgd 60  
QY 1 SRTLLLAIFGLCLPWLQGSADSVCPQGKYIHPQNSICCTCKHKYLYNDPCPGPD 60  
Db 61 tdccessgsftaseenhlrlcsckrkemgyreisctvdrtdtvcgcrnoryhwe 120  
QY 61 TDCESSGSFTASENHLRLCSCKRKEGVEISCTVDRDTCGCRNORRYHWE 120  
Db 121 nlfqfncslngtlvhsceqkntvctchagffirencvscncklslectklspq 180  
QY 121 NLFQFNCSLNGTLVHSCQEKONTVCTCHAGFFIRENCEVSCNCKLSLECTKLSPQ 180  
Db 121 lenvgyredagttgagapgcpectlqenpffgagapblqcmccfrrayptlrskktm 240  
QY 121 LENVGYREDAGTTGAGAPGCPECTLQENPFFGAGAPBLQCMCCFRRAYPTLRSKKTM 240  
Db 241 lvqkntvscavakynrvvmgfkfvenhtachscvtyhks 285  
QY 241 LVQKNVTSESTCVAKSYNRTVVMGFKFVENHTACHSCVTYHKS 285

RESULT 3  
ID W33358 standard; Protein; 307 AA.  
AC W33358;  
DE 19-MAR-1998 (first entry)  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW beta subunit; hCG-beta.  
OS Homo sapiens.  
PN MO9730161-A1.  
PD 21-AUG-1997.  
PF 20-FEB-1997; U02315.  
PR 20-FEB-1996; US-011936.  
PI (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chappe SC, Jameson BA;  
DR WPI: 97-425036/39.  
DR N-PSDB: T94008.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PT hormone, especially FSH, for inducing follicular maturation  
PS Example; Pages 34-35; 60pp; English.  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotropin-beta subunit  
CC (hCG-beta) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.  
SQ Sequence 307 AA;

Query Match 66.2%; Score 1321; DB 26; Length 307;  
Best Local Similarity 98.8%; Pred. No. 6.46e-132;  
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 srtlllaifglclpwlqgsadsvcpqgkylhpqnsicctckhkylyndcpqpgd 60  
QY 1 SRTLLLAIFGLCLPWLQGSADSVCPQGKYIHPQNSICCTCKHKYLYNDPCPGPD 60  
Db 61 tdccessgsftaseenhlrlcsckrkemgyreisctvdrtdtvcgcrnoryhwe 120  
QY 61 TDCESSGSFTASENHLRLCSCKRKEGVEISCTVDRDTCGCRNORRYHWE 120  
Db 121 nlfqfncslngtlvhsceqkntvctchagffirencvscagapgc 171  
QY 121 NLFQFNCSLNGTLVHSCQEKONTVCTCHAGFFIRENCEVSCAGAPGC 171

RESULT 4  
ID W33360 standard; Protein; 336 AA.  
AC W33360;  
DE 19-MAR-1998 (first entry)  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW beta subunit; hCG-beta.  
OS Homo sapiens.  
PN MO9730161-A1.  
PD 21-AUG-1997.  
PF 20-FEB-1997; U02315.  
PR 20-FEB-1996; US-011936.  
PI (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chappe SC, Jameson BA;  
DR WPI: 97-425036/39.  
DR N-PSDB: T94022.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PT hormone, especially FSH, for inducing follicular maturation  
PS Example; Pages 39-40; 60pp; English.

CC A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric receptor chain or ligand, with ligand-receptor binding activity, CC bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with CC the hormone's other subunits. The fusion protein, e.g. the thymopoietin (TPO)/human chorionic gonadotropin-beta subunit CC (hCG-beta) fusion protein denoted by the present sequence, CC significantly increases the biological activity of the hormone CC component, reducing the requirement for hormone itself and the CC number of injections needed.

SQ Sequence 336 AA;

Query Match 64.7%; Score 1291; DB 26; Length 336;  
Best Local Similarity 99.4%; Pred. No. 1,466-128;

Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 streliafqlclpwlqgsadsvcpqkyihpqnslcctckhgtlylndcpqpgqd 60

Qy 1 SRTSLIAFLGLCLPWLQGSADSVCPQGXVYHPQNNISICTCKHKGTYLVNDGCPGQD 60

Db 61 tdcrcsgsgftasenhrlhrlscskcrkengvqeisctvdrtvcgrnqyrhywse 120

Qy 61 TDCRCESGSGFTASENHLRLCLSCSKCRKENGVEISCTVDRTVCGCRNQRHYWSE 120

Db 121 nlfcfncslclngtlhscgkqkntvctchagfflirencvcs 165

Qy 121 NLFQCFNCSLCLNGTIVHLSGCKQKNTVCTCHAGFFLIRENECVCSA 165

RESULT 5  
ID R27496 standard; protein; 161 AA.  
AC R27496;

DT 09-MAR-1993 (first entry)  
DE Native 30 kD TNF inhibitor.

KW Tumour necrosis factor; ethylene glycol; pharmacokinetic;  
KM adult respiratory distress syndrome; rheumatoid arthritis;

OS Homo sapiens.  
PN W09216221-A.

PD 01-OCT-1992.  
PF 13-MAR-1992; U02122.

PR 15-MAR-1991; US-669862.  
PR 17-JUN-1992; US-822296.

PA (SYND) SYNERGEN INC.  
PI Ames LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;

PT New ethylene glycolated polypeptide(s) with improved  
PT pharmacokinetic properties - for treating e.g. TNF and IL-1

PT mediated diseases, e.g. adult respiratory distress syndrome,  
PT rheumatoid arthritis, septic shock etc.

PS Claim 54; Fig 2; 100pp; English.

CC The sequence shows a native 30 kD TNF inhibitor which may be  
CC modified to contain at least one non-native cysteine residue, pref.

CC at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is  
CC joined to a non-peptidic polymer, pref. monomethoxy PEG via

CC thio-ether bonds. Two such TNF inhibitor mols. may be linked via  
CC this non-peptidic spacer. The modified polypeptides show improved

CC pharmacokinetic properties, i.e. increased mol. wt. hence reduced  
CC clearance rate following s.c. or systemic administration. Increased

CC sol. of native TNF inhibitors, and reduced antigenicity. The  
CC polypeptides may be used for treatment of TNF mediated diseases such

CC as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid  
CC arthritis, inflammatory bowel disease and septic shock. The same  
CC method may be applied to the interleukin-1 receptor antagonist

CC IL-1ra.  
SQ Sequence 161 AA; See also R27495.

Query Match 56.4%; Score 1124; DB 5; Length 161;  
Best Local Similarity 99.3%; Pred. No. 6,196-110;

Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 dsvepqgkyihpqnslcctckhgtlylndcpqpgqdtdecresgsgftasenhrlhrl 60

Qy 23 DSVCPQGXVYHPQNNISICTCKHKGTYLVNDGCPGQDTDCREESGSGFTASENHLRLCL 82

Db 61 scskcrkmgvqeisctvdrtvcgrkngyrhywseqlfcfncslclngtlhscgqe 120

Qy 83 SCSCSKCRKMGVEISCTVDRTVCGCRKNQRYHYWSENLFQCFNCSLCLNGTIVHLSGQE 142

Db 121 kntvctchagfflirencvcs 143

Qy 143 KNTVCTCHAGFFLIRENECVCSA 165

RESULT 6

ID R24080 standard; protein; 199 AA.

AC R24080; 05-NOV-1992 (first entry)

DE Truncated TNF-alpha 55kD receptor.

KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;

KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.

OS Homo sapiens.  
PN W09207076-A.

PD 30-APR-1992.  
PE 18-OCT-1991; G01826.

PR 18-OCT-1990; GB-022648.  
PA (CHAR-) CHARLING CROSS SUNLEY RES CENT.

PI Brennan FM, Feldmann M, Gray PW, Turner MC;  
DR WPI; 92-167156/20.

DR N-PSDB: Q24441.

PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for

PT treating autoimmune disease, septic shock, HIV etc.  
PS Example; Fig 7; 43pp; English.

CC This sequence is a truncated TNF-alpha receptor derivative, as encoded  
CC in pTRFrec. This was produced as described in Q24440.

CC This derivative lacks the 81 carboxyl terminal residues of the  
CC cytoplasmic domain. The derivative could be used in the

CC regulation of TNF-alpha mediated responses by binding and  
CC sequestering human TNF-alpha e.g. in the treatment of pulmonary

CC diseases, septic shock, HIV infection, malaria, viral meningitis,  
CC graft versus host disease and autoimmune diseases, esp. rheumatoid

CC arthritis.  
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8

SQ Sequence 199 AA;

Query Match 56.4%; Score 1124; DB 4; Length 199;  
Best Local Similarity 99.3%; Pred. No. 6,196-110;

Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvepqgkyihpqnslcctckhgtlylndcpqpgqdtdecresgsgftasenhrlhrl 100

Qy 23 DSVCPQGXVYHPQNNISICTCKHKGTYLVNDGCPGQDTDCREESGSGFTASENHLRLCL 82

Db 101 scskcrkmgvqeisctvdrtvcgrkngyrhywseqlfcfncslclngtlhscgqe 160

Qy 83 SCSCSKCRKMGVEISCTVDRTVCGCRKNQRYHYWSENLFQCFNCSLCLNGTIVHLSGQE 142

Db 161 kntvctchagfflirencvcs 183

Qy 143 KNTVCTCHAGFFLIRENECVCSA 165

RESULT 7

ID R70108 standard; protein; 309 AA.

AC R70108; 10-NOV-1995 (first entry)

DE TNF-R-GBPH fusion protein.  
KW Hybrid peptide; malaria parasite; plasmodium falciparum; fusion protein;

KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;  
KW GBP 130; GBP; glycoprotein binding peptide homologue; glycoprotein A;

OS Chimeric Homo sapiens.

OS Chimeric Plasmodium falciparum.  
 FH Key Location/Qualifiers  
 FT misc\_difference 230..269  
 FT /label=repeat\_region  
 FT /note="can be repeated n times, where n is a real  
 number"  
 PD W09506737-A.  
 PD 09-MAR-1995.  
 PR 01-SEP-1994; G01900.  
 PR 03-SEP-1993; GB-018350.  
 PR 23-AUG-1994; GB-017021.  
 PA (PREN/) PRENDERGAST K F.  
 PI Prendergast KF;  
 DR WPI: 95-115452/15.  
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PT malaria parasite peptide capable of binding a red blood cell and  
 PT a receptor peptide  
 PS Example A, Page 54-55; 93pp: English.  
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples  
 CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor  
 CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
 CC and glycoprotein binding protein (GBP) homologue (GBP). The  
 CC use of cytokine receptors not normally found on RBCs means that the  
 CC cytokine can bind harmlessly to the RBC without deleterious effect.  
 CC The RBC protects the hybrid peptides from excretion from the kidney, and  
 CC due to steric hindrance prevents the cytokines binding to a receptor in  
 CC another cell. GBP 130 or GBP are the pref. malaria parasite peptides  
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA  
 CC (pre major merozoite surface antigen) and the Duffy binding receptor  
 CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to  
 CC pref. glycoprotein A, B and C, sialo glycoproteins, found on the surface  
 CC of RBCs. The hybrid peptides are thus used to lower the levels of free  
 CC cytokines in the circulation to reduce pathological damage.  
 SQ Sequence 309 AA;

Query Match 56.4%; Score 1124; DB 13; Length 309;  
 Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 20 davecpqkylhpnmsicctckhkylylndcpgpddtcreesgsftasehnlrhl 79  
 |||||||  
 QY 23 dsvcpqkylhpnmsicctckhkylylndcpgpddtcreesgsftasehnlrhl 82  
 |||||||

DB 80 scskckemgvyelsctdrvtvcgcrnryhysenlfcfnscslngtvhlsce 139  
 |||||||  
 QY 83 scskckemgvyelsctdrvtvcgcrnryhysenlfcfnscslngtvhlsce 142

DB 140 kntvctchagfflreneecvscs 162  
 |||||||  
 QY 143 KONTVCTCHAGFFLRENECVSCA 165

RESULT 8  
 ID R07449 standard; protein; 371 AA.  
 AC R07449;  
 DT 29-JAN-1991 (first entry)  
 DE Tumour Necrosis Factor-binding Protein from pTNF-BP15 cDNA.  
 KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
 KW pTNF-BP15; infectious disease; parasitic disease; cachexia;  
 KW autoimmune disease; shock.  
 OS Homo sapiens.  
 PN EP-393438-A.  
 PD 24-OCT-1990.  
 PR 06-APR-1990; 106624.  
 PR 21-APR-1989; DE-913101.  
 PR 21-JUN-1989; DE-920282.  
 PA (BOHR) BOHRINGER INGELHEIMINT.  
 PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stralowa C;  
 DR WPI: 90-321987/43.  
 DR N-PEDB; Q06282.  
 PT DNA encoding TNF binding protein and TNF-receptor - used in

PT tumour treatment and to understand mechanism to TNF action  
 PS Disclosure: Fig 1(1-3); 51pp: German.  
 CC Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of  
 CC e.g. COS7 cells. The expressed proteins are useful  
 CC prophylactically and therapeutically to control disorders which  
 CC involve the damaging effects of TNF-alpha or beta (e.g. infectious or  
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
 CC respiratory distress syndrome etc., or side effects of treatment with  
 CC TNF-alpha). They can also be used as diagnostic reagents for  
 CC assaying TNF and in study of TNF-receptor interactions.  
 CC See also Q06282-Q06285.  
 SQ Sequence 371 AA;

Query Match 56.4%; Score 1124; DB 2; Length 371;  
 Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 41 davecpqkylhpnmsicctckhkylylndcpgpddtcreesgsftasehnlrhl 100  
 |||||||  
 QY 23 dsvcpqkylhpnmsicctckhkylylndcpgpddtcreesgsftasehnlrhl 82  
 |||||||

DB 101 scskckemgvyelsctdrvtvcgcrnryhysenlfcfnscslngtvhlsce 160  
 |||||||  
 QY 83 scskckemgvyelsctdrvtvcgcrnryhysenlfcfnscslngtvhlsce 142

DB 161 kntvctchagfflreneecvscs 183  
 |||||||  
 QY 143 KONTVCTCHAGFFLRENECVSCA 165

RESULT 9  
 ID R70107 standard; protein; 451 AA.  
 AC R70107;  
 DT 10-NOV-1995 (first entry)  
 DE TNF-R-GBP 130 fusion protein.  
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
 KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;  
 KW GBP 130; GBP; glycoprotein binding peptide homologue; glycoprotein A.  
 OS Chimeric Homo sapiens.  
 OS Chimeric Plasmodium falciparum.  
 PN W09506737-A.  
 PD 09-MAR-1995.  
 PR 01-SEP-1994; G01900.  
 PR 03-SEP-1993; GB-018350.  
 PR 23-AUG-1994; GB-017021.  
 PA (PREN/) PRENDERGAST K F.  
 PI Prendergast KF;  
 DR WPI: 95-115452/15.  
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PT malaria parasite peptide capable of binding a red blood cell and  
 PT a receptor peptide  
 PS Example A, Page 53-54; 93pp: English.  
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples  
 CC of these hybrid peptides. R70107 is a fusion of tumour necrosis factor  
 CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
 CC and glycoprotein binding protein (GBP) 130. The use of cytokine  
 CC receptors not normally found on RBCs means that the cytokine can bind  
 CC harmlessly to the RBC without deleterious effect. The RBC protects the  
 CC hybrid peptides from excretion from the kidney, and due to steric  
 CC hindrance prevents the cytokines binding to a receptor in another cell.  
 CC GBP 130 or GBP (GBP homologue) are the pref. malaria parasite peptides  
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
 CC PMMSA (pre major merozoite surface antigen) and the Duffy binding  
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
 CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on  
 CC the surface of RBCs. The hybrid peptides are thus used to lower  
 CC the levels of free cytokines in the circulation to reduce pathological  
 CC damage.  
 SQ Sequence 451 AA;

Query Match 56.4%; Score 1124; DB 13; Length 451;

Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 20 dsvcpqgkylhpnmsicctckhkgtylyndcpgpddtccrecesgftasenhrlhcl 79  
|||||  
Qy 23 dsvcpqgkylhpnmsicctckhkgtylyndcpgpddtccrecesgftasenhrlhcl 82  
|||||  
Db 80 scskckremgveissctdrdtvcgcrkngryhysenlfgcfnslclngtvlhscqe 139  
|||||  
Qy 83 scskckremgveissctdrdtvcgcrkngryhysenlfgcfnslclngtvlhscqe 142  
|||||

Db 140 kqntvctchagfflirenevcs 162  
|||||  
Qy 143 kqntvctchagfflirenevcs 165  
|||||

RESULT 10  
ID R42059 standard; Protein: 455 AA.  
AC R42059;  
DT 29-APR-1994 (first entry)  
DE Lambda derived TNF-R  
KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
pulmonary fibrosis; silicosis; allograft rejection;  
KW graft versus host disease; sepsis; inflammation; allergy;  
KW autoimmune dysfunction.  
OS Homo sapiens.  
OS Lambda-gli-0-7c1nfbp.  
FH Key Location/Qualifiers  
FT peptide 1..40  
FT protein /note="Signal peptide"  
FT 41..455  
FT /note="Mature hTNF-R"  
PN W09319777-A.  
PD 14-OCT-1993.  
PE 26-MAR-1993; U02938.  
PR 30-MAR-1993; US-860710.  
PA (IMMV) IMMUNEX CORP.  
PI Smith CA;  
DR WPI: 93-336592/42.  
DR N-PSDB: Q49932.  
PT New fusion protein tumour necrosis factor and human interleukin-1  
PT receptor - useful in therapy, diagnosis and assays of e.g.  
PT rheumatoid arthritis; diabetes; cerebral malaria; sepsis, etc.  
PS Disclosure; Page 57-59; 85pp; English.  
CC The sequences given in R42058-59 represent human tumour necrosis  
CC factor receptor (TNF-R) and the sequences in R42060-61 represent  
CC human interleukin-1 receptor (IL-1R). These sequences were used in  
CC the production of a fusion protein which conformed to one of the  
CC formulae:  
CC TNF-R-linker-TNF-R-linker-IL-1R  
CC IL-1R-linker-TNF-R-linker-TNF-R or  
CC TNF-R-linker-TNF-R  
CC The linker may comprise 5-100 amino acids selected from Gly, Asp,  
CC Ser, Thr and Ala. These linkers separate the individual moieties  
CC by such a distance that each component of the fusion protein is  
CC capable of folding into the secondary or tertiary structure required  
CC for its biological activity. These fusion proteins may be used in  
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
CC particularly in conditions in which both TNF and IL-1 play a causative  
CC role. They may be used to treat cachexia, rheumatoid arthritis,  
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
CC cerebral malaria, allograft and xenograft rejection in graft versus  
CC host disease, sepsis, septic shock, inflammation, allergies and  
CC autoimmune dysfunctions.  
SQ Sequence 455 AA;

Query Match 56.4%; Score 1124; DB 8; Length 455;

Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvcpqgkylhpnmsicctckhkgtylyndcpgpddtccrecesgftasenhrlhcl 100

|||||  
Qy 23 dsvcpqgkylhpnmsicctckhkgtylyndcpgpddtccrecesgftasenhrlhcl 82  
|||||  
Db 101 scskckremgveissctdrdtvcgcrkngryhysenlfgcfnslclngtvlhscqe 160  
|||||  
Qy 83 scskckremgveissctdrdtvcgcrkngryhysenlfgcfnslclngtvlhscqe 142  
|||||  
Db 161 kqntvctchagfflirenevcs 183  
|||||  
Qy 143 kqntvctchagfflirenevcs 165  
|||||

RESULT 11  
ID R10986 standard; Protein: 455 AA.  
AC R10986;  
DT 13-MAY-1991 (first entry)  
DE 30KD TNF inhibitor precursor.  
KW Tumour necrosis factor; inhibitor.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT cleavage\_site 40..41  
FT note="cleavage gives active protein"  
PN AU9058976-A.  
PD 24-JAN-1991.  
PE 16-JUL-1990; 058976.  
PR 18-JUL-1989; US-381080.  
PR 11-DEC-1988; US-450329.  
PR 07-FEB-1990; US-479661.  
PA (SYNE-) SYNERGEN INC.  
DR WPI: 91-073847/11.  
DR N-PSDB: Q10883.  
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha  
PT and -beta, useful as therapeutic agent.  
PS Disclosure; Fig 21; 142pp; English.  
CC The sequence comprises the entire 30 kD TNF inhibitor. The clone  
CC from which the sequence was deduced was isolated from a cDNA  
CC library prep. from RNA from U937 cells treated with PMA/PMA.  
CC The whole gene can be inserted into expression vectors for prepn.  
CC of TNF inhibitor for use in the treatment of inflammatory and  
CC degenerative diseases. The active protein is claimed (Claim 8).  
CC See also R10984 and R11001.  
SQ Sequence 455 AA;

Query Match 56.4%; Score 1124; DB 2; Length 455;  
Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvcpqgkylhpnmsicctckhkgtylyndcpgpddtccrecesgftasenhrlhcl 100  
|||||  
Qy 23 dsvcpqgkylhpnmsicctckhkgtylyndcpgpddtccrecesgftasenhrlhcl 82  
|||||  
Db 101 scskckremgveissctdrdtvcgcrkngryhysenlfgcfnslclngtvlhscqe 160  
|||||  
Qy 83 scskckremgveissctdrdtvcgcrkngryhysenlfgcfnslclngtvlhscqe 142  
|||||  
Db 161 kqntvctchagfflirenevcs 183  
|||||  
Qy 143 kqntvctchagfflirenevcs 165  
|||||

RESULT 12  
ID R20787 standard; Protein: 455 AA.

AC R20787;  
DT 11-MAY-1992 (first entry)  
DE TNF-alpha binding protein.  
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin;  
KW extracellular domain.

OS Homo sapiens.  
FH Key Location/Qualifiers  
FT peptide 1..40  
FT /note="Signal peptide"  
FT 41..455  
FT /note="Mature peptide"

FT domain 30..199  
 FT /note= "extracellular domain"  
 FT domain 212..234  
 FT /note= "transmembrane domain"  
 FT modified\_site 145..147  
 FT /note= "potential N-glycosylation site"  
 FT modified\_site 151..153  
 FT /note= "potential N-glycosylation site"  
 PN GB2246569-A.  
 PD 05-FEB-1992.  
 PR 15-JUN-1990: 013410.  
 PR 15-JUN-1990: GB-013410  
 PA (CHAR.) CHARING CROSS SUNT.E.  
 PI Feldman M, Gray P, Turner M, Brennan F;  
 DR WPI: 92-043613/06.  
 DR N-PSDB: 020973.  
 PT New tumour necrosis factor alpha binding protein and polypeptide  
 PT - useful in treating cachexia, sepsis and autoimmune diseases  
 PS e.g. Rheumatoid arthritis.  
 CC The amino acid sequence is that of tumour necrosis factor alpha  
 CC binding protein which contains the extracellular domain of human TNF  
 CC alpha receptor. It is soluble and can be used in the regulation of  
 CC TNF-mediated responses by binding and sequestering the cytokine. It  
 CC can therefore be used therapeutically to treat disorders such as  
 CC cachexia, sepsis and autoimmune diseases, specifically rheumatoid  
 CC arthritis.  
 SQ Sequence 455 AA;

Query Match 56.4%; Score 1124; DB 4; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsavpqqkylhpnmsicctckhkytylyndcpqgddtdeceassgfssenhrlnc1 100  
 |||||||  
 QY 23 DSVCPQGKTHPNNSICTCKHKTYLYNDCPPGQDTRBCESSGFTASENHLRHCL 82  
 |||||||  
 Db 101 scskcrkmgvseissctvdtdtcgcrknqyryhwsenlfqcfncslclngvtlscqe 160  
 |||||||  
 QY 83 SCSKCRKMGVEISSCTVDTRDTVCGRKNQRYHWSENLFCFCNCSCLNGVTLSCQE 142  
 |||||||  
 Db 161 kqntvctchagffilrenecvacs 183  
 |||||||  
 QY 143 KQNTVCTCHAGFFILRENECVASCA 165  
 |||||||

RESULT 13  
 ID R75084 standard; Protein; 455 AA.  
 AC R75084;  
 DT 19-JAN-1996 (first entry)  
 DE p55 TNF-R.  
 KW p55: tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;  
 KW phorbol myristate acetate; PMA.  
 OS Homo sapiens.

PH Key  
 FT peptide 41..53  
 FT /note= "N terminus of soluble p55 TNF-R"  
 FT modified\_site 54..56  
 FT /note= "glycosylation site"  
 FT modified\_site 145..147  
 FT /note= "glycosylation site"  
 FT modified\_site 161..163  
 FT /note= "glycosylation site"  
 FT peptide 193..210  
 FT /note= "peptide used in creation of chimeras"  
 FT region 198..210  
 FT /note= "spacer region"  
 FT misc\_difference 201  
 FT /note= "major C terminus for soluble p55 TNF-R"  
 FT misc\_difference 202  
 FT /note= "essential for shedding reaction"  
 FT misc\_difference 203

FT region /note= "minor C terminus for soluble p55 TNF-R"  
 FT region 212..234  
 FT /note= "transmembrane region"  
 PN A09475742-A.  
 PD 04-MAY-1995.  
 PR 11-OCT-1994: 075742.  
 PR 12-OCT-1993: IL-107268.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;  
 DR WPI: 95-194342/26.  
 DR N-PSDB: 090513.  
 PT New protease capable of cleaving soluble tumour necrosis factor  
 PT (TNF) receptor - from cell-bound TNF-receptor, useful for  
 PT antagonising deleterious effects of TNF.  
 PS Disclosure: Fig 1; 40pp; English.  
 CC This sequence represents human p55 tumour necrosis factor (TNF-R).  
 CC Expression of this receptor is regulated by shedding of the extracellular  
 CC receptor fragment. The p55 TNF-R can be shed in response to different  
 CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell  
 CC type. The only region of the receptor whose structure affects the  
 CC shedding response is the spacer region (see R75012) in the extracellular  
 CC domain. This region is located close to a site of cleavage of the  
 CC molecule, and links the Cys rich module to the transmembrane domain. The  
 CC spacer region of the encoded protein was used to create the chimeras  
 CC between human p55 TNF-R and murine epidermal growth factor receptor  
 CC (EGF-R) that are represented by R75007-11. This spacer region was  
 CC subjected to deletion mutations (R75013-25) and substitutions  
 CC (R75026-47). Of the spacer region, the most important residues are  
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most  
 CC important of these. The shedding of the receptor is independent of the  
 CC side chain identity of these residues, with the exception of a limited  
 CC dependence on the identity of Val 173. Mutations which alter the  
 CC conformation of the protein adversely effect the shedding process.  
 CC The mutations shown in R75013-47 were introduced in order to create an  
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R  
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in  
 CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can  
 CC be used for enhancing TNF function.  
 SQ Sequence 455 AA;

Query Match 56.4%; Score 1124; DB 14; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsavpqqkylhpnmsicctckhkytylyndcpqgddtdeceassgfssenhrlnc1 100  
 |||||||  
 QY 23 DSVCPQGKTHPNNSICTCKHKTYLYNDCPPGQDTRBCESSGFTASENHLRHCL 82  
 |||||||  
 Db 101 scskcrkmgvseissctvdtdtcgcrknqyryhwsenlfqcfncslclngvtlscqe 160  
 |||||||  
 QY 83 SCSKCRKMGVEISSCTVDTRDTVCGRKNQRYHWSENLFCFCNCSCLNGVTLSCQE 142  
 |||||||  
 Db 161 kqntvctchagffilrenecvacs 183  
 |||||||  
 QY 143 KQNTVCTCHAGFFILRENECVASCA 165  
 |||||||

RESULT 14  
 ID R07451 standard; Protein; 455 AA.  
 AC R07451;  
 DT 29-JAN-1991 (first entry)  
 DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 CDNA insert.  
 KW Tumour necrosis factor binding protein; TNF-R; TNF-receptor;  
 KW infectious disease; parasitic disease; cachexia;  
 KW autoimmune disease; shock; lambdaTNF-R2; ratTNF-R8.  
 OS Homo sapiens.  
 PN EP-393438-A.  
 PD 24-OCT-1990.  
 PR 06-APR-1990: 106624.  
 PR 21-APR-1989: DE-913101.  
 PR 21-JUN-1989: DE-920282.  
 PA (BOER ) BOEHRINGER INGELHEIMINT.  
 PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;



DR WPI: 90-321987/43.  
 DR N-PSDB: 006285.  
 PT DNA encoding TNF binding protein and TNF-receptor - used in  
 CC tumour treatment and to understand mechanism to TNF action  
 PS disclosure; Fig 91(1-2): 51pp; German.  
 CC ratTNF-R8 (006284) was used to screen the HS913T cDNA library.  
 CC lambdaTNF-R2 encodes the complete human TNF-R2 and was used to  
 CC construct a plasmid (pADTNF-R) expressing the product the same way  
 CC as pADTNF-BP (see 006282). The expressed proteins are useful  
 CC prophylactically and therapeutically to control disorders which  
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
 CC respiratory distress syndrome etc.) or side effects of treatment with  
 CC TNF-alpha). They can also be used as diagnostic reagents for  
 CC assaying TNF and in study of TNF-receptor interactions.  
 CC See also 006282-006285.  
 SQ Sequence 455 AA:

Query Match 56.4%; Score 1124; DB 2; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvcpqgkylhpnmsicctckhkgtylyndcpgpqtddcreceagstfaenhlrhl 100  
 QY 23 dsvcpqgkylhpnmsicctckhkgtylyndcpgpqtddcreceagstfaenhlrhl 82  
 Db 101 scskcrkemgveisactvdrtvcgcrknqyrhwsenlfqfncslcngtvlhscge 160  
 QY 83 scskcrkemgveisactvdrtvcgcrknqyrhwsenlfqfncslcngtvlhscge 142  
 Db 161 kqntvctchagfflreneecvscs 183  
 QY 143 kqntvctchagfflreneecvscs 165

RESULT 15  
 ID R11082 standard; Protein: 455 AA.  
 AC R11082:

DE 24-MAR-1991 (first entry)  
 DE Human 55kD TNF-binding protein.  
 KW Tumour Necrosis factor; binding proteins; septic shock;  
 KW autoimmune glomerulonephritis; lymphokine; cytokine.  
 FH Key Location/Qualifiers  
 FT modified\_site 54  
 FT /label= putative N-glycosylation site  
 FT modified\_site 145  
 FT /label= putative N-glycosylation site  
 FT modified\_site 151  
 FT /label= putative N-glycosylation site  
 FT modified\_site 270  
 FT /label= putative N-glycosylation site  
 FT region 212..230  
 FT /label= transmembrane region  
 FT peptide 1..28  
 FT /label= signal peptide  
 PN EP-417563-A.  
 PD 20-MAR-1991.  
 PE 31-AUG-1990; 116707.  
 PR 12-SEP-1989; CH-003319.  
 PR 08-MAR-1990; CH-000746.  
 PR 20-APR-1990; CH-001347.  
 PA (HOFF ) HOFFMANN-LA ROCHE AG.  
 PI Brochhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
 PI Schlaeger EJ;  
 DR WPI: 91-081851/12.  
 DR N-PSDB: 010955.  
 PT Insoluble tumour necrosis factor binding proteins - and DNA  
 PT encoding them, useful in pharmaceutical prods. and for antibody  
 PT prods.  
 PS Claim 1; Fig 1; 26pp; German.  
 CC Partial amino acid sequences were determined for the 55 and 75kD  
 CC TNF-BPs (see R11072-R11081) and oligonucleotide primers were  
 CC synthesised based on these partial sequences. The primers were used







CC to produce a cDNA fragment for use as a probe to screen a human  
 CC placental cDNA bank constructed in lambda gtl1. Positive clones were  
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding  
 CC sequence may also contain a fragment encoding a human Ig domain.  
 CC Recombinant constructs are used to transform cells to confer  
 CC improved TNF-binding properties.  
 CC See also 010956.  
 SQ Sequence 455 AA:

Query Match 56.4%; Score 1124; DB 2; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 6.19e-110;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvcpqgkylhpnmsicctckhkgtylyndcpgpqtddcreceagstfaenhlrhl 100  
 QY 23 dsvcpqgkylhpnmsicctckhkgtylyndcpgpqtddcreceagstfaenhlrhl 82  
 Db 101 scskcrkemgveisactvdrtvcgcrknqyrhwsenlfqfncslcngtvlhscge 160  
 QY 83 scskcrkemgveisactvdrtvcgcrknqyrhwsenlfqfncslcngtvlhscge 142  
 Db 161 kqntvctchagfflreneecvscs 183  
 QY 143 kqntvctchagfflreneecvscs 165

Search completed: Wed May 6 08:52:53 1998  
 Job time : 114 secs.

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20-33      #disulfide_bonds\
23-42      #disulfide_bonds\
45-60      #disulfide_bonds\
63-78      #disulfide_bonds\
66-86      #disulfide_bonds\
88-104     #disulfide_bonds\
107-119    #disulfide_bonds\
110-127    #disulfide_bonds\
129-140    #disulfide_bonds\
143-156    #disulfide_bonds\
146-152    #disulfide_bonds\

SUMMARY
#length 158 #molecular-weight 17827 #checksum 5022

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Best Local Similarity 99.3%;  Pred. No.2,23e-230;
Matches 142;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Db 2  DSVCPQGRYIHPPNNSICTCKHKGTYLNDPCPGPDPTDCRECESGSFTASENHLRHCL 61
Oy 23 DSVCPQGRYIHPPNNSICTCKHKGTYLNDPCPGPDPTDCRECESGSFTASENHLRHCL 82
Db 62  SCSCKRKMGGVYEISCTYVDRDTVCGCRNNQYRHWSENLFOCFNCSLCLNGTVHLSCE 121
Oy 83  SCSCKRKMGGVYEISCTYVDRDTVCGCRNNQYRHWSENLFOCFNCSLCLNGTVHLSCE 142
Db 122 KONTVCTCHAGFFLENECVSCS 144
Oy 143 KONTVCTCHAGFFLENECVSCA 165

RESULT 2
ENTRY  GQHUT1      #type complete

TITLE  tumor necrosis factor receptor type 1 precursor - human|ALTERNATE_NAMES
CONTAINS
ORGANISM  HUMAN
DATE

ACCESSIONS
REFERENCE
#authors  Fuchs, P.; Strühl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.
#journal  Genomics (1992) 13:219-224
#title    Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and
          localization to chromosome 12p13.
#accession A38208
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#residues  1-455 ##label FUC
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          PID:g339750

REFERENCE
#authors  Loetscher, H.; Pan, Y.C.E.; Lahn, H.W.; Gentz, R.; Brockhaus,
#journal  M.; Tabuchi, H.; Lesslauer, W.
#title    Cell (1990) 61:351-359
          Molecular cloning and expression of the human 55 kd tumor
          necrosis factor receptor.
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#cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754
#experimental_source Placenta
#note     mature protein, confirmed by protein sequencing

REFERENCE  A34900
#authors  Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
#journal  Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
#title    H.; Kohr, W.J.; Goeddel, D.V.
          Cell (1990) 61:361-370
          Molecular cloning and expression of a receptor for human
          tumor necrosis factor.
#cross-references MUID:90235285

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#accession A34900
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##residues 1-455 ##label SCH
##cross-references GB:M3294; NID:g339744; PID:g339745
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#authors Hammler, A.; Maurer-Fogy, I.; Krenke, M.; Scheulich, P.;
#titles Pfizenmaier, K.; Lantzy, M.; Olsson, I.; Hauptmann, R.;
#titles Stromow, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
#titles Molecular cloning and expression of human and rat tumor
#titles necrosis factor receptor chain (p60) and its soluble
#titles derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
#accession A35555
##molecule_type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:g339755; PID:g339756
#accession C36555
##molecule_type protein
#residues 30-38:41-53,'X',55-79,'XX',82-94,'NK','XX',100-104,
#residues 107-128;162-167,'X',169-201 ##label H12
#titles the purified protein, called tumor necrosis factor
#titles binding protein, is a soluble derivative of the
#titles receptor
REFERENCE
#authors Gray, P.W.; Barrett, K.; Chantiry, D.; Turner, M.; Feldmann,
#titles M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#titles Cloning of human tumor necrosis factor (TNF) receptor cDNA
#titles and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
##molecule_type mRNA
##residues 1-455 ##label GRA
##cross-references GB:M37764
#titles the authors translated the codon TGG for residue 371 as
#titles Thr, AAG for residue 372 as Leu, and GAC for residue
#titles 427 as Asn
REFERENCE
#authors Noplar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang
#titles R.; Aderka, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278
#titles Soluble forms of tumor necrosis factor receptors (TNF-Rs).
#titles The cDNA for the type I TNF-R, cloned using amino acid
#titles sequence data of its soluble form, encodes both the cell
#titles surface and a soluble form of the receptor.
#cross-references MUID:91006021
#accession S12057
##molecule_type mRNA
##residues 1-455 ##label NOP
##cross-references EMBL:X5313; NID:g37223; PID:g37224
#titles parts of soluble TNF binding protein 1, including its
#titles amino and carboxyl ends, were confirmed by protein
#titles sequencing
REFERENCE
#authors JTO758
#titles Kemper, O.; Wallach, D.
#journal Gene (1993) 134:209-216
#titles Cloning and partial characterization of the promoter for the
#titles human p55 tumor necrosis factor (TNF) receptor.
#accession JTO758
##molecule_type DNA
##residues 1-13 ##label KEM
REFERENCE
#authors A60231
#titles Seelinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
#titles J.M.
#journal Eur. J. Immunol. (1990) 20:1167-1174
#titles Tumor necrosis factor inhibitor: purification, NH-2-terminal
#titles amino acid sequence and evidence for anti-inflammatory and
#titles immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
##molecule_type protein
#residues 41-45,'X',45-53,'X',55-57 ##label SEC

```

REFERENCE A38258  
#authors Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucet III, J.A.; Jeffes, E.W.B.; Lentz, R.; Tomlich, J.; Yamamoto, R.S.; Granger, G.A.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784  
#title Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.  
#cross-references A38258  
#accession A38258  
#molecule-type protein  
#residues 41-60 #label GAT  
#experimental\_source cancer patient serum  
REFERENCE A60594  
#authors Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
#journal Eur. J. Haematol. (1989) 42:270-275  
#title Isolation and characterization of a tumor necrosis factor binding protein from urine.  
#accession A60594  
#molecule-type protein  
#residues 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 #label OLS  
#experimental\_source renal failure patient urine  
REFERENCE A35010  
#authors Engelmann, H.; Novick, D.; Wallach, D.  
#journal J. Biol. Chem. (1990) 265:1531-1536  
#title Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.  
#cross-references MUID:90110215  
#accession A35010  
#molecule-type protein  
#residues 41-45 #label ENG  
#experimental\_source normal urine  
REFERENCE JC2404  
#authors Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
#journal Biochem. Biotechnol. Biochem. (1994) 58:2266-2268  
#title Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.  
#accession JC2404  
#molecule-type protein  
#residues 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 #label KAJ  
#experimental\_source urine  
COMMENT This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).  
GENETICS GDB:TNFRL  
#gene ##cross-references GDB:125913; OMIM:191190  
#map\_position 12p13.2-12p13.2  
#introns 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology  
KEYWORDS duplication; glycoprotein; receptor; transmembrane protein  
FEATURE  
1-21 #domain signal sequence #status predicted #label SIG  
22-45 #product tumor necrosis factor receptor type 1 #status predicted #label MAT  
41-201 #domain extracellular #status predicted #label EXN  
30-211 #product TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status experimental #label TBPL  
44-82 #domain NGF receptor repeat homology #label NG1  
86-126 #domain NGF receptor repeat homology #label NG2  
127-167 #domain NGF receptor repeat homology #label NG3  
168-196 #domain NGF receptor repeat homology #label NG4  
212-234 #domain transmembrane #status predicted #label MEM  
235-455 #domain intracellular #status predicted #label INT  
54,145,151 #binding\_site carbonyl (Asn) (covalent) #status predicted  
SUMMARY #length 455 #molecular-weight 50494 #checksum 153  
Query Match 56.4%; Score 1124; DB 1; Length 455;

Best Local Similarity 99.3%; Pred. No. 2,23e-230;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 41 DSVCGQKTIHPQNNSTCTCKHKTYLYNCPGQOTDCECGSGSFTASENLRCL 100  
Qy 23 DSVCPQGYIHPQNNSTCTCKHKTYLYNCPGQOTDCECGSGSFTASENLRCL 82  
Db 101 SCSCKRKEKGOVEISSCTVDNRDTCGCKRNOYRHVWSENLPFCFNCISLCTNGLVLSQOE 160  
Qy 83 SCSCKRKEKGOVEISSCTVDNRDTCGCKRNOYRHVWSENLPFCFNCISLCTNGLVLSQOE 142  
Db 161 KONTVCTCHAGFFLENECVSCS 183  
Qy 143 KONTVCTCHAGFFLENECVSCA 165  
RESULT 3  
ENTRY 3  
TITLE tumor necrosis factor receptor extracellular domain, chain A  
PDB-TITLE extracellular domain of the 55kDa tumor necrosis factor receptor. crystallized at pH3.7 in p 21 21 21.  
ORGANISM #formal\_name Homo sapiens #common\_name man  
#note expressed in Escherichia coli, the construct contains residues 12 to 172 of the mature sequence of the entire receptor. residue 11 is mutated to met as a result of the expression system  
REFERENCE A65560  
#authors Nalsmith, J.H.; Sprang, S.R.  
#accession submitted to the Brookhaven Protein Data Bank, July 1996  
#cross-references PDB:1EXT  
REFERENCE TN026248  
#authors Nalsmith, J.H.; Devine, T.O.; Brandhuber, B.J.; Sprang, S.R.  
#journal J. Biol. Chem. (1995) 270:13303  
#title Crystallographic evidence for dimerization of unliganded tumor necrosis factor receptor.  
REFERENCE TN026249  
#authors Rodese, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale, K.; Nalsmith, J.H.; Sprang, S.R.  
#journal J. Mol. Biol. (1994) 239:332  
#title Two crystal forms of the extracellular domain of type 1 tumor necrosis factor receptor.  
REFERENCE A40737  
#authors Banner, D.W.; D'Arcy, A.; Jones, W.; Gentz, R.; Schoenfeld, H.-J.; Broger, C.; Doetscher, H.; Lesslauer, W.  
#journal Cell (1993) 73:431-445  
#title Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for TNF receptor activation.  
COMMENT Resolution: 1.85 angstroms  
COMMENT Determination: X-ray diffraction  
COMMENT R-value: no refinement  
KEYWORDS binding protein; cytokine; signalling protein  
FEATURE  
66-68 #region helix (right hand 3-10)\\  
141-143 #region helix (right hand 3-10)\\  
151-154 #region helix (right hand alpha)\\  
7-9,17-19 #region beta sheet\\  
131-134,137-140 #region beta sheet\\  
25-29,39-42 #region beta sheet\\  
71-74,83-85 #region beta sheet\\  
90-96,99-104 #region beta sheet\\  
111-115,124-127 #region beta sheet\\  
3-17 #region beta sheet\\  
18-31 #disulfide\_bonds\\  
21-40 #disulfide\_bonds\\  
43-58 #disulfide\_bonds\\  
61-76 #disulfide\_bonds\\  
64-84 #disulfide\_bonds\\  
86-102 #disulfide\_bonds\\  
105-117 #disulfide\_bonds\\  
127-138 #disulfide\_bonds\\

141-154 #disulfide\_bonds\  
144-150 #disulfide\_bonds  
SUMMARY #length 160 #molecular-weight 18065 #checksum 2297

Query Match 56.1%; Score 118; DB 5; Length 160;  
Best Local Similarity 99.3%; Pred. No. 5,83e-229;  
Matches 141; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 SVCPGKXIHPPNNISICTCKHKGTYLYNDGPGGDDTDCRECESSGFTASENHLRHCLIS 60  
QY 24 SVCPGKXIHPPNNISICTCKHKGTYLYNDGPGGDDTDCRECESSGFTASENHLRHCLIS 83

Db 61 CSKRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 120  
QY 84 CSKRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 143

Db 121 NTVCTCHAGFFLRENECVSCS 142  
QY 144 NTVCTCHAGFFLRENECVSCA 165

RESULT 4  
ENTRY 1NCFB #type complete

TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
Chain B - hu

ALTERNATE\_NAMES stnfr1; type 1 receptor  
ORGANISM #formal\_name Homo sapiens #common\_name man  
#note expressed in Escherichia coli, residue 11 is mutated to met  
as a result of the expression system

REFERENCE A66195  
#authors Nalsmith, J.H.; Sprang, S.R.  
#submission submitted to the Brookhaven Protein Data Bank, October 1994  
#cross-references PDB:1NCF  
REFERENCE TN029041  
#authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,  
J. Mol. Biol. (1994) 239:332  
#journal R.; Nalsmith, J.H.; Sprang, S.R.  
#title Two crystal forms of the extracellular domain of type 1 tumor  
necrosis factor receptor.  
A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
#journal Cell (1993) 73:431-445  
#title Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
binding protein; cytokine; signalling protein

COMMENT Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
binding protein; cytokine; signalling protein

KEYWORDS #disulfide\_bonds\  
FEATURE 2-16 #disulfide\_bonds\  
17-30 #disulfide\_bonds\  
20-39 #disulfide\_bonds\  
42-57 #disulfide\_bonds\  
60-75 #disulfide\_bonds\  
63-83 #disulfide\_bonds\  
85-101 #disulfide\_bonds\  
104-116 #disulfide\_bonds\  
107-124 #disulfide\_bonds\  
126-137 #disulfide\_bonds\  
SUMMARY #length 142 #molecular-weight 16046 #checksum 1225

Query Match 55.9%; Score 114; DB 5; Length 142;  
Best Local Similarity 99.3%; Pred. No. 5.14e-228;  
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 VCPGKXIHPPNNISICTCKHKGTYLYNDGPGGDDTDCRECESSGFTASENHLRHCLIS 60  
QY 25 VCPGKXIHPPNNISICTCKHKGTYLYNDGPGGDDTDCRECESSGFTASENHLRHCLIS 84

Db 61 SKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 120  
QY 85 SKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 144

Db 121 NTVCTCHAGFFLRENECVSCS 141  
QY 145 NTVCTCHAGFFLRENECVSCA 165

RESULT 5  
ENTRY 1TNRR #type complete

TITLE tumor necrosis factor receptor type 1 (p55 extracellular  
#formal\_name Homo sapiens #common\_name man  
#note recombinant form expressed in Baculovirus SP9  
A52442  
REFERENCE #authors Banner, D.W.  
#submission submitted to the Brookhaven Protein Data Bank, May 1994  
#cross-references PDB:1TNR  
REFERENCE A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
#journal Cell (1993) 73:431-445  
#title Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
TN034093  
#authors D'Arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;  
Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;  
Lesslauer, W.  
#journal J. Mol. Biol. (1993) 229:555  
#title Crystalization and preliminary analysis of tnfr-beta and a  
tnfr-beta-55 kd tnfr receptor complex.  
Resolution: 2.85 angstroms  
Determination: X-ray diffraction  
Complex(LymphokineRECEPTOR)

COMMENT Resolution: 2.85 angstroms  
Determination: X-ray diffraction  
Complex(LymphokineRECEPTOR)

KEYWORDS #disulfide\_bonds\  
FEATURE 1-15 #disulfide\_bonds\  
16-29 #disulfide\_bonds\  
19-38 #disulfide\_bonds\  
41-56 #disulfide\_bonds\  
59-74 #disulfide\_bonds\  
62-82 #disulfide\_bonds\  
84-100 #disulfide\_bonds\  
103-115 #disulfide\_bonds\  
106-123 #disulfide\_bonds\  
125-136 #disulfide\_bonds\  
SUMMARY #length 139 #molecular-weight 15746 #checksum 5335

Query Match 55.4%; Score 1105; DB 5; Length 139;  
Best Local Similarity 100.0%; Pred. No. 6.85e-226;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CPCKXIHPPNNISICTCKHKGTYLYNDGPGGDDTDCRECESSGFTASENHLRHCLIS 60  
QY 26 CPCKXIHPPNNISICTCKHKGTYLYNDGPGGDDTDCRECESSGFTASENHLRHCLIS 85

Db 61 KCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 120  
QY 86 KCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 145

Db 121 TVCTCHAGFFLRENECVSC 139  
QY 146 TVCTCHAGFFLRENECVSCA 164

RESULT 6  
ENTRY 1NCFB #type complete

TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
Chain A - hu

ALTERNATE\_NAMES stnfr1; type 1 receptor

ORGANISM #formal\_name Homo sapiens #common\_name man  
#note expressed in Escherichia coli, residue 11 is mutated to met  
as a result of the expression system

REFERENCE A66195  
#authors Naismith, J.H.; Sprang, S.R.  
#submission submitted to the Brookhaven Protein Data Bank, October 1994  
#cross-references PDB:INCF  
REFERENCE TM029039  
#authors Rodesth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,  
K.; Naismith, J.H.; Sprang, S.R.  
#journal J. Mol. Biol. (1994) 239:332  
#title Two crystal forms of the extracellular domain of type 1 tumor  
necrosis factor receptor.  
#authors Banner, D.W.; D'Arcy, A.; Jones, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
#journal Cell (1993) 73:431-445  
#title Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.

COMMENT Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement

KEYWORDS binding protein; cytokine; signalling protein

FEATURE  
5-19 #disulfide\_bonds\  
20-33 #disulfide\_bonds\  
23-42 #disulfide\_bonds\  
45-60 #disulfide\_bonds\  
63-78 #disulfide\_bonds\  
66-86 #disulfide\_bonds\  
88-104 #disulfide\_bonds\  
107-119 #disulfide\_bonds\  
110-127 #disulfide\_bonds\  
129-140 #disulfide\_bonds\  
SUMMARY #length 140 #molecular-weight 15889 #checksum 6622

Query Match 55.1%; Score 1098; DB 5; Length 140;  
Best Local Similarity 100.0%; Pred. No. 3.08e-224;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 DSVCPGKXTHPNNISCTCKHKGTYLNDGPGPDIDRCRCESGFTASENHLRHCL 61  
|||  
QY 23 DSVCPGKXTHPNNISCTCKHKGTYLNDGPGPDIDRCRCESGFTASENHLRHCL 82  
|||  
Db 62 SCSKCKREKGOYEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLGLNGVHLSCE 121  
|||  
QY 83 SCSKCKREKGOYEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLGLNGVHLSCE 142  
|||  
Db 122 KONTVCTCHAGFFLRENEC 140  
|||  
QY 143 KONTVCTCHAGFFLRENEC 161  
|||

RESULT 7 Jc4302 #type complete

ENTRY Jc4302 #type complete

TITLE tumor necrosis factor receptor p55 - pigORGANISM #formal\_name S

DATE 23-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change

ACCESSION Jc4302; PC4093

REFERENCE Jc4302  
#authors Suter, B.; Pauli, U.  
#journal Gene (1995) 163:263-266  
#title Cloning of the cDNA encoding the porcine p55 tumor necrosis  
factor receptor.  
#accession Jc4302  
#molecule\_type mRNA  
#residues 1-461 #label SURT  
#cross-references GB:019944; NID:g1141752; PID:g1141753  
#accession PC4093  
#molecule\_type protein  
#residues 1-7 #label SUR2

#experimental\_source kidney cell line 15

GENETICS

CLASSIFICATION #gene tnfr  
#superfamily tumor necrosis factor receptor type 1; NGF  
receptor repeat homology  
glycoprotein; kidney; receptor; transmembrane protein; tumor

KEYWORDS  
FEATURE  
1-29 #domain signal sequence #status predicted #label SIG\  
30-461 #product tumor necrosis factor receptor p55 #status  
44-194 #domain extracellular cysteine rich #status predicted  
44-82 #domain NGF receptor repeat homology #label NG1\  
211-231 #domain transmembrane #status predicted #label TMV\  
361-447 #domain signal transduction #status predicted #label  
SIG\  
54,145,151 #binding\_site carbohydrate (asn) (covalent) #status  
predicted

SUMMARY #length 461 #molecular-weight 50696 #checksum 8079

Query Match 48.2%; Score 962; DB 2; Length 461;  
Best Local Similarity 69.8%; Pred. No. 3.26e-192;  
Matches 120; Conservative 22; Mismatches 26; Indels 4; Gaps 4;

Db 41 ESICPGKXTHPNNISCTCKHKGTYLNDGPGPDIDRCRCESGFTASENHLRHCL 100  
|||  
QY 23 DSVCPGKXTHPNNISCTCKHKGTYLNDGPGPDIDRCRCESGFTASENHLRHCL 82  
|||  
Db 101 SCSKCKREKGOYEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLGLNGVHLSCE 160  
|||  
QY 83 SCSKCKREKGOYEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLGLNGVHLSCE 142  
|||  
Db 161 KODTINCCHGFFLRENECVCYNCKNADCKNCPATSTRNDPQDTTVL 212  
|||  
QY 143 KONTVCTCHAGFFLRENECVCAG-AAQCP-C-TLQENPF-FSQPGAPIL 190  
|||

RESULT 8 I57826 #type complete

ENTRY I57826 #type complete

TITLE tumor necrosis factor receptor - mouseORGANISM #formal\_name

DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change

ACCESSION I57826

REFERENCE I57826  
#authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;  
Steinmetz, M.  
#journal Mol. Immunol. (1993) 30:165-176  
#title Genomic organization and promoter function of the murine  
tumor necrosis factor receptor beta gene.  
#cross-references MUID:93156721  
#accession I57826  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 1-454 #label RES  
#cross-references GB:M76556; NID:g202100; PID:g202102

GENETICS

CLASSIFICATION #gene TNFR-2  
#superfamily tumor necrosis factor receptor type 1; NGF  
receptor repeat homology  
cytokine receptor

KEYWORDS  
SUMMARY #length 454 #molecular-weight 50030 #checksum 4267

Query Match 42.2%; Score 841; DB 2; Length 454;  
Best Local Similarity 70.6%; Pred. No. 7.05e-164;  
Matches 101; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Db 41 DSVCPGKXTHPNNISCTCKHKGTYLNDGPGPDIDRCRCESGFTASENHLRHCL 100  
|||  
QY 23 DSVCPGKXTHPNNISCTCKHKGTYLNDGPGPDIDRCRCESGFTASENHLRHCL 82  
|||  
Db 101 SCSKCKREKGOYEISCTVDRTVCGCRKQYRHYSENLFQCFNCSLGLNGVHLSCE 160  
|||

Oy	83	SCSKRCKMGQYIISCTYDRDTCGCRKNQRYHYSENLFGCFNLSCLNGVHLSQCE	142
Db	161	TONTYCNCCHAGFFLRSECVPCS	183
Oy	143	KONTVCCTCHAGFFLRNECVCSCA	165
RESULT ENTRY	9	GOMST1 #type complete	
TITLE		tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES	
ORGANISM		#formal_name mus musculus #common_name house mouse	
DATE		30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Sep-1997	
ACCESSIONS REFERENCE		A38634; B40254; S16677; S19021; I54532 A38634	
#authors		Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.	
#journal		Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834	
#title		Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.	
#cross-references	MUID:9187885		
#accession	A38634		
#molecule_type	mRNA		
#residues	1-454 ##label LEW		
REFERENCE		#cross-references GB:M60468; NID:g199825; PID:g199826 A40254	
#authors		Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.L.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.	
#journal		Mol. Cell. Biol. (1991) 11:3020-3026	
#title		Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.	
#cross-references	MUID:91246168		
#accession	B40254		
#molecule_type	mRNA		
#residues	1-454 ##label GO2		
REFERENCE		#cross-references GB:M60468; NID:g199825; PID:g199826 S16677	
#authors		Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.	
#journal		Eur. J. Immunol. (1991) 21:1649-1656	
#title		Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.	
#cross-references	MUID:91285014		
#accession	S16677		
#molecule_type	mRNA		
#residues	1-454 ##label BAR		
REFERENCE		#cross-references EMBL:X59238; NID:g53578; PID:g53579 S19021	
#authors		Rothe, J.G.; Brockhaus, M.; Gentz, R.; Leaslaue, W.	
#journal		Immunogenetics (1991) 34:338-340	
#title		Molecular cloning and expression of the mouse Tnf receptor type b.	
#cross-references	MUID:92039815		
#accession	S19021		
#molecule_type	mRNA		
#residues	1-454 ##label ROT		
REFERENCE		#cross-references EMBL:X57796; NID:g54848; PID:g54849 I54532	
#authors		Bebo, B.F.	
#journal		Immunogenetics (1994) 39:450-451	
#title		Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.	
#cross-references	MUID:94245292		
#accession	I54532		
#status		translated from GB/EMBL/DDBT	
#molecule_type	mRNA		
#residues	1-454 ##label RES		
#cross-references	GB:L26349; NID:g430732; PID:g430733		
COMMENT		This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).	

CLASSIFICATION	#superfamily tumor necrosis factor receptor type 1: NGF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS	
FEATURE	
1-29	
30-454	
30-212	#domain signal sequence #status predicted #label SIG\
44-82	#product tumor necrosis factor receptor type 1 #status predicted #label MAT\
84-126	#domain extracellular #status predicted #label EXT\
127-167	#domain NGF receptor repeat homology #label NG1\
168-204	#domain NGF receptor repeat homology #label NG2\
213-235	#domain NGF receptor repeat homology #label NG3\
236-454	#domain transmembrane #status predicted #label NG4\
54,151,202	#domain intracellular #status predicted #label NGM\
	#binding_site carbohydrate (asn) (covalent) #status predicted
SUMMARY	#length 454 #molecular-weight 50129 #checksum 4839
Query Match	42.2% Score 841; DB 1; Length 454;
Best Local Similarity	70.6%; Pred. No. 7, 05e-164;
Matches 101;	Conservative 23; Mismatches 19; Indels 0; Gaps 0;
Db	41 DSLPQGRKYVHAKNNKSICTCHKRGYLYSDPSPGRDVCRCCEKGFETASQNTYRQL 100
Qy	23 DSVGPGRKYTHPNQNSICTCHKRGYLYNDGPGRQDIDRCESGGSFTASENTRCL 82
Db	101 SCTCRKEMSGVEISPCQADKDTVCGCKENQFORLYSETHFQCVDCSPFCNGVTYIPCKE 160
Qy	83 SCSCKRCKMGVEISCTVDKDTVCGCKRNQRYHSENLFCFCNCSLCLNQTVALSCOE 142
Db	161 TQNTVNCNAGFPLRESECPGS 183
Qy	143 KQNTVCTCHAGFPLRENEVCSA 165
RESULT 10	
ENTRY	GQRTT1 #type complete
TITLE	tumor necrosis factor receptor type 1 precursor - ratCONTRAINS
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat
DATE	30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 05-Sep-1997
ACCESSIONS	B36555
REFERENCE	A36555
#authors	Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfeffermayer, K.; Lantiz, M.; Olsson, I.; Hauptmann, R.; Stratowa, C.; Adolf, G.R.
#journal	DNA Cell Biol. (1990) 9:705-715
#title	Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.
#cross-references	MUID:91090841
#accession	B36555
##molecule_type	mRNA
#residues	1-461 ##label HIM
#cross-references	GB:M63122; NID:g207361; PID:g207362
COMMENT	This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION	#superfamily tumor necrosis factor receptor type 1: NGF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS	
FEATURE	
1-29	
30-461	
30-211	#domain signal sequence #status predicted #label SIG\
30-201	#product tumor necrosis factor receptor type 1 #status predicted #label MAT\
44-82	#domain extracellular #status predicted #label EXT\
84-126	#domain NGF receptor repeat homology #label NG1\
127-167	#domain NGF receptor repeat homology #label NG2\
168-204	#domain NGF receptor repeat homology #label NG3\
212-234	#domain transmembrane #status predicted #label NG4\



235-461	#domain intracellular	#status predicted	#label INT\
54,151,201			#binding-site carbonyl: (asn) (covalent) #status predicted
SUMMARY	#length 461	#molecular-weight 50969	#checksum 1617
Query Match	40.6%	Score 809;	DB 1; Length 461;
Best Local Similarity	68.5%	Pred. No. 2,056-156;	
Matches	98; Conservative	21; Mismatches	24; Indels 0; Gaps 0;
Db	41	DNLCPGKRVAPRPNKNSICTCTCHKGTLYLSDCPSPGQETVCEVCDKGTFTASQNHVRCGL	100
Oy	23	DSVCPGKVIHPRPNNSICTCTCHKGTLYLSDCPSPGQETVCEVCDKGTFTASQNHVRCGL	82
Db	101	SCRTCKRKMFOVEISPCADMDTVCGCKKNQFQRYLSTFTFCQVDCSPCENGVTYTIPEK	160
Oy	83	SCSRKREMGVEIISCTVDRDTCGCKRKNQRYHYSNLTFCQFNCISLNGTVHLSCE	142
Db	161	KONTVCNCHAGFPLSGNCTPCS	183
Oy	143	KONTVCNCHAGFPLSGNCTPCS	165
RESULT	11	TTHVAP	#type complete
TITLE		glycoprotein hormones alpha chain precursor - humanALTERNATE_NAMES	
ORGANISM		alpha chain; follitropin alpha chain; interstitial cell-stimulating hormone alpha chain; lutelizing hormone alpha chain; lutropin alpha chain; thyroid-stimulating hormone alpha chain; thyrotropin alpha chain	
DATE		#format.name Homo sapiens #common.name man 13-Jul-1981 #sequence_revision 23-Oct-1981 #text_change 05-Sep-1997	
ACCESSIONS		A93213; A92832; B92303; A90751; A90179; A91461; A92184; A84552; B92181; A92141; J58200; A01481	
REFERENCE		A93213 Fiddes, J.C.; Goodman, H.M. Nature (1979) 281:351-356	
#journal		Isolation, cloning and sequence analysis of the cDNA for the alpha-subunit of human chorionic gonadotropin.	
#title		alpha-subunit of human chorionic gonadotropin.	
#cross-references		MUID:80011660	
#accession		A93213	
#molecule_type		mRNA	
#residues		1-116 #label FTD	
#cross-references		GB:V00518; NID:g31868; PID:g31869	
REFERENCE		A92832	
#authors		Fiddes, J.C.; Goodman, H.M.	
#journal		J. Mol. Appl. Genet. (1981) 1:3-18	
#title		The gene encoding the common alpha subunit of the four human glycoprotein hormones.	
#cross-references		MUID:82267643	
#accession		A92832	
#molecule_type		DNA	
#residues		1-98 #label F12	
#cross-references		GB:V00484	
REFERENCE		A92303	
#authors		Birren, S.; Fetherston, J.; Canfield, R.; Bolme, I.	
#journal		J. Biol. Chem. (1981) 256:1816-1823	
#title		The amino acid sequences of the prepeptides contained in the alpha and beta subunits of human chorionadotropin.	
#cross-references		MUID:81117268	
#accession		B92303	
#molecule_type		protein	
#residues		1-24 #label BIR	
#note		restriction endonuclease evidence indicates that a single gene codes for the alpha chain common to the four dimeric hormones: thyrotropin, lutropin, follitropin, and chorionadotropin	
#note		previously the mature alpha chain (residues 25-116) was isolated from each of the hormones and its sequence was determined, as documented below	
REFERENCE		A90751	
#authors		Saltram, M.R.; Li, C.H.	

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#journal      Can. J. Biochem. (1977) 55:755-760
#title        Human pituitary thyrotropin. The primary structure of the
              alpha and beta subunits.
#cross-references MUID:77243687
#accession    A90751
#molecule_type protein
#residues     28-107,'SC',110-116 ##label SAI
REFERENCE
#authors      A90179
#journal      Saitam, M.R.; Papkoff, H.; Li, C.H.
#title        Biochem. Biophys. Res. Commun. (1972) 48:530-537
              Human pituitary interstitial cell stimulating hormone:
              primary structure of the alpha subunit.
#cross-references MUID:72242988
#accession    A90179
#molecule_type protein
#residues     28-107,'SC',110-116 ##label SA2
REFERENCE
#authors      A91461
#journal      Keutmann, H.T.; Williams, R.M.; Bishop, W.H.; Ryan, R.J.
#title        Fed. Proc. (1978) 37:1828
              Structure of human luteinizing hormone.
#accession    A91461
#molecule_type protein
#residues     28-116 ##label KRU
REFERENCE
#authors      A92184
#journal      Rathnam, P.; Saxena, B.B.
#title        J. Biol. Chem. (1975) 250:6735-6746
              Primary amino acid sequence of follicle-stimulating hormone
              from human pituitary glands.
#cross-references MUID:76005558
#accession    A92184
#molecule_type protein
#residues     25-28,'E',30-116 ##label RAT
REFERENCE
#authors      A94552
#journal      Shome, B.; Parlow, A.F.
#title        Submitted to the Atlas, April 1975
#accession    A94552
#molecule_type protein
#residues     28-116 ##label SHO
REFERENCE
#authors      A92181
#journal      Morgan, F.J.; Birken, S.; Canfield, R.E.
#title        J. Biol. Chem. (1975) 250:5247-5258
              The amino acid sequence of human chorionic gonadotropin. The
              alpha subunit and beta subunit.
#cross-references MUID:75211304
#accession    B92181
#molecule_type protein
#residues     25-116 ##label MOR
              heterogeneity is found at the amino end. Approximately
              10 and 30% of the chains lack residues 1-2 and 1-3,
              respectively
#cross-references MUID:74011266
#accession    A92141
#molecule_type protein
#residues     25-116 ##label BEL
REFERENCE
#authors      A92760
#journal      Shome, B.; Parlow, A.F.
#title        J. Clin. Endocrinol. Metab. (1974) 39:199-202
              Human follicle stimulating hormone (hFSH): first proposal for
              the amino acid sequence of the alpha-subunit (hFSHalpha)
              and first demonstration of its identity with the
              alpha-subunit of human luteinizing hormone (hLHalpha).
#cross-references MUID:74262937
#contents     annotation
#accession    A90632
#authors      Fujiki, Y.; Rathnam, P.; Saxena, B.B.
#journal      Biochem. Biophys. Acta (1980) 624:428-435
#title        Studies on the disulfide bonds in human pituitary
              follicle-stimulating hormone.

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REFERENCE	#journal	#title	#contents	#authors	#journal	#title	#contents	#authors	#journal	#title	#contents	#authors
cross-references	MUID:81021713	annotation: preliminary disulfide bonds										
REFERENCE	A44674	Lapthorn, A.U.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs, N.W.										
#journal	1994	369:455-461										
#title		Crystal structure of human chorionic gonadotropin.										
#contents		annotation: X-ray crystallography, 3.0 angstroms; correction of disulfide bonds										
REFERENCE	158200	Miyoshi, I.; Kasai, N.; Hayashizaki, Y.										
#journal	1994	52:940-947										
#title		Nippon Rinsho (1994) 52:940-947										
#contents		Structure and regulation of human thyroid-stimulating hormone (TSH) gene).										
cross-references	MUID:94254248											
accession	158200											
#status	preliminary; translated from GB/EMBL/DBJ											
#molecule-type	DNA											
#residues	1-116	#label	RES									
cross-references	GB:S70585; NID:9546844; PID:9546845											
GENETICS												
#gene	GDB:CGA											
cross-references	GDB:119774; OMIM:118850											
#map-position	6q14-6q21											
#introns	30/1; 91/3											
CLASSIFICATION	#superfamily	glycoprotein hormones alpha chain										
KEYWORDS	glycoprotein; heterodimer; hormone; pituitary											
FEATURE												
1-24												
25-116												
31-55,34-84,52-106,												
56-108,83-111												
76,102												
SUMMARY												
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Db	25	APVDQCECTLDENPFSSQPGAPILQMGCCFSRAYTPRKRKTMVQRNVTSESTCC	84									
Qy	165	AGAAGGPECTLDENPFSSQPGAPILQMGCCFSRAYTPRKRKTMVQRNVTSESTCC	224									
Db	85	VAKSYNRYTVMGFRVNHHTACHCSTCYHKS	116									
Qy	225	VAKSYNRYTVMGFRVNHHTACHCSTCYHKS	256									
RESULT	12											
ENTRY	1HRA	#type complete										
TITLE		chorionic gonadotropin, chain A - humanORGANISM										
#note		placental origin, urinary extracted										
REFERENCE	A52806	Lapthorn, A.U.; Harris, D.C.; Isaacs, N.W.										
#authors		submitted to the Brookhaven Protein Data Bank, August 1994										
#submission		cross-references pms:1HRA										
cross-references	pms:1HRA											

COMMENT	Determination: X-ray diffraction
KEYWORDS	hormone
FEATURE	
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7-57	#disulfide_bonds\
25-79	#disulfide_bonds\
29-81	#disulfide_bonds\
56-84	#disulfide_bonds
SUMMARY	#length 86 #molecular-weight 9572 #checksum 1371
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Best Local Similarity	95.3%; Pred. No. 6 89e-119;
Matches	82; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db	1 T0DCPCTLQENPFPSQPGAPILQMGCCFSRAYPTPLRSKRTMLVQKNVTSESTCCVAK 60
QY	168 APCGECTLQENPFPSQPGAPILQMGCCFSRAYPTPLRSKRTMLVQKNVTSESTCCVAK 227
Db	61 SYNRYTMGKFEVNHRTACHCSTCY 86
QY	228 SYNRYTMGKFEVNHRTACHCSTCY 253
RESULT 13	
ENTRY	1XUUA #type complete
TITLE	chorionic gonadotropin, chain A - humanPDB_TITLE
ORGANISM	receptor complexed with human chorionic gonadotropin
REFERENCE	#formal_name Homo sapiens #common_name man
#authors	Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N.
#submission	submitted to the Brookhaven Protein Data Bank, December 1996
#cross-references	PDB:1XUUA
REFERENCE	TN032623
#authors	Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N.
#journal	Structure (London) (1996) 3:1341
#title	Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions structure.
REFERENCE	TN032624
#authors	Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.; Hendrickson, W.A.
#journal	Structure (London) (1994) 2:545
#title	Structure of human chorionic gonadotropin at 2.6 Å resolution from mad analysis of the selenomethionyl protein.
COMMENT	Resolution: not applicable
COMMENT	Determination: theoretical model
KEYWORDS	complex; glycoprotein hormone receptor glycoprotein; hormone; phosphorylation; receptor
FEATURE	
37-41	#region helix (right hand alpha)\
7-10, 22-25	#region beta sheet\
49-53, 26-34	#region beta sheet\
61-65, 71-75	#region beta sheet\
55-60, 77-81	#region beta sheet\
3-27	#disulfide_bonds\
6-56	#disulfide_bonds\
24-78	#disulfide_bonds\
28-80	#disulfide_bonds\
55-83	#disulfide_bonds
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Best Local Similarity	98.8%; Pred. No. 1 99e-119;
Matches	82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db	3 CPECTLQENPFPSQPGAPILQMGCCFSRAYPTPLRSKRTMLVQKNVTSESTCCVAKSYN 62
QY	171 CPECTLQENPFPSQPGAPILQMGCCFSRAYPTPLRSKRTMLVQKNVTSESTCCVAKSYN 230
Db	63 RVTYMGKFEVNHRTACHCSTCY 85

OY 231 RVTWGGFVENHTGCHCSTCY 253

RESULT 14 1HCNA #type complete

TITLE Human chorionic gonadotropin, chain A - humanORGANISM  
REFERENCE A52587  
#authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;  
Hendrickson, W.A.  
#submission Submitted to the Brookhaven Protein Data Bank, July 1994  
#cross-references PDB:1HCN  
REFERENCE TN020262  
#authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;  
Hendrickson, W.A.  
#journal Structure (1994) 2:545  
#title Structure of human chorionic gonadotropin at 2.6 angstroms resolution from mad analysis of the selenomethionyl protein.

COMMENT Resolution: 2.6 angstroms  
KEYWORDS Determination: X-ray diffraction  
FEATURE Hormone

36-43 #region helix (right hand alpha)\  
4-11,21-28 #region beta sheet\  
29-35,48-54 #region beta sheet\  
3-27 #disulfide\_bonds\  
6-56 #disulfide\_bonds\  
24-78 #disulfide\_bonds\  
28-80 #disulfide\_bonds\  
55-83 #disulfide\_bonds  
SUMMARY #length 85 #molecular-weight 9471 #checksum 9656

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Best Local Similarity 98.8%; Pred. No. 1.99e-118;  
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 3 CPECTLOENPFESOGAPILQCMGCCFSRAYPTPLRSKKTMLVOKNVTSESTCCVAKSYN 62  
OY 171 CPECTLOENPFESOGAPILQCMGCCFSRAYPTPLRSKKTMLVOKNVTSESTCCVAKSYN 230

Db 63 RVTWGGFVENHTGCHCSTCY 85  
OY 231 RVTWGGFVENHTGCHCSTCY 253

RESULT 15 A39555 #type complete

TITLE glycoprotein hormones alpha chain precursor - rhesus macaqueORGANISM  
DATE 08-Nov-1991 #sequence\_revision 08-Nov-1991 #text\_change 13-Jan-1995

ACCESSIONS A39555  
REFERENCE A39555  
#authors Golos, T.G.; Durning, M.; Fisher, J.M.  
#journal DNA Cell Biol. (1991) 10:367-380  
#title Molecular cloning of the rhesus glycoprotein hormone alpha-subunit gene.  
#cross-references MUID:91321740  
#accession A39555

##status preliminary; not compared with conceptual translation  
##molecule\_type DNA  
##residues 1-120 #label GOL  
CLASSIFICATION #superfamily glycoprotein hormones alpha chain glycoprotein  
KEYWORDS  
SUMMARY #length 120 #molecular-weight 13785 #checksum 5074

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Best Local Similarity 83.5%; Pred. No. 6.48e-97;  
Matches 71; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Db 35 CPECKPRENKFSPGAPIYQCMGCCFSRAYPTPLRSKKTMLVOKNVTSESTCCVAKSLT 94

OY 171 CPECTLOENPFESOGAPILQCMGCCFSRAYPTPLRSKKTMLVOKNVTSESTCCVAKSYN 230  
Db 95 RVTWGGFVENHTGCHCSTCYHK 119  
OY 231 RVTWGGFVENHTGCHCSTCYHK 255

Search completed: Wed May 6 08:50:40 1998  
Job time : 39 secs.

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FT	REPEAT	43	82	TNFR-CYS 1.
FT	REPEAT	83	125	TNFR-CYS 2.
FT	REPEAT	126	166	TNFR-CYS 3.
FT	REPEAT	167	195	TNFR-CYS 4.
FT	DOMAIN	362	447	DEATH DOMAIN.
FT	DISULFID	44	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	81	BY SIMILARITY.
FT	DISULFID	84	99	BY SIMILARITY.
FT	DISULFID	102	117	BY SIMILARITY.
FT	DISULFID	105	125	BY SIMILARITY.
FT	DISULFID	127	143	BY SIMILARITY.
FT	DISULFID	146	158	BY SIMILARITY.
FT	DISULFID	149	166	BY SIMILARITY.
FT	DISULFID	182	179	BY SIMILARITY.
FT	DISULFID	182	190	BY SIMILARITY.
FT	DISULFID	185	194	BY SIMILARITY.
FT	CARBOHYD	54	54	POTENTIAL.
FT	CARBOHYD	86	86	POTENTIAL.
FT	CARBOHYD	145	145	POTENTIAL.
FT	CARBOHYD	151	151	POTENTIAL.
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Db	101	SCSKRSEMSQVEISPTVDYBDYVCGCKRKNQYRRYVSETLTFQCLNCSLCPNGTVQLPCLE	160	
Qy	83	SCSKCRKEMGQVEISSCTVDYBDYVCGCKRKNQYRRYVSENLTFQCLNCSLCPNGTVQLPCLE	142	
Db	161	KODTICNHSFELRDKECVSCVCKNADCNLCIPRISSETNDQDGTIVL	212	
Qy	143	KONTVCTHAEFLRENECVSCAG-AAPGCE-C-TIGENPF-EPGAPIL	190	
RESULT				
ID	3	STANDARD;	PRT;	454 AA.
AC	P25118;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).			
GN	TNFR1 OR TNFR-1.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUFARCTA; METAOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 9118785.			
RA	LEWIS M., TATAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,			
RA	WONG G.H., CHEN E.Y., GOEDEL D.V.;			
RA	PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE; 91246168.			
RX	GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANDAN C.I.,			
RA	COPELAND N.G., JENKINS N.A., SMITH C.A.;			
RA	MOL. CELL. BIOL. 11:3020-3026(1991).			
RL	[3]			
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RP	MEDLINE; 91285014.			
RX	BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,			
RA	GRAY P.W., FELDMANN M., FOXWELL B.M.J.;			
RA	EUR. J. IMMUNOL. 21:1649-1656(1991).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE-SPLEEN;			
RC				

RX	MEDLINE: 92039815.
RA	ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL	IMMUNOGENETICS 34:338-340(1991).
RN	[5]
RP	SEQUENCE FROM N.A.
RX	MEDLINE: 94245292.
RA	BEBO B.F., LINTHICUM D.S.;
RL	IMMUNOGENETICS 39:450-451(1994).
RN	[6]
RP	SEQUENCE FROM N.A.
RX	MEDLINE: 93156721.
RA	ROTHE J., BLUTHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL	MOL. IMMUNOL. 30:165-175(1993).
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (APARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMODIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR	EMBL: M60466; G199826; -
DR	EMBL: M59377; G202097; -
DR	EMBL: X59238; G53579; -
DR	EMBL: X57796; G54849; -
DR	EMBL: L26349; G430733; -
DR	EMBL: M76656; G202102; -
DR	EMBL: M88067; G202102; JOINED.
DR	EMBL: M76655; G202102; JOINED.
DR	PIR: A38634; GQMST1.
DR	PIR: S16677; S16677.
DR	PIR: S19021; S19021.
DR	HSSP: P19438; 1TNR.
DR	MGI: P98781; TNFR1.
DR	PROSITE: PS00652; TNFR_NGFR_1; 3.
DR	PROSITE: PS50050; TNFR_NGFR_2; 3.
KW	PROSITE: PS50017; DEATH_DOMAIN: 1.
DR	RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS. POTENTIAL.
FT	SIGNAL 1 21
FT	CHAIN 22 454
FT	DOMAIN 22 212
FT	TRANSSEM 213 235
FT	DOMAIN 236 454
FT	DOMAIN 43 196
FT	REPEAT 43 82
FT	REPEAT 83 125
FT	REPEAT 126 166
FT	REPEAT 167 196
FT	DOMAIN 356 441
FT	DISULFID 44 58
FT	DISULFID 59 72
FT	DISULFID 62 81
FT	DISULFID 84 99
FT	DISULFID 102 125
FT	DISULFID 105 125
FT	DISULFID 127 143
FT	DISULFID 146 158
FT	DISULFID 149 166
FT	DISULFID 168 179
FT	DISULFID 182 191
FT	DISULFID 185 195
FT	CARBOHYD 54 54
FT	CARBOHYD 151 151
FT	CARBOHYD 202 202
FT	CONFLICT 394 394
FT	R -> G (IN REF. 6).

[illegible]

FT	DISULFID	84	99	BY SIMILARITY.
FT <th>DISULFID</th> <td>102</td> <td>117</td> <td>BY SIMILARITY.</td>	DISULFID	102	117	BY SIMILARITY.
FT <th>DISULFID</th> <td>105</td> <td>125</td> <td>BY SIMILARITY.</td>	DISULFID	105	125	BY SIMILARITY.
FT <th>DISULFID</th> <td>127</td> <td>143</td> <td>BY SIMILARITY.</td>	DISULFID	127	143	BY SIMILARITY.
FT <th>DISULFID</th> <td>146</td> <td>158</td> <td>BY SIMILARITY.</td>	DISULFID	146	158	BY SIMILARITY.
FT <th>DISULFID</th> <td>149</td> <td>166</td> <td>BY SIMILARITY.</td>	DISULFID	149	166	BY SIMILARITY.
FT <th>DISULFID</th> <td>168</td> <td>179</td> <td>BY SIMILARITY.</td>	DISULFID	168	179	BY SIMILARITY.
FT <th>DISULFID</th> <td>182</td> <td>191</td> <td>BY SIMILARITY.</td>	DISULFID	182	191	BY SIMILARITY.
FT <th>DISULFID</th> <td>185</td> <td>195</td> <td>BY SIMILARITY.</td>	DISULFID	185	195	BY SIMILARITY.
FT <th>CARBOHYD</th> <td>54</td> <td>54</td> <td>POTENTIAL.</td>	CARBOHYD	54	54	POTENTIAL.
FT <th>CARBOHYD</th> <td>151</td> <td>151</td> <td>POTENTIAL.</td>	CARBOHYD	151	151	POTENTIAL.
FT <th>CARBOHYD</th> <td>201</td> <td>201</td> <td>POTENTIAL.</td>	CARBOHYD	201	201	POTENTIAL.
SO <th>SEQUENCE</th> <td>461 AA;</td> <td>50969 MM;</td> <td>82F66B08 CRC32;</td>	SEQUENCE	461 AA;	50969 MM;	82F66B08 CRC32;
Query Match				
Best Local Similarity		40.6%;	Score 809;	DB 1; Length 461;
Matches 98;		Conservative 21;	Mismatches 24;	Indels 0; Gaps 0;
Db	41	DNLDPGKVAHPKRNKSTICTGCHGTGLVSPSPGQETVCEVDKKTFTFASQHNHNOCL	100	
Qy	23	DSVCGQGYTHPNNSICTCKHGTGLVNCPEPGDPTDCRESGSSFTASENHLPHCL	82	
Db	101	SKCTCKRMEFVEIISPCKADMDTYCGCKKNQFORLYLSETHPQCSPPCENGTYTTPCKE	160	
Qy	83	SCSNCRKMGVGEVSSCTGYRDRDTYCGCKRKNYRHYRSENLEFGCCNCSLCLNGTYHLSQCE	142	
Db	161	KONTVCNCHAGFTLSGNECTPCS	183	
Qy	143	KONTVCNCHAGFTLRENECVSCA	165	
RESULT 5				
ID	5	STANDARD;	PRT;	116 AA.
AC	P01215;			
DT	21-JUL-1986	(REL. 01, CREATED)		
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)		
DE	GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.			
GN	CGA.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 8001160.			
RA	FIDDES J.C., GOODMAN H.M.;			
RA	MIYOSHI I., KASAI N., HAYASHIZANI Y.;			
RA	NIPON RINSHO 52:940-947(1994).			
RN	[3]			
RP	SEQUENCE OF 1-98 FROM N.A.			
RX	MEDLINE; 82267643.			
RA	FIDDES J.C., GOODMAN H.M.;			
RA	J. MOL. APPL. GENET. 1:3-18(1981).			
RN	[4]			
RP	SEQUENCE OF 1-24.			
RX	MEDLINE; 81117268.			
RA	BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;			
RA	J. BIOL. CHEM. 256:1816-1823(1981).			
RN	[5]			
RP	SEQUENCE OF 28-116.			
RX	MEDLINE; 77243687.			
RA	SAIRAM M.R., LI C.H.;			
RA	CAN. J. BIOCHEM. 55:755-760(1977).			
RN	[6]			
RP	SEQUENCE OF 28-116.			
RX	MEDLINE; 72242988.			
RA	SAIRAM M.R., PARKOFF H., LI C.H.;			
RA	BIOCHEM. BIOPHYS. RES. COMMON. 48:530-537(1972).			
RN	[7]			

RP SEQUENCE, AND REVISIONS.  
RA KEUTMANN H.T., WILLIAMS R.M., BISHOP W.H., RYAN R.J.;  
RL FED. PROC. 37:1828-1828(1978).  
RN [8]  
RP SEQUENCE OF 25-116.  
RX MEDLINE; 76005558.  
RA RATHNAM P., SAXENA B.B.;  
RL J. BIOL. CHEM. 250:6735-6746(1975).  
RN [9]  
RP SEQUENCE OF 28-116.  
RX MEDLINE; 74262937.  
RA SHOME B., PARLOW A.F.;  
RL J. CLIN. ENDOCRINOL. METAB. 39:199-202(1974).  
RN [10]  
RP SEQUENCE OF 25-116.  
RX MEDLINE; 7521304.  
RA MORGAN F.J., BIRKEN S., CANFIELD R.E.;  
RL J. BIOL. CHEM. 250:5247-5258(1975).  
RN [11]  
RP SEQUENCE OF 25-116.  
RX MEDLINE; 74011266.  
RA BELITSARIO R., CARLSEN R.B., BAHL O.P.;  
RL J. BIOL. CHEM. 248:6796-6809(1973).  
RN [12]  
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
RX MEDLINE; 81021713.  
RA FUJIKI Y., RATHNAM P., SAXENA B.B.;  
RL BIOCHIM. BIOPHYS. ACTA 624:428-435(1980).  
RN [13]  
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
RX MEDLINE; 81006887.  
RA MISE T., BAHL O.P.;  
RL J. BIOL. CHEM. 255:8516-8522(1980).  
RN [14]  
RP STRUCTURE OF CARBOHYDRATES.  
RX MEDLINE; 91122088.  
RA WEISSHAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;  
RL EUR. J. BIOCHEM. 195:257-268(1991).  
RN [15]  
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RX MEDLINE; 94261179.  
RA LATHMON A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,  
RA CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;  
RL NATURE 369:455-461(1994).  
RN [16]  
RP STRUCTURE BY NMR.  
RX MEDLINE; 97054614.  
RA DE BEER T., VAN ZUYLEN C.W.E.M., LEEFLANG B.R., HARD K., BOELEN S.,  
RA KAPTEIN R., KAMERLING J.P., VLEGENTHART J.F.G.;  
RL EUR. J. BIOCHEM. 241:229-242(1996).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CC CHAIN WHICH CONFERNS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC EMBL; J00152; G183319; -;  
DR EMBL; J00150; G183319; JOINED.  
DR EMBL; J00151; G183319; JOINED.  
DR EMBL; S70585; G546845; -;  
DR EMBL; S70583; G546845; JOINED.  
DR EMBL; S70584; G546845; JOINED.  
DR EMBL; V00518; G31869; -;  
DR EMBL; V00485; G669156; -;  
DR EMBL; V00486; G669156; JOINED.  
DR EMBL; V00487; G669156; JOINED.  
DR PIR; A01481; TTH0AP.  
DR PDB; 1HCP; 30-SEP-94.  
DR PDB; 1HRP; 01-NOV-94.  
DR MIM; 118850; -;  
DR MIM; 188530; -;  
DR PROSITE; PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE; PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
DR HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.  
FT SIGNAL 1 24  
FT CHAIN 25 116 GLYCOPROTEIN HORMONES ALPHA CHAIN.

FT DISULFID 31 55  
FT DISULFID 34 84  
FT DISULFID 52 106  
FT DISULFID 56 108  
FT DISULFID 83 111  
FT CARBOHYD 63 63  
FT CARBOHYD 76 76  
FT CARBOHYD 102 102  
FT CONFLICT 29 29  
FT CONFLICT 108 109  
SQ SEQUENCE 116 AA; 13075 MW; 3BA19E2F CRC32;  
O -> E (IN REF. 8).  
CS -> SC (IN REF. 5 AND 6).  
Query Match 33.5%; Score 667; DB 1; Length 116;  
Best Local Similarity 93.5%; Pred. No. 3 28e-145;  
Matches 86; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Db 25 APDVDDCEPTIQENPFESQGPAPILQCGCCFSRAYPTPLRSKTKMLVQKNVTSSTCC 84  
165 AGAPGCEPTIQENPFESQGPAPILQCGCCFSRAYPTPLRSKTKMLVQKNVTSSTCC 224  
QY 165 AGAPGCEPTIQENPFESQGPAPILQCGCCFSRAYPTPLRSKTKMLVQKNVTSSTCC 224  
Db 85 VAKSYNRYTVMGFVFNHTACHCSTCYHKS 116  
225 VAKSYNRYTVMGFVFNHTACHCSTCYHKS 256  
QY 225 VAKSYNRYTVMGFVFNHTACHCSTCYHKS 256  
RESULT 6  
ID GLHA\_MACMU STANDARD; PRT; 120 AA.  
AC P22762;  
DT 01-AUG-1991 (REL. 19, CREATED)  
DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.  
GN CGA.  
OS MACACA MULATTA (RHESUS MACAQUE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 91321740.  
RA GOLOS T.G., DURNING M., FISHER J.M.;  
RL DNA CELL BIOL. 10:367-380(1991).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CC CHAIN WHICH CONFERNS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC PIR; A39555; A39555.  
DR HSSP; P01215; 1HCN.  
DR PROSITE; PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE; PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KM HORMONE; GLYCOPROTEIN; SIGNAL.  
FT SIGNAL 1 24  
FT CHAIN 25 120  
FT DISULFID 35 59  
FT DISULFID 38 88  
FT DISULFID 56 110  
FT DISULFID 60 112  
FT DISULFID 87 115  
FT CARBOHYD 67 67  
FT CARBOHYD 80 80  
FT CARBOHYD 106 106  
SQ SEQUENCE 120 AA; 13785 MW; 85E1F9F4 CRC32;  
Query Match 27.6%; Score 551; DB 1; Length 120;  
Best Local Similarity 83.5%; Pred. No. 6 39e-114;  
Matches 71; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
Db 35 CPECKREKPFKSGAPLYOCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCVAKSLT 94  
171 CPECKREKPFKSGAPLYOCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCVAKSLT 230  
QY 171 CPECKREKPFKSGAPLYOCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCVAKSLT 230  
Db 95 RYVMGSEVENHTCHCSTCYHKS 119  
231 RYVMGSEVENHTCHCSTCYHKS 255  
QY 231 RYVMGSEVENHTCHCSTCYHKS 255

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RESULT 7
ID GLHA_BOVIN STANDARD; PRT: 120 AA.
AC POL217;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN CGA.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84041490.
RA GOODWIN R.G., MONCMAN C.L., ROTTMAN F.M., NILSON J.H.;
RL NUCLEIC ACIDS RES. 11:6873-6882(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84024633.
RA ERWIN C., CROYLE M.L., DONELSON J., MAURER R.;
RL BIOCHEMISTRY 22:4856-4860(1983).
RN [3]
RP SEQUENCE OF 8-133 FROM N.A.
RX MEDLINE; 83161058.
RA NILSON J.H., THOMASON A.R., CSEBBAK M.T., MONCMAN C.L., WOYCHIK R.P.;
RL J. BIOL. CHEM. 258:4679-4682(1983).
RN [4]
RP SEQUENCE OF 25-120.
RX MEDLINE; 71111428.
RA LIAO T.-H., PIERCE J.G.;
RL J. BIOL. CHEM. 246:850-865(1971).
RN [5]
RP PRELIMINARY PARTIAL SEQUENCE.
RX MEDLINE; 71111429.
RA PIERCE J.G., LIAO T.-H., CARLSEN R.B., REIMO T.;
RL J. BIOL. CHEM. 246:866-872(1971).
RN [6]
RP SEQUENCE OF 80-91 AND 100-120.
RX MEDLINE; 72012932.
RA MAGHOUN-ROGISTER G., HENNEN G.P.;
RL EUR. J. BIOCHEM. 21:489-497(1971).
RN [7]
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX MEDLINE; 74307752.
RA CORNELL J.S., PIERCE J.G.;
RL J. BIOL. CHEM. 249:4166-4174(1974).
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC EMBL; X00003; E274391; -.
DR EMBL; X00004; E274391; JOINED.
DR EMBL; X00050; G607; -.
DR PIR; A01483; TTBOA.
DR PIR; A05132; A05132.
DR HSSP; P01215; LHGN.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 120
FT DISULFID 35 59 GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 56 110 BY SIMILARITY.
FT DISULFID 60 112 BY SIMILARITY.
FT DISULFID 87 115 BY SIMILARITY.
FT CARBOHYD 80 80
FT CARBOHYD 106 106
FT CONFLICT 13 13 A -> T (IN REF. 2).
FT CONFLICT 37 37 E -> Q (IN REF. 4).
FT CONFLICT 52 52 P -> A (IN REF. 2).
FT CONFLICT 84 84 EATC -> ACCT (IN REF. 6).
SQ SEQUENCE 120 AA; 13616 MW; 99C153C5 CRC32;

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Query Match 27.5%; Score 548; DB 1; Length 120;
Best Local Similarity 77.0%; Pred. No. 4,06e-113;
Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

DB 34 GCPECKLEKNKFSKPDAPVIOCGCCFSRAYPTPARSKTMTLPKNTSEATCCVAKAF 93
QY 170 GCPCTIQENFFSQPAPILQMGCCFSRAYPTPLRSKTMVLQKNVTSSTCCVAKSY 229
DB 94 TKATVNGNVRENTBCHSCSTCYHKS 120
QY 230 NRTVMGCFVENVHTGCHSCSTCYHKS 256

RESULT 8
ID GLHA_SHEEP STANDARD; PRT: 120 AA.
AC POL218;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN CGA.
OS OVIS ARIES (SHEEP).
OC EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90098887.
RA BELLO P.A., MOUNTFORD P.S., BRANDON M.R., ADAMS T.E.;
RL NUCLEIC ACIDS RES. 17:10494-10494(1989).
RN [2]
RP SEQUENCE OF 25-120.
RX MEDLINE; 72211144.
RA LIU W.-K., NAHM H.S., SWEENEY C.M., LANKIN W.M., BAKER H.N.;
RL J. BIOL. CHEM. 247:4351-4364(1972).
RN [3]
RP SEQUENCE OF 25-120.
RX MEDLINE; 73190034.
RA SAIRAM M.R., PARKOFF H., LI C.H.;
RL ARCH. BIOCHEM. BIOPHYS. 153:554-571(1972).
RN [4]
RP SEQUENCE OF 25-120.
RX MEDLINE; 82113052.
RA SAIRAM M.R.;
RL BIOCHEM. J. 197:535-539(1981).
RN [5]
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RA CHUNG D., SAIRAM M.R., LI C.H.;
RL ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973).
RN [6]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE; 91006170.
RA WEISSHAAR G., HIYAMA J., RENNICK A.G.C.;
RL EUR. J. BIOCHEM. 192:741-751(1990).
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC EMBL; X16977; G1366; -.
DR EMBL; X16977; G1366; -.
DR PIR; A01483; TTBOA.
DR PIR; A01484; UTSHA.
DR PIR; S06935; S06935.
DR PIR; S13200; S13200.
DR HSSP; P01215; LHGN.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 120
FT DISULFID 35 59 GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 56 110 BY SIMILARITY.
FT DISULFID 60 112 BY SIMILARITY.

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FT	DISULFID	87	115		BY SIMILARITY.
FT	CARBOHYD	80	80		
FT	CARBOHYD	106	106		
FT	CONFLICT	27	27	D -> N (IN REF. 2).	
FT	CONFLICT	29	29	E -> Q (IN REF. 2).	
FT	CONFLICT	37	37	E -> Q (IN REF. 2 TO 4).	
FT	CONFLICT	112	113	CS -> SC (IN REF. 3).	
SO	SEQUENCE	120 AA;	13588 MM;	13BADDEL CAC32;	
Query Match 27.5%; Score 548; DB 1; Length 120;					
Best Local Similarity 77.0%; Pred. No. 4,06e-113;					
Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;					
Db	34 GCPECKLKENVYFKSPADPIYQCGCCFSRAVPPPARSKTMTLVPKNTSEATCCVAKAF 93				
Oy	170 GCPECTLDENFFSOPGAPILQCGCCFSRAVPPPLRSKTMVLQKNVTSSTCCVAKSY 229				
Db	94 TKATVMGNVRYENHTCHSTCYHYKS 120				
Oy	230 NRYVMGSGFYVENHTGCHSTCYHYKS 256				
RESULT	9	STANDARD;	PRT;	96 AA.	
ID	GLHA_RABIT				
AC	P07474;				
DT	01-APR-1988 (REL. 07, CREATED)				
DT	01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)				
DE	GLYCOPROTEIN HORMONES ALPHA CHAIN.				
GN	CGA.				
OS	ORYCTOLAGUS CUNICULUS (RABBIT).				
OC	EUMAROTIA; METAPOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	EUTHERIA; LAGOMORPHA.				
RN	[1]				
RP	SEQUENCE.				
RA	GLENN S.D., NAHM H.S., WARD D.N.;				
RL	J. PROTEIN CHEM. 3:143-156(1984).				
CC	-1- SUBUNIT: HEMERODIMER OF A COMMON ALPHA CHAIN AND A UNIOE BETA				
CC	CHAIN WHICH CONTERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,				
CC	LUTROTROPIN, FOLLITROPIN AND GONADOTROPIN.				
DR	PIR: A05096; A05096.				
DR	HSSP: P01233; IHRP.				
DR	PROSITE: PS00779; GLYCO_HORMONE_ALPHA_1; 1.				
DR	PROSITE: PS00780; GLYCO_HORMONE_ALPHA_2; 1.				
FT	HORMONE; GLYCOPROTEIN.				
FT	DISULFID	11	35	BY SIMILARITY.	
FT	DISULFID	14	64	BY SIMILARITY.	
FT	DISULFID	32	86	BY SIMILARITY.	
FT	DISULFID	36	88	BY SIMILARITY.	
FT	DISULFID	63	91	BY SIMILARITY.	
FT	CARBOHYD	56	56	BY SIMILARITY.	
FT	CARBOHYD	82	82		
SO	SEQUENCE	96 AA;	10663 MM;	CD56D255 CRC32;	
Query Match 27.4%; Score 546; DB 1; Length 96;					
Best Local Similarity 76.7%; Pred. No. 1.39e-112;					
Matches 69; Conservative 6; Mismatches 15; Indels 0; Gaps 0;					
Db	7 AMOGPECKLKENVYFKSLGAPYQCGCCFSRAVPPPARSKTMTLVPKNTSEATCCVAA 66				
Oy	167 AAPGPECKTLDENFFSOPGAPILQCGCCFSRAVPPPLRSKTMVLQKNVTSSTCCVAA 226				
Db	67 KAFKATVMGNVRYENHTCHSTCYHYKS 96				
Oy	227 KSYNRYVMGSGFYVENHTGCHSTCYHYKS 256				
RESULT	10	STANDARD;	PRT;	120 AA.	
ID	GLHA_RAT				
AC	P11662; P70516;				
DT	01-OCT-1989 (REL. 12, CREATED)				
DT	01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				

DE	GLYCOPROTEIN HORMONES ALPHA CHAIN 1 PRECURSOR.
OC	RATTUS NORVEGICUS (RAT).
OC	EUARCTOTA, METAFOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA,
OC	EUTHERIA, RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RP	STRAIN-SPRAGUE-DAWLEY; TISSUE=PIUITARY;
RX	MEDLINE; 8221405.
RA	GODINE J.E., CHIN W.W., HABENER J.F.;
RL	J. BIOL. CHEM. 257:8368-8371(1982).
RN	[2]
RP	SEQUENCE FROM N.A.
RP	STRAIN-SPRAGUE-DAWLEY; TISSUE=PIUITARY;
RX	MEDLINE; 89196918.
RA	BURNSIDE J., BUCKLAND P.R., CHIN W.W.;
RL	GENE 70:67-74(1988).
RN	[3]
RP	SEQUENCE FROM N.A.
RP	STRAIN-WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;
RA	KATO Y., EZASHI T., HIRAI T., KATO T.;
RL	ZOOL. SCI. 7:877-885(1990).
CC	-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC	CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC	EMBL; V01252; G56580; -
DR	EMBL; J00757; G206111; -
DR	EMBL; M22829; - NOT_ANNOTATED_CDS.
DR	EMBL; M23543; G204470; -
DR	EMBL; M25544; G204471; -
DR	EMBL; D00575; G220842; -
DR	PIR; J04048; TTRTA.
DR	PIR; S27385; S27385.
DR	HSSP; P01233; IHRP.
DR	PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR	PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW	HORMONE; GLYCOPROTEIN; SIGNAL.
FT	SIGNAL 1 24
FT	CHAIN 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN 1.
FT	DISULFID 35 59 BY SIMILARITY.
FT	DISULFID 38 88 BY SIMILARITY.
FT	DISULFID 56 110 BY SIMILARITY.
FT	DISULFID 60 112 BY SIMILARITY.
FT	DISULFID 87 115 BY SIMILARITY.
FT	CARBOHYD 80 80 PROBABLE.
FT	CARBOHYD 106 106 PROBABLE.
FT	CONFLICT 84 84 E -> Q (IN G206111).
SO	SEQUENCE 120 AA; 13453 MW; 5E507A0D CRC32;.
Query Match	27.3%; Score 544; DB 1; Length 120;
Best Local Similarity	78.2%; Pred. No. 4,78e-112;
Matches 68; Conservative	6; Mismatches 13; Indels 0; Gaps 0.
Db	34 GCEPKLKENVYFSLGLAPIYQCGCCFSRAYPTPARSKKTMVLPKNITSATCCVAKSF 93
Oy	170 GCPECTLOENFFESOPGAPILQCGCCFSRAYPTPLASKRTMLVQKNVTSBSTCCVAKSY 229
Db	94 TKATVGNARVYENTDCHSTCYTHKS 120
Oy	230 NRVTVMGGEFVYENHTGCHSCSTCYTHKS 256
RESULT 11	
ID	GLHA_BALAC STANDARD; PRT; 96 AA.
AC	P37036;
DT	01-JUN-1994 (REL. 29, CREATED)
DT	01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE	GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN	CGA.
OS	BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER ROBOUUL).
OC	EUARCTOTA, METAFOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;
OC	EUTHERIA; CETACEA.
RN	[1]
RP	SEQUENCE.

RA KARASEV V.S., PANKOV Y.A.;  
RC BLOKHIMIA 50:1972-1986(1985).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC PIR: P01038; P01038.  
DR HSSP: P01215; 1HCN.  
DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
KW PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KW HORMONE; GLYCOPROTEIN.  
FT DISULFID 11 35 BY SIMILARITY.  
FT DISULFID 14 64 BY SIMILARITY.  
FT DISULFID 32 86 BY SIMILARITY.  
FT DISULFID 36 88 BY SIMILARITY.  
FT DISULFID 63 91 BY SIMILARITY.  
FT CARBOHYD 56 56 PROBABLE.  
FT CARBOHYD 82 82 PROBABLE.  
SQ SEQUENCE 96 AA; 10720 MW; E2CD30DF CRC32;

Query Match 27.1%; Score 541; DB 1; Length 96;  
Best Local Similarity 70.1%; Pred. No. 3.03e-111;  
Matches 61; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Db 10 GCEPCKLKEKRYSKLAPLYQCGCCFSRAYPTLPKSKTMTLVKNTSEATCCVAKAF 69  
QY 170 GCEPCKLQENPFPSQAPAPLQCGCCFSRAYPTLPKSKTMTLVKNTSEATCCVAKSY 229  
Db 70 TKATVMGARVYENHTZCHCSTCYTHKS 96  
QY 230 NRYTVMGFVYENHTZCHCSTCYTHKS 256

RESULT 12  
ID GLH2\_RAT STANDARD; PRT; 120 AA.  
AC P11963;  
DT 01-OCT-1989 (REL. 12, CREATED)  
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
DE GLYCOPROTEIN HORMONES ALPHA CHAIN 2 PRECURSOR.  
OS RATRUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE; 82214055.  
RX GODINE J.E., CHIN W.W., HABENER J.F.;  
RL J. BIOL. CHEM. 257:8368-8371(1982).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC EMBL; V01253; G56583; -.  
DR PIR; S27386; S27386.  
DR HSSP: P01215; 1HCN.  
DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KW HORMONE; GLYCOPROTEIN; SIGNAL.  
FT CHAIN 1 24  
FT SIGNAL 1 24  
FT DISULFID 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN 2.  
FT DISULFID 35 59 BY SIMILARITY.  
FT DISULFID 38 88 BY SIMILARITY.  
FT DISULFID 56 110 BY SIMILARITY.  
FT DISULFID 60 112 BY SIMILARITY.  
FT DISULFID 87 115 BY SIMILARITY.  
FT CARBOHYD 80 80 PROBABLE.  
FT CARBOHYD 106 106 PROBABLE.  
SQ SEQUENCE 120 AA; 13565 MW; 4E4FAB2E CRC32;

Query Match 27.1%; Score 541; DB 1; Length 120;  
Best Local Similarity 77.0%; Pred. No. 3.03e-111;  
Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Db 34 GCEPCKLKEKRYSKLAPLYQCGCCFSRAYPTLPKSKTMTLVKNTSEATCCVAKAF 93  
QY 170 GCEPCKLQENPFPSQAPAPLQCGCCFSRAYPTLPKSKTMTLVKNTSEATCCVAKSY 229

QY 170 GCEPCKLQENPFPSQAPAPLQCGCCFSRAYPTLPKSKTMTLVKNTSEATCCVAKSY 229  
Db 94 TKATVMGARVYENHTZCHCSTCYTHKS 120  
QY 230 NRYTVMGFVYENHTZCHCSTCYTHKS 256

RESULT 13  
ID GLH\_MOUSE STANDARD; PRT; 120 AA.  
AC P01216;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.  
GN CGA.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 82060239.  
RA CHIN W.W., KROENBERG H.M., DEE P.C., MALOOF F., HABENER J.F.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 78:5329-5333(1981).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 89170115.  
RA GORDON D.F., WOOD W.M., RIDGWAY E.C.;  
RL DNA 7:679-690(1988).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC EMBL; J00643; G202180; -.  
DR EMBL; V00852; G54799; -.  
DR EMBL; M22991; -: NOT\_ANNOTATED\_CDS.  
DR EMBL; M22992; G575520; -.  
DR PIR; A01482; TTMSA.  
DR PIR; A31598; A31598.  
DR HSSP: P01215; 1HCN.  
DR MGD; MGI:88390; CGA.  
DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KW HORMONE; GLYCOPROTEIN; SIGNAL.  
FT CHAIN 1 24  
FT SIGNAL 1 24  
FT DISULFID 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN.  
FT DISULFID 35 59 BY SIMILARITY.  
FT DISULFID 38 88 BY SIMILARITY.  
FT DISULFID 56 110 BY SIMILARITY.  
FT DISULFID 60 112 BY SIMILARITY.  
FT DISULFID 87 115 BY SIMILARITY.  
FT CARBOHYD 80 80 PROBABLE.  
FT CARBOHYD 106 106 PROBABLE.  
SQ SEQUENCE 120 AA; 13565 MW; 86F1F31A CRC32;

Query Match 27.1%; Score 541; DB 1; Length 120;  
Best Local Similarity 77.0%; Pred. No. 3.03e-111;  
Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Db 34 GCEPCKLKEKRYSKLAPLYQCGCCFSRAYPTLPKSKTMTLVKNTSEATCCVAKAF 93  
QY 170 GCEPCKLQENPFPSQAPAPLQCGCCFSRAYPTLPKSKTMTLVKNTSEATCCVAKSY 229

Db 94 TKATVMGARVYENHTZCHCSTCYTHKS 120  
QY 230 NRYTVMGFVYENHTZCHCSTCYTHKS 256

RESULT 14  
ID GLH\_PIG STANDARD; PRT; 120 AA.  
AC P01219;  
DT 21-JUL-1986 (REL. 01, CREATED)  
DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.

GN CGA.  
OS EMBRYO SCROFA (PIG).  
OC EMBRYOTA; METAPODA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; ARTIODACTYLA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 89325834.  
RA HIRAI T., TAKIKAWA H., KATO Y.;  
RL MOL. CELL. ENDOCRINOL. 63:209-217(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA KATO Y., EZASHI T., HIRAI T., KATO T.;  
RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [3]  
RP SEQUENCE OF 31-120.  
RX MEDLINE: 74075725.  
RA MAGHJIN-ROGISTER G., COMBARNOUS Y., HENNEN G.;  
RL EUR. J. BIOCHEM. 39:255-263(1973).  
RN [4]  
RP PRELIMINARY SEQUENCE OF 25-120.  
RA CLOSSET J., MAGHJIN-ROGISTER G., HENNEN G.;  
RL ENDOCRINOL. EXP. 8:164(1974).  
RN [5]  
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
RX MEDLINE: 75093922.  
RA COMBARNOUS Y., HENNEN G.;  
RL BIOCHEM. SOC. TRANS. 2:915-917(1974).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC EMBL: D00768; G217689; -.  
DR EMBL: D00768; G217689; JOINED.  
DR PIR: A01485; UTGA.  
DR PIR: A30339; A30339.  
DR HSSP: P01215; IHCN.  
DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KM HORMONE; GLYCOPROTEIN; SIGNAL.  
FT SIGNAL 1 24  
FT CHAIN 1 20  
FT DISULFID 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN.  
FT DISULFID 35 59 BY SIMILARITY.  
FT DISULFID 38 88 BY SIMILARITY.  
FT DISULFID 56 110 BY SIMILARITY.  
FT DISULFID 60 112 BY SIMILARITY.  
FT DISULFID 87 115 BY SIMILARITY.  
FT CARBOHYD 80 80  
FT CARBOHYD 106 106  
SQ SEQUENCE 120 AA; 13532 MW; 8749DBA5 CRC32;  
Query Match 27.1%; Score 541; DB 1; Length 120;  
Best Local Similarity 77.0%; Pred. No. 3.03e-11;  
Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
Db 34 GCECKLGENPFESKRGAPVYOCCTGCFRSPAYPTLRSKKTMVLPKNITSEATCCVAKAF 93  
QY 170 GCECKLGENPFESKRGAPVYOCCTGCFRSPAYPTLRSKKTMVLPKNITSEATCCVAKSY 229  
Db 94 TKATVGNARVENHTECHSCSTCYHKS 120  
QY 230 NRVTVMGFKVENHTECHSCSTCYHKS 256  
RESULT 15  
ID GLHA\_STRCA STANDARD: PRT; 96 AA.  
AC P80665;  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE GLYCOPROTEIN HORMONES ALPHA CHAIN.  
OS STRUTHIO CAMELUS (OSTRICH).  
OC EUKARYOTA; METAPODA; CHORDATA; VERTEBRATA; TETRAPODA; AVES;  
OC PALAEOGNATHAE; STRUTHIONIFORMES.  
RN [1]

RP SEQUENCE. 97025333.  
RX MEDLINE: 74075725.  
RA KOIDE Y., PAKOFF H., KANAUCHI H.;  
RL EUR. J. BIOCHEM. 240:262-267(1996).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KM HORMONE; GLYCOPROTEIN.  
FT DISULFID 11 35 BY SIMILARITY.  
FT DISULFID 14 64 BY SIMILARITY.  
FT DISULFID 32 86 BY SIMILARITY.  
FT DISULFID 36 88 BY SIMILARITY.  
FT DISULFID 63 91 BY SIMILARITY.  
FT CARBOHYD 56 56 POTENTIAL.  
FT CARBOHYD 82 82 POTENTIAL.  
SQ SEQUENCE 96 AA; 10781 MW; DDF7B4BB CRC32;  
Query Match 27.0%; Score 538; DB 1; Length 96;  
Best Local Similarity 74.7%; Pred. No. 1.92e-10;  
Matches 65; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
Db 10 GCECKLGENPFESKRGAPVYOCCTGCFRSPAYPTLRSKKTMVLPKNITSEATCCVAKAF 69  
QY 170 GCECKLGENPFESKRGAPVYOCCTGCFRSPAYPTLRSKKTMVLPKNITSEATCCVAKSY 229  
Db 70 TKATVGNARVENHTECHSCSTCYHKS 96  
QY 230 NRVTVMGFKVENHTECHSCSTCYHKS 256

Search completed: Wed May 6 08:48:07 1998  
Job time : 35 secs.

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MSrch\_PP protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed May 6 08:47:32 1998: MasPar time 7.91 Seconds  
Tabular output not generated. 811.687 Million cell updates/sec

Title: >US-08-804-166-2  
Description: (1-256) from US08804166.pep  
Perfect Score: 1994  
Sequence: 1 SRTSLLAFLGLCLPMLQEG.....GFKVENHGCHCTCYHKS 256

Scoring table: PAM 150  
Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot35  
1:swiss1

Statistics: Mean 42.029; Variance 63.165; scale 0.665

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description	Pred. No.
1	1124	56.4	455 1	TNRI_HUMAN TUMOR NECROSIS FACTOR	3.586-271
2	962	48.2	461 1	TNRI_PIG TUMOR NECROSIS FACTOR	3.536-226
3	841	42.2	454 1	TNRI_MOUSE TUMOR NECROSIS FACTOR	8.776-193
4	809	40.6	461 1	TNRI_RAT TUMOR NECROSIS FACTOR	5.456-184
5	667	33.5	116 1	GLHA_HUMAN GLYCOPROTEIN HORMONES	3.286-145
6	551	27.6	120 1	GLHA_MACMU GLYCOPROTEIN HORMONES	6.396-114
7	548	27.5	120 1	GLHA_BOVIN GLYCOPROTEIN HORMONES	4.066-113
8	548	27.5	120 1	GLHA_SHEEP GLYCOPROTEIN HORMONES	4.066-113
9	546	27.4	96 1	GLHA_RABIT GLYCOPROTEIN HORMONES	1.396-112
10	544	27.3	120 1	GLHA_RAT GLYCOPROTEIN HORMONES	3.036-111
11	541	27.1	96 1	GLHA_BALAC GLYCOPROTEIN HORMONES	3.036-111
12	541	27.1	120 1	GLHA_RAT GLYCOPROTEIN HORMONES	3.036-111
13	541	27.1	120 1	GLHA_MOUSE GLYCOPROTEIN HORMONES	3.036-111
14	541	27.1	120 1	GLHA_PIG GLYCOPROTEIN HORMONES	3.036-111
15	538	27.0	96 1	GLHA_STRCA GLYCOPROTEIN HORMONES	1.926-110
16	539	27.0	120 1	GLHA_CALJA GLYCOPROTEIN HORMONES	1.046-110
17	537	26.9	120 1	GLHA_MELGA GLYCOPROTEIN HORMONES	3.556-110
18	535	26.8	96 1	GLHA_PHYCA GLYCOPROTEIN HORMONES	1.226-109
19	503	25.4	118 1	GLHA_CYPKA GLYCOPROTEIN HORMONES	3.346-102
20	503	25.2	120 1	GLHA_EDVAS GLYCOPROTEIN HORMONES	4.106-101
21	501	25.1	96 1	GLHA_HORSE GLYCOPROTEIN HORMONES	1.396-100
22	500	25.1	118 1	GLHA_HYPMO GLYCOPROTEIN HORMONES	2.576-100
23	500	25.1	118 1	GLHA_CYPKA GLYCOPROTEIN HORMONES	2.576-100

24	500	25.1	118 1	GLHA_CTEID GLYCOPROTEIN HORMONES	2.576-100
25	499	25.0	116 1	GLHA_CLAGA GLYCOPROTEIN HORMONES	4.746-100
26	478	24.0	93 1	GLHA_MURCI GLYCOPROTEIN HORMONES	1.746-94
27	476	23.9	97 1	GLHA_RANCA GLYCOPROTEIN HORMONES	5.906-94
28	474	23.8	117 1	GLHA_ANGAN GLYCOPROTEIN HORMONES	1.996-93
29	448	22.5	114 1	GLH2_ONCKE GLYCOPROTEIN HORMONES	1.436-86
30	447	22.4	108 1	GLH1_ONCKE GLYCOPROTEIN HORMONES	2.626-86
31	427	21.4	94 1	GLHA_THUOB GLYCOPROTEIN HORMONES	4.606-81
32	424	21.3	117 1	GLHA_ACALA GLYCOPROTEIN HORMONES	2.806-80
33	377	18.9	125 1	GLHA_TUNHE GLYCOPROTEIN HORMONES	4.566-68
34	273	13.7	417 1	WSL1_HUMAN WSL-1 PROTEIN PRECURSOR	8.976-42
35	221	11.6	435 1	TNRC_HUMAN TUMOR NECROSIS FACTOR	1.406-31
36	225	11.3	325 1	VT2_SEVKA TUMOR NECROSIS FACTOR	3.766-30
37	221	11.1	326 1	TNRC_MOUSE TUMOR NECROSIS FACTOR	3.336-29
38	215	10.8	415 1	TNRC_MOUSE LYMPHOTOXIN-BETA RECEPTOR	8.656-28
39	214	10.7	349 1	VC22_VARV PROTEIN C22/B28 HOMOLOG	1.496-27
40	212	10.6	474 1	TNRI_MOUSE TUMOR NECROSIS FACTOR	4.376-27
41	207	10.4	425 1	NGFR_RAT LOW-AFFINITY NERVE GROWTH	6.446-26
42	207	10.4	427 1	NGFR_HUMAN LOW-AFFINITY NERVE GROWTH	6.446-26
43	204	10.2	260 1	CD27_HUMAN CD27 RECEPTOR PRECURSOR	3.216-25
44	188	9.4	323 1	PASG_BOVIN PASL RECEPTOR PRECURSOR	1.526-21
45	183	9.2	595 1	CD30_HUMAN CD30 RECEPTOR PRECURSOR	2.066-20

## ALIGNMENTS

RESULT ID	1	TNRI_HUMAN	STANDARD:	PRT:	455 AA.
AC	P19438;				
DT	01-FEB-1991 (REL. 17, CREATED)				
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).				
GN	TNFR1 OR TNFR.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.				
CC	[1]				
RC	SEQUENCE FROM N.A.				
RC	TISSUE-PLACENTA;				
RX	MEDLINE: 90235285.				
RA	SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W., GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDEL D.V., CELT 61:361-370(1990).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 90235284.				
RA	LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M., TABUCHI H., LESSLAUER W.;				
RL	CELL 61:351-359(1990).				
RP	[3]				
RX	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.				
RA	MEDLINE: 91016021.				
RL	NOPAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R., ADERKA D., HOLTSMANN H., WALLACH D.;				
RL	EMBO J. 9:3269-3278(1990).				
RP	[4]				
RX	SEQUENCE FROM N.A.				
RA	MEDLINE: 91090841.				
RA	HIMMLER A., NAURER-FOGY I., KROENKE M., SCHURICH P., PITZENMAIER K., LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;				
RL	DNA CELL BIOL. 9:705-715(1990).				
RP	[5]				
RX	SEQUENCE FROM N.A.				
RC	TISSUE-PLACENTA;				
RA	MEDLINE: 91017509.				
RL	GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).				
RP	[6]				
RX	SEQUENCE FROM N.A.				
RA	MEDLINE: 92250049.				
RA	FUCHS P., STREHL S., DMORZAK M., HIMMLER A., AMBROS P.F.;				



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[W] [O] [R] [E] [H] (TM)  
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MSPRCH\_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Wed May 6 08:48:26 1998; Maspar time 13.91 Seconds

Tabular output not generated. 775.210 Million cell updates/sec

Title: >US-08-804-166-2

Description: (1-256) from US08804166.pep

Perfect Score: 1994

Sequence: 1 SRTSLLAFLGLCLPWLQEG.....GKVENHTGCHCTCYHKS 256

Scoring table:

PAM 150  
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

sptrembl5  
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal  
5:sp\_mhc 6:sp\_oranella 7:sp\_phase 8:sp\_plant  
9:sp\_bacteria 10:sp\_rudent 11:sp\_virus 12:sp\_vertebrate  
13:sp\_unclassified

Statistics: Mean 41.143; Variance 64.343; scale 0.639

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	945	47.4	180	4	Q95185	TUMOUR NECROSIS FACTOR	3.15e-213
2	895	44.9	471	4	Q19131	TUMOR NECROSIS FACTOR	6.13e-200
3	454	22.8	108	12	Q90287	GONADOTROPIN ALPHA SUB	6.53e-85
4	453	22.7	107	12	Q90286	GONADOTROPIN ALPHA SUB	1.17e-84
5	451	22.6	119	12	Q91370	GONADOTROPIN ALPHA 1	3.76e-84
6	446	22.4	114	12	Q91371	GONADOTROPIN ALPHA 2	6.95e-83
7	433	21.7	117	12	Q91119	GLYCOPROTEIN HORMONES	1.34e-79
8	333	16.7	55	10	Q62589	ALPHA SUBUNIT OF GLYCO	1.06e-54
9	273	13.7	253	2	Q00276	LYMPHOCYTE ASSOCIATED	3.29e-40
10	273	13.7	380	2	Q00280	LYMPHOCYTE ASSOCIATED	3.29e-40
11	273	13.7	418	2	Q00275	LYMPHOCYTE ASSOCIATED	3.29e-40
12	257	12.9	277	2	Q14865	SOLUBLE DEATH RECEPTOR	2.00e-36
13	257	12.9	426	2	Q14866	SOLUBLE DEATH RECEPTOR	2.00e-36
14	214	10.7	348	11	Q85407	HOMOLOG OF VACCINIA VI	1.76e-26
15	214	10.7	349	11	Q85408	SOMALIA-1977 RIGHT NEA	1.76e-26
16	210	10.5	349	11	Q85409	GARCIA-1966 RIGHT NEAR	1.76e-26
17	210	10.5	355	11	Q85308	SECRETED RECEPTOR BIND	1.42e-25
18	206	10.3	459	10	Q62327	TUMOR NECROSIS FACTOR	1.13e-24
19	187	9.4	267	4	Q02764	OX40 PRECURSOR (FRAGME	1.89e-20
20	182	9.1	259	2	Q14755	TRAIL RECEPTOR 3.	2.34e-19

RESULT	ID	PRELIMINARY	PRT	180 AA.	HERPESVIRUS ENTRY MEDI	6.38e-19
21	180	9.0	283	2	Q92956	6.38e-19
22	180	9.0	299	2	Q14798	6.38e-19
23	179	9.0	425	2	Q16042	1.05e-18
24	178	8.9	324	10	Q63199	1.73e-18
25	174	8.7	411	2	Q15508	1.27e-17
26	174	8.7	411	2	Q15517	1.27e-17
27	174	8.7	411	2	Q14720	1.27e-17
28	174	8.7	440	2	Q15531	1.27e-17
29	174	8.7	440	2	Q14763	1.27e-17
30	167	8.4	202	2	Q14405	3.98e-16
31	167	8.4	217	2	Q16631	3.98e-16
32	161	8.1	468	2	Q00220	3.98e-16
33	160	8.0	202	2	Q14643	7.40e-15
34	160	8.0	245	2	Q14644	1.20e-14
35	155	7.8	217	2	Q14407	1.33e-13
36	156	7.8	372	2	Q00279	8.22e-14
37	154	7.7	199	2	Q14406	2.14e-13
38	153	7.7	401	2	Q00300	3.45e-13
39	153	7.7	625	10	Q35305	3.45e-13
40	152	7.6	401	10	Q08712	5.55e-13
41	150	7.5	274	2	Q13663	1.43e-12
42	147	7.4	217	4	Q07367	5.90e-12
43	148	7.4	401	10	Q08727	5.68e-12
44	146	7.3	217	4	Q07369	9.42e-12
45	143	7.2	212	4	Q07368	3.82e-11

#### ALIGNMENTS

RESULT 1  
ID Q95185 PRELIMINARY; PRT; 180 AA.

AC Q95185:  
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).  
GN TNFR-1.  
OS FELIS SILVESTRIS CATUS (CAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; CARNIVORA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA DUTHIE S., NASIR L., ECKERSALL P.D.;  
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; U72344; G1613880; -.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
FT NON\_TER 1 180  
FT NON\_TER 1 180  
SQ SEQUENCE 180 AA; 20399 MW; 5452A6B2 CRC32;

Query Match 47.4%; Score 945; DB 4; Length 180;  
Best Local Similarity 86.0%; Pred. No. 3.15e-213;  
Matches 117; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

DB	45	CPQGYIHQDMSICCTKHKSTLYLNDAGRGDLTDCECNGTFAENLRQCLSCS	104
QY	26	CPQGYIHQDMSICCTKHKSTLYLNDAGRGDLTDCECNGTFAENLRQCLSCS	85
DB	105	KRKEMGYVEISPCYRDYVGCGRKQRYRYWSETHFOCLNCSLCLNGTVOISCRETN	164
QY	86	KRKEMGYVEISPCYRDYVGCGRKQRYRYWSETHFOCLNCSLCLNGTVOISCRETN	145
DB	165	TVCTCHAGFFLRGNEC 180	
QY	146	TVCTCHAGFFLRGNEC 161	
RESULT	2	PRELIMINARY; PRT; 471 AA.	
ID	Q19131		
AC	Q19131		
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)		

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DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR-RECEPTOR 1.
GN TNR-RI.
OS BOS TAURUS (BOVINE).
OC EURKAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-AORTA;
RA LEE E.-K., TALYOR M.J., KEHRLI M.E.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U90937; G2290398; -.
DR PROSITE; PS00652; TNR_NGFR_1; 3.
SQ SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;

Query Match
Best Local Similarity 73.2%; Score 895; DB 4; Length 471;
Matches 104; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

Db 41 ESPCGKYNHPONSTICTCKHKGTYLYNDOPGPRDTCRVCAPTTALLENHRLCL 100
QY 23 DSVCPGGYTHIPNNSICTCKHKTLYXNDOPGGRDTCRVCAPTTALLENHRLCL 82
DB 101 SCSRCRDEMFVEISPCVVDVDCGCRKNQYREYWGTFGRCLNCLCPNGTVNIPCOE 160
QY 83 SCSRCRDEMFVEISPCVVDVDCGCRKNQYREYWGTFGRCLNCLCPNGTVNIPCOE 142
DB 161 RODTCHGMEFPLGAKCISC 182
QY 143 KONTVCTCHAGFEFLNEKCVSC 164

RESULT 3
ID 090287 PRELIMINARY; PRT; 108 AA.

AC 090287;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS CARASSIUS AURATUS (GOLDFISH).
OC EURKAROTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEIFHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RA KOBAYASHI M., KATO Y., YOSHIDARA Y., AIDA K.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; D86552; G1469838; -.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12129 MW; B2B1A212 CRC32;

Query Match
Best Local Similarity 72.8%; Score 454; DB 12; Length 108;
Matches 59; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

Db 28 GCECKLKENNIFSPGAPVYOCGCCFSRAYPTPLRSKKTMLVPKNTSRTATCCVAKEV 87
QY 170 GCECKLKENNIFSPGAPVYOCGCCFSRAYPTPLRSKKTMLVOKNVTSESTCCVAKSY 229
DB 88 KRVLV-DVRLVNHDTCHCSTC 108
QY 230 NRYVTVMGFKVENHTGCHCSTC 251

RESULT 4
ID 090286 PRELIMINARY; PRT; 107 AA.

AC 090286;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
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DE GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).
OS CARASSIUS AURATUS (GOLDFISH).
OC EURKAROTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEIFHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RA KOBAYASHI M., KATO Y., YOSHIDARA Y., AIDA K.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; D86551; G1469836; -.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11959 MW; 880C6840 CRC32;

Query Match
Best Local Similarity 72.7%; Score 453; DB 12; Length 107;
Matches 59; Conservative 7; Mismatches 15; Indels 1; Gaps 1;

Db 27 GCECKLKENNIFSPGAPVYOCGCCFSRAYPTPLRSKKTMLVPKNTSRTATCCVAKEV 86
QY 170 GCECKLKENNIFSPGAPVYOCGCCFSRAYPTPLRSKKTMLVOKNVTSESTCCVAKSY 229
DB 87 KRVLV-DVRLVNHDTCHCSTC 107
QY 230 NRYVTVMGFKVENHTGCHCSTC 251

RESULT 5
ID 091370 PRELIMINARY; PRT; 119 AA.

AC 091370;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GONADOTROPIN ALPHA 1 SUBUNIT.
OS ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC EURKAROTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEIFHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RA GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;
RL J. MOL. ENDOCRINOL. 11:265-273(1993).
DR EMBL; S69273; G546258; -.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ SEQUENCE 119 AA; 13131 MW; 2EEF28F4 CRC32;

Query Match
Best Local Similarity 72.6%; Score 451; DB 12; Length 119;
Matches 59; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

Db 34 GCECKLKENNIFSPGAPVYOCGCCFSRAYPTPLRSKKTMLVPKNTSRTATCCVAKEV 93
QY 170 GCECKLKENNIFSPGAPVYOCGCCFSRAYPTPLRSKKTMLVOKNVTSESTCCVAKSY 229
DB 94 ERV-VVONIKRLNTECMCNCTYHKS 119
QY 230 NRYVTVMGFKVENHTGCHCSTCYTHKS 256

RESULT 6
ID 091371 PRELIMINARY; PRT; 114 AA.

AC 091371;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GONADOTROPIN ALPHA 2 SUBUNIT.
OS ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).
OC EURKAROTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEIFHTHYES; ACTINOPTERYGII; SALMONIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE: 94197892.
RA GEN K., MARYAMA O., KATO T., TOMIZAWA K., MAKABAYASHI K., KATO Y.;
RL J. MOL. ENDOCRINOL. 11:265-273(1993).
DR EMBL: S69274; G546260; -.
DR PROSITE: PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE: PS00780; GLYCO_HORMONE_ALPHA_2; 1.
SQ SEQUENCE 114 AA; 12519 MW; 47303C83 CRC32;

Query Match 22.4%; Score 446; DB 12; Length 114;
Best Local Similarity 71.3%; Pred. No. 6,956-83;
Matches 62; Conservative 6; Mismatches 15; Indels 4; Gaps 2;

Db 32 GCECTLKPNIF--PN--IIQTCGCFRATPTLRKSTMLVKNITSEATCCVAKG 87
OY 170 GCEPCTIQENFEFSQAPILQCMGCCSRATPTLRKSTMLVKNITSEATCCVAKSY 229
DB 88 ERVTTKDGPVNTHTCHSTCYVHKS 114
OY 230 NRYTVMGKFKVENHTGCHSTCYVHKS 256

RESULT 7
ID Q91119 PRELIMINARY; PRT; 117 AA.

AC Q91119;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (CONADOTROPIN ALPHA
DE CHAIN) (GTH-ALPHA).
OS MORONE SAKATILIS (STRIPED BASS).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OC OSTEOCHITES; ACTINOPTERYGII; PERCIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PITUITARY GLAND;
RX MEDLINE: 96020549.
RA HASSIN S., ELIZUR A., ZOHAR Y.;
RL J. MOL. ENDOCRINOL. 15:23-35(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-PITUITARY GLAND;
RA HASSIN S.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDGENESIS (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
DR EMBL: L35071; G2322657; -.
DR PROSITE: PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE: PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 117 GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT DISULFID 34 57 BY SIMILARITY.
FT DISULFID 37 86 BY SIMILARITY.
FT DISULFID 54 107 BY SIMILARITY.
FT DISULFID 58 109 BY SIMILARITY.
FT DISULFID 85 112 BY SIMILARITY.
FT CARBOHYD 78 78 POTENTIAL.
FT CARBOHYD 103 103 POTENTIAL.
SQ SEQUENCE 117 AA; 13066 MW; CAFB9DOC CRC32;

Query Match 21.7%; Score 433; DB 12; Length 117;
Best Local Similarity 65.5%; Pred. No. 1,346-79;
Matches 57; Conservative 14; Mismatches 12; Indels 4; Gaps 4;

Db 33 GCECTLKRNVEFR-DBPYVOCGCCSRATPTLRKSTMLVKNITSEATCCVAKHS 91
OY 170 GCEPCTIQENFEFSQAPILQCMGCCSRATPTLRKSTMLVKNITSEATCCVAKS-S 228
DB 92 YE-TEV-AGIKVNRHTDCHSTCYVH 116
OY 229 YNRVTVMGKFKVENHTGCHSTCYVH 255

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RESULT 8
ID Q62589 PRELIMINARY; PRT; 55 AA.

AC Q62589;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ALPHA SUBUNIT OF GLYCOPROTEIN HORMONES (FRAGMENT).
DE PHODOPUS SUNGORUS (STRIPED HAIRY-FOOTED HAMSTER) (DUONGARIAN HAMSTER).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PITUITARY;
RX MEDLINE: 96198779.
RA BOCKMANN J., BOCKERS T.M., VENNEMANN B., NIKLOWITZ P., MULLER J.,
RA WITKOWSKI W., SABEL B., KREUTZ M.R.;
RL ENDOCRINOLOGY 137:1804-1813(1996).
DR EMBL: X90776; E195654; -.
FT NON_TER 1 1
SQ SEQUENCE 55 AA; 6047 MW; E5AAE0F8 CRC32;

Query Match 16.7%; Score 333; DB 10; Length 55;
Best Local Similarity 76.4%; Pred. No. 1,066-54;
Matches 42; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 1 PTPARSKTMLVKNITSEATCCVAKFTKATVGNARVNTCHSTCYVHKS 55
OY 202 PTPARSKTMLVKNITSEATCCVAKFTKATVGNARVNTCHSTCYVHKS 256

RESULT 9
ID Q00276 PRELIMINARY; PRT; 253 AA.

AC Q00276;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA SCHEATON G., XU X.N., OLSEN A., COMPER A., TAN R., MICHAEL A.,
RA BELL J.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U94503; G2071953; -.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
SQ SEQUENCE 253 AA; 26934 MW; A21C863E CRC32;

Query Match 13.7%; Score 273; DB 2; Length 253;
Best Local Similarity 32.4%; Pred. No. 3,296-40;
Matches 60; Conservative 34; Mismatches 74; Indels 17; Gaps 13;

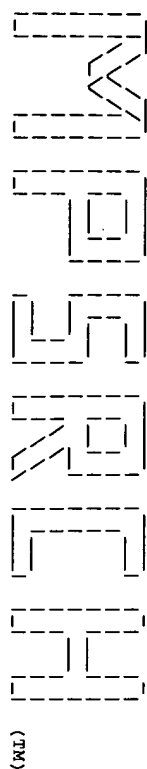
Db 13 AALLLV--LIG-AARAQGTSPRCADGF-HKRIIGFCRCGCPAGHYLAKPCTEPCGNS 68
OY 3 TSLILAGLGLPMLQESADSVC-P-QGKYTHPQNNISICCKHKGTYLVNDGPGDGT 61
DB 69 TGLVCPDPTFLAMENHNHNSCARCOACDEQASVALENCASVADTRCGCKRGMFEVCOVS 128
OY 62 DCRCESSGFSFASNNHR-HCLSCSKCKEKMGVEISCTYDRDTVCGCKRNOYRHYW-S 119
DB 129 QCVSSPFYQCPCLDCGALHHTRLIC-SRBDTCGCTLPFEYHGGGCVSCPTSLGSC 187
OY 120 ENLFQC-FNCSCLN-GIVH---LSCQEKONTVC-TCHAGFLRENDCVSAGAAPE-C 171
DB 188 PERCA 192
OY 172 PE-CT 175

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Db	40	HNLCCLSPGPTGYASTALCQSKT~NQCPCGGFTFSNNHLPAQLSCNQ~RQNSQVET	97
		:::	
		:::	
Qy	37	NSICQTKKHGFTLYLNDCCPGQPDIDCCNECSGSFTASENHLRCLSCSCKREMQVET	96
Db	98	RSCNTTHNRICDESPGY	115
Qy	97	SSCTVDADTVCGCRKMQY	114

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Run on: Wed May 6 12:57:57 1998; Maspar time 1227.99 Seconds  
Tabular output not generated. 1496.959 Million cell updates/sec

Title: >US-08-804-166-3  
Description: (1-1202) from US08804166.seq  
Perfect Score: 1202  
N.A. Sequence: 1 CTCGAGATGGCTACAGGTA.....CCCGCATCTCCACAAATA 1202  
Comp: GAGCTCTACCGATGTCCANT.....GGGCGTAGAGGGGTGTATT

Scoring table:  
TABLE default  
Gap 6

Nmatch STD : DBase 0; Query 0

Searched: 436399 seqs, 764661465 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

emb153  
1:em\_hn 2:em\_or 3:em\_om 4:em\_ov 5:em\_pl 6:em\_htg  
7:em\_hum1 8:em\_hum2 9:em\_ha 10:em\_ro 11:em\_un 12:em\_v1  
13:em\_pat  
genbank105

14:gb\_ro 15:gb\_om 16:gb\_ov 17:gb\_hn 18:gb\_pl 19:gb\_ha  
20:gb\_st 21:gb\_v1 22:gb\_ph 23:gb\_sy 24:gb\_un 25:gb\_pat  
26:gb\_htg 27:gb\_pr1 28:gb\_pr2

Statistics: Mean 11.143; Variance 5.206; scale 2.140

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	424	35.3	483	25	A29099		Synthetic DNA for TNF-	0.00e+00
2	424	35.3	510	25	A21525		oligonucleotide probe.	0.00e+00
3	424	35.3	600	25	A20257		Synthetic nucleotide s	0.00e+00
4	424	35.3	1331	25	A29103		H.sapiens mRNA for TNF-	0.00e+00
5	424	35.3	1368	25	A29098		Synthetic DNA for TNF-	0.00e+00
6	424	35.3	2050	27	HUMTNFRP		Human tumor necrosis f	0.00e+00
7	424	35.3	2062	25	I43805		Sequence 24 from paten	0.00e+00
8	424	35.3	2087	25	A21522		TNF alpha gene.	0.00e+00
9	424	35.3	2087	27	HUMTNFR		Human tumor necrosis f	0.00e+00
10	424	35.3	2111	27	HUMTNFRB		Homo sapiens tumor nec	0.00e+00
11	424	35.3	2111	25	A26412		CDNA for (55kd TNF-BP)	0.00e+00
12	424	35.3	2112	27	HUMTNFR		Human tumor necrosis f	0.00e+00
13	424	35.3	2161	27	HSTNFR1A		H.sapiens TNF-R mRNA f	0.00e+00
14	424	35.3	2175	25	A43873		Sequence 1 from Patent	0.00e+00

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16	424	35.3	2176	25	A19907		Synthetic nucleotide s	0.00e+00
17	424	35.3	6889	25	I26928		Sequence 2 from patent	0.00e+00
18	420	34.9	600	25	I43808		Sequence 47 from patent	0.00e+00
19	417	34.7	2061	25	A20255		55kD receptor gene for	0.00e+00
20	414	34.4	539	27	HUMGB		Human chorionic gonado	0.00e+00
21	381	31.7	504	25	I43813		Sequence 56 from patent	0.00e+00
22	381	31.7	504	25	A20713		Synthetic nucleotide s	0.00e+00
23	379	31.5	501	25	I43786		Sequence 1 from patent	0.00e+00
24	372	30.9	500	25	A20254		Synthetic nucleotide 5	1.79e-236
25	370	30.8	372	25	A20253		Synthetic nucleotide 5	1.14e-234
26	370	30.8	372	25	I43787		Sequence 3 from patent	1.14e-234
27	330	27.5	642	27	BABBCGA		Baboon beta-chorionic	1.27e-238
28	330	27.5	642	27	HUMGHCSA		Human growth hormone (	1.27e-238
29	308	25.6	1665	27	HSG602		Human chorionic gonado	7.42e-237
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31	306	25.5	475	27	HUMGBBL03		Human chorionic gonado	4.63e-237
32	306	25.5	1665	27	HSG601		Human chorionic gonado	4.63e-237
33	303	25.2	1826	25	I02855		Sequence 1 from Patent	2.27e-234
34	302	25.1	581	15	FCU72344		Felis catus tumour nec	1.79e-233
35	302	25.1	1964	27	HUMGH		Human growth hormone (	1.79e-233
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37	302	25.1	2771	25	I41411		Sequence 5 from patent	1.11e-231
38	300	25.0	474	25	I43809		Sequence 49 from patent	1.11e-231
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40	301	25.0	2657	27	HUMGHN		Human growth hormone g	1.41e-232
41	301	25.0	4283	25	I63120		Sequence 3 from patent	1.41e-232
42	293	24.4	2004	15	SSU19994		Sus scrofa p55 TNF rec	2.08e-215
43	283	23.5	426	25	I08477		Sequence 18 from Patent	1.86e-216
44	255	21.2	477	25	A20263		Synthetic nucleotide s	1.84e-191
45	255	21.2	477	25	I43811		Sequence 53 from patent	1.84e-191

## ALIGNMENTS

RESULT	1	LOCUS	A29099	483 bp	DNA	PAT	03-JUL-1995
DEFINITION			Synthetic DNA for TNF-binding polypeptide from patent EP0393438.				
ACCESSION			A29099				
NID			91248893				
KEYWORDS			unidentified.				
SOURCE			unidentified.				
ORGANISM			unclassified.				
REFERENCE			1 (bases 1 to 483)				
AUTHORS			Hauptmann, R., Himmeler, A., Maurer-Fogy, I. and Stratowa, C.				
TITLE			TNF-receptor, TNF-binding protein and DNA coding therefor				
JOURNAL			Patent: EP 0393438-A 49 24-OCT-1990;				
			BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H				
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BASE COUNT			130 a 124 c 123 g 106 t				
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Query Match			35.3%; Score 424; DB 25; Length 483;				
Best Local Similarity			99.8%; Pred. No. 0.00e+00;				
Matches			425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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OY	345	GATAGGTGTGTCCTCCCAAGAAATATATCCACCCCAAAATGATGATTCCTTAC	404				
Db	61	AAGTGCACAAAGAACCTACTGTGACATGACTGTCCAGCCCGGCGCAGATACGAC	120				
OY	405	AAGTGCACAAAGAACCTACTGTGACATGACTGTCCAGCCCGGCGCAGATACGAC	464				
Db	121	TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACCACTCAGACACTGCTC	180				

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QY 525 AGCTGCTCCAATGCGAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 584  
Db 241 CGGACACCGGTGTGGCTGCAAGAAACAGTACCGGCAATTATGGAGTGAACCTT 300  
QY 585 CGGACACCGGTGTGGCTGCAAGAAACAGTACCGGCAATTATGGAGTGAACCTT 644  
Db 301 TTCAGTCTTCAATTGACGCTCGCTCAATGGACCGTGCACCTCTCTGCGACAGAG 360  
QY 645 TTCAGTCTTCAATTGACGCTCGCTCAATGGACCGTGCACCTCTCTGCGACAGAG 704  
Db 361 AAACAGAACACCGTGTGCACTGCATGCAGTTCTTCTAAGAGAAACGAGTGTGC 420  
QY 705 AAACAGAACACCGTGTGCACTGCATGCAGTTCTTCTAAGAGAAACGAGTGTGC 764  
Db 421 TCGTGT 426  
QY 765 TCGTGT 770

RESULT 2  
LOCUS A21525 510 bp DNA PAT 26-JUL-1994  
DEFINITION oligonucleotide probe.  
ACCESSION A21525  
NID 9583574  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 510)  
AUTHORS  
JOURNAL  
FEATURES  
Source  
BASE COUNT 136 a 132 c 133 g 109 t  
ORIGIN

Query Match 35.3%; Score 424; DB 25; Length 510;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 34 GATAGTGTGTGTCGCCAAGAAATATATCCACCTCAAAATTAATGATTTGCTGTACC 93  
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QY 405 AAGTGCCACAAGAACCTTGTACATGACTGTCCAGGCGCGGGCAGGATACGGAC 464  
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QY 465 TGCAGGAGTGTGAGAGGGCTCTTACCGCTTCAGAAAACCACTGACACTGCTC 524  
Db 214 AGCTGCTCCAATGCGAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 273  
QY 525 AGCTGCTCCAATGCGAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 584  
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QY 705 AAACAGAACACCGTGTGCACTGCATGCAGTTCTTCTAAGAGAAACGAGTGTGC 764  
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QY 765 TCGTGT 770

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LOCUS A20257 600 bp DNA PAT 20-SEP-1995  
DEFINITION Synthetic nucleotide sequence of plasmid p-TNFrecd.  
ACCESSION A20257  
NID 91247896  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 600)  
AUTHORS  
TITLE MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR  
JOURNAL Patent: WO 9207076-A 25 30-APR-1992;  
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Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCGCCAAGAAATATATCCACCTCAAAATTAATGATTTGCTGTACC 180  
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Db 181 AAGTGCCACAAGAACCTTGTACATGACTGTCCAGGCGCGGGCAGGATACGGAC 240  
QY 405 AAGTGCCACAAGAACCTTGTACATGACTGTCCAGGCGCGGGCAGGATACGGAC 464  
Db 241 TGCAGGAGTGTGAGAGGGCTCTTACCGCTTCAGAAAACCACTGACACTGCTC 300  
QY 465 TGCAGGAGTGTGAGAGGGCTCTTACCGCTTCAGAAAACCACTGACACTGCTC 524  
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QY 525 AGCTGCTCCAATGCGAAGAAATGGGTGAGTGAATCTCTTTCGACAGTGGAC 584  
Db 361 CGGACACCGGTGTGGCTGCAAGAAACAGTACCGGCAATTATGGAGTGAACCTT 420  
QY 585 CGGACACCGGTGTGGCTGCAAGAAACAGTACCGGCAATTATGGAGTGAACCTT 644  
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QY 645 TTCAGTCTTCAATTGACGCTCGCTCAATGGACCGTGCACCTCTCTGCGACAGAG 704  
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QY 705 AAACAGAACACCGTGTGCACTGCATGCAGTTCTTCTAAGAGAAACGAGTGTGC 764  
Db 541 TCGTGT 546  
QY 765 TCGTGT 770

RESULT 4  
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DEFINITION H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.  
ACCESSION A29103

NID	KEYWORDS	g1247517
SOURCE	human.	
ORGANISM	human.	
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Carnivora; Homnidae; Homo. 1 (bases 1 to 1331)	
AUTHORS	Hauptmann, R., Himmeler, A., Maurer-Fogy, I. and Stratowa, C.	
JOURNAL	TNF-receptor, TNF-binding protein and DNA coding therefor	
FEATURES	Patent: EP 0393438-A 53 24-OCT-1990; BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H	
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Best Local Similarity	99.8%; Pred. No. 0.00e+00;	
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Oy	345 GATAGTGTGTCCCAAGAAATATATCCACCCTCAAAATATTCGATTGCTGACC	4004
Db	393 AAGTCCCAAGAAAGAACCTACTTGTACATGATGTCAGGCCCGGGGCAAGATACGAC	4523
Oy	405 AAGTCCCAAGAAAGAACCTACTTGTACATGATGTCAGGCCCGGGGCAAGATACGAC	4644
Db	453 TGCAGGGATGTGAGAGGGGCTCCTTACCCCTTCAGAAACACCTCAGACACTGCTC	5124
Oy	465 TGCAGGGATGTGAGAGGGGCTCCTTACCCCTTCAGAAACACCTCAGACACTGCTC	5244
Db	513 AGCTGCTCCAATGCGCAAGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGACAGTGGAC	5724
Oy	525 AGCTGCTCCAATGCGCAAGAAAGAAATGGGTGAGGTGAGATCTCTTCTTGACAGTGGAC	5844
Db	573 CGGACACACGCTGTGTGCTGACAGGAAGAACCGACATTAATTGGAGTGAACCTT	6323
Oy	585 CGGACACACGCTGTGTGCTGACAGGAAGAACCGACATTAATTGGAGTGAACCTT	6444
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Oy	645 TTCCAGTCTTCAATGTCAGCCTCTGCTCTCAATGGAGACCTGTCTCTCTGCCAGAG	7044
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Oy	705 AAACGACACACGCTGTGACCTGACCTGACATGAGTTCTTTCAAGAGAAACGAGTGTGTC	7644
Db	753 TCCCTGT 758	
Oy	765 TCCCTGT 770	
RESULT	5	
LOCUS	A29098 1368 bp DNA PAT 03-JUL-1995	
DEFINITION	Synthetic DNA for TNF-receptor from patent EP0393438.	
ACCESSION	A29098	
NID	g1248892	
KEYWORDS	unidentified.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 1368)	
AUTHORS	Hauptmann, R., Himmeler, A., Maurer-Fogy, I. and Stratowa, C.	
TITLE	TNF-receptor, TNF-binding protein and DNA coding therefor	
JOURNAL	Patent: EP 0393438-A 48 24-OCT-1990;	
FEATURES	BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H	
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Qy	405 AAGTCCCAAAAGAACCTTACTTGTACATGATGTCCAGGCCCGGGCAGATACGGAC	464
Db	241 TCGAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAAACACCTCAGACACTGCTC	300
Qy	465 TCGAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAAACACCTCAGACACTGCTC	524
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Qy	585 CGGACACCGTGTGTGGCTGCAGAGAACACAGTACCGGCAATATTCGATGAACCTT	644
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Qy	645 TTCAGTCTTCAATTGACAGCTTGCCTCAATGGACCGTGCACCTCTCTGCGAGAG	704
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Qy	705 AAACGAACACCGTGTGCACCTGCATGACAGTCTTCTTAAGAGAAACGAGTGTGC	764
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DEFINITION	Human tumor necrosis factor receptor (TNF) mRNA, complete cds.	
ACCESSION	M60275 M57764	
NID	9339759	
KEYWORDS	TNF receptor; transmembrane receptor; tumor necrosis factor receptor.	
SOURCE	Human placenta, cDNA to mRNA.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2050)	
AUTHORS	Gray,P.W., Barrett,K.J., Chantry,D., Turner,M. and Feldman,M.	
TITLE	Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)	
MEDLINE	91017509	
COMMENT	Draft entry and computer-readable sequence for (Proc. Natl. Acad. Sci. U.S.A. (1990) in press, 13-Aug-1990. by P.W.Gray, 13-Aug-1990.	
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BASE COUNT 429 a 617 c 573 g 443 t  
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Query Match 35.3%; Score 424; DB 25; Length 2062;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 275 GATGAGTGTGTGCCCCAAGAAATATATCCACCCCAAAATATGATTTGCTTACC 334  
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Db 335 AAGTGCACAAAGAAAGAACTTGTACATGACTGTCCAGGCCGGGCGAGATACGAG 394  
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Qy 585 CGGACACCGCTGTGTGCTGTCAGAGAAACAGTACCGGATTTAGAGTGAACCTT 644  
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Db 575 TTCAGTGTTCATATGACAGCTTGTCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 634  
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Qy 645 TTCAGTGTTCATATGACAGCTTGTCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 704  
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Db 635 AAACAGAACACCGGTGTGACCTGTCATGCAAGTTCTTCTTAAGAAAAAGAGTGTTC 694  
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Db 695 TCCTGT 700  
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Qy 765 TCCTGT 770

RESULT 9 HUMNFR 2087 bp mRNA PRI 10-NOV-1993  
LOCUS  
DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION M33294  
NID 9339744  
KEYWORDS cell surface receptor; tumor necrosis factor receptor.  
SOURCE Human placenta, cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 2087)  
Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Wong, G.H.,  
Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Kohr, W.J. and  
Goeddel, D.V.  
Molecular cloning and expression of a receptor for human tumor  
necrosis factor  
Cell 61, 361-370 (1990)  
JOURNAL MEDLINE 90235285  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
by T.Schall, 26-MAR-1990.  
FEATURES  
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182..1549  
/note="tumor necrosis factor receptor"

CDS  
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KONTVCTCHAGFLRENEVCASNKSECTKILCLPOLIENVKGTEDSGTLLPLV  
FFGLISLFIPLGMYRYORBMKSKLYSIYVCKSTPEKGELETTKRLANPSPT  
PGFTPTGSPVSPSTSSSTYPCDPAARBPAPYOCADPLIARALASDPI  
PNPLQKEDSHKPOSIDTDPAFLIAYEVNPPPLRKPEYFRRLGSLSHEDRLQ  
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BASE COUNT 433 a 624 c 581 g 449 t  
ORIGIN

Query Match 35.3%; Score 424; DB 27; Length 2087;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 302 GATGAGTGTGTGCCCCAAGAAATATATCCACCCCAAAATATGATTTGCTTACC 361  
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Qy 345 GATGAGTGTGTGCCCCAAGAAATATATCCACCCCAAAATATGATTTGCTTACC 404  
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Db 362 AAGTGCACAAAGAAAGAACTTGTACATGACTGTCCAGGCCGGGCGAGATACGAG 421  
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Qy 405 AAGTGCACAAAGAAAGAACTTGTACATGACTGTCCAGGCCGGGCGAGATACGAG 464  
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Db 422 TCCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 481  
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Qy 465 TCCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 524  
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Db 482 AGCTGTCCAAATGCCGAAAGAAATGGGTCAAGTGAATCTCTTGTGCACAGTGGAC 541  
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Qy 525 AGCTGTCCAAATGCCGAAAGAAATGGGTCAAGTGAATCTCTTGTGCACAGTGGAC 584  
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Db 542 CGGACACCGCTGTGTGCTGTCAGAGAAACAGTACCGGATTTAGAGTGAACCTT 601  
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Qy 705 AAACAGAACACCGGTGTGACCTGTCATGCAAGTTCTTCTTAAGAAAAAGAGTGTTC 764  
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Db 722 TCCTGT 727  
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Qy 765 TCCTGT 770

RESULT 10 HUMNFRB 2111 bp mRNA PRI 14-NOV-1990  
LOCUS  
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION M58286  
NID 9339753  
KEYWORDS tumor necrosis factor receptor.  
SOURCE Human cell line HL60, cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 2111)  
Loetscher, H., Par, Y.-C.E., Lahm, H.-W., Gentz, R., Brockhaus, M.,  
Tabuchi, H. and Lesslauer, W.  
Molecular cloning and expression of the human 55 kd tumor necrosis  
factor receptor  
Cell 61, 351-359 (1990)  
JOURNAL MEDLINE 90235284  
COMMENT

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187..1554

/gene="TNF receptor"  
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SKCRKMGVOYISSCTVDRTDVGCRKNQRYHWSBNLFCQFNCISLNGTVHLSCE  
KONTVCTCHAGFLRENECVSCNCKSLCTKLCLOIENYKGTEDSGTTLPLVI  
FEGICLSLFLFGLMYRQRMKSLYSIVCGKSTPERKEBEGTTKPLAPNPSFPT  
PGFTPLGSPVPSSTFTSSSTYTPGDCNFAAPREVAAPYOGADPIIATLASDPI  
PNPLOWEDSAHKPOSIDTDPAITLYAVENVPPLRKEVEYRLGLSDHEIDLELON  
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187 . 1554  
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/gene="TNF receptor"  
/product="tumor necrosis factor receptor"  
BASE COUNT 445 a 629 c 587 g 450 t  
ORIGIN

Query Match 35.3%; Score 424; DB 27; Length 2111;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 307 GATAGTGTGTGTCGCCAAGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 366  
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OY 345 GATAGTGTGTGTCGCCAAGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 404  
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Db 367 AAGTGCCCAAGAACCTACTGTACATGACTGTCCAGGCCCGGGGAGAGATACGGAC 426  
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OY 405 AAGTGCCCAAGAACCTACTGTACATGACTGTCCAGGCCCGGGGAGAGATACGGAC 464  
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Db 427 TGCAGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTACAGACTGCCTC 486  
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OY 465 TGCAGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTACAGACTGCCTC 524  
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Db 487 AGCTGCTCCAAATGCCGAAGAAATGGTCAAGTGGAGATCTCTTCTTGACAGTGGAC 546  
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Db 547 CGGACACCGTGTGTGCTGCAGAGAACAGTACCGGATTAATGGAGTGAACCTT 606  
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Db 667 AAACAGAACACCGTGTGACCTGCATGCAAGTTCTTTCTAAGAGAAAACGAGTGTGC 726  
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OY 705 AAACAGAACACCGTGTGACCTGCATGCAAGTTCTTTCTAAGAGAAAACGAGTGTGC 764  
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Db 727 TCCTGT 732  
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OY 765 TCCTGT 770

RESULT 11  
LOCUS A26412 2111 bp DNA PAT 26-APR-1995  
DEFINITION cDNA for (55KD TNF-BP) tumor necrosis factor binding protein from  
ACCESSION A26412  
NID 9904968  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2111)  
AUTHORS Brockhaus, M., Dembic, Z., Gentz, R., Lesslauer, W., Loetscher, H. and  
Schlaefer, E. J.

TITLE TNF-binding proteins  
JOURNAL Patent: EP 0417563-A 24 20-MAR-1991;  
F. HOFFMANN-IA ROCHE AG  
FEATURES  
source location/Qualifiers  
CDS  
1. 2111  
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SKCRKMGVOYISSCTVDRTDVGCRKNQRYHWSBNLFCQFNCISLNGTVHLSCE  
KONTVCTCHAGFLRENECVSCNCKSLCTKLCLOIENYKGTEDSGTTLPLVI  
FEGICLSLFLFGLMYRQRMKSLYSIVCGKSTPERKEBEGTTKPLAPNPSFPT  
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PNPLOWEDSAHKPOSIDTDPAITLYAVENVPPLRKEVEYRLGLSDHEIDLELON  
GRLREAOYSMLATWRRRTPREATLELLGRVLRDMDLGLCLEDIEALCGPALPPA  
PSLLR"  
BASE COUNT 445 a 629 c 587 g 450 t  
ORIGIN

Query Match 35.3%; Score 424; DB 25; Length 2111;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 307 GATAGTGTGTGTCGCCAAGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 366  
|||||  
OY 345 GATAGTGTGTGTCGCCAAGAAATATATCCACCCTCAAAATTAATTCGATTGCTGTACC 404  
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Db 367 AAGTGCCCAAGAACCTACTGTACATGACTGTCCAGGCCCGGGGAGAGATACGGAC 426  
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OY 405 AAGTGCCCAAGAACCTACTGTACATGACTGTCCAGGCCCGGGGAGAGATACGGAC 464  
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Db 427 TGCAGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTACAGACTGCCTC 486  
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Db 607 TTCAGAGCTTCATTTGACAGCTCTGCCTCAATGGAGACCGTGCACCTCTCTGCCAGAG 666  
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OY 645 TTCAGAGCTTCATTTGACAGCTCTGCCTCAATGGAGACCGTGCACCTCTCTGCCAGAG 704  
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Db 667 AAACAGAACACCGTGTGACCTGCATGCAAGTTCTTTCTAAGAGAAAACGAGTGTGC 726  
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OY 705 AAACAGAACACCGTGTGACCTGCATGCAAGTTCTTTCTAAGAGAAAACGAGTGTGC 764  
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Db 727 TCCTGT 732  
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OY 765 TCCTGT 770

RESULT 12  
LOCUS HUMTNFR 2112 bp mRNA PRI 30-SEP-1991  
DEFINITION Human tumor necrosis factor receptor (TNF receptor) mRNA, complete  
ACCESSION M63121 M75861  
NID 9339755  
KEYWORDS tumor necrosis factor receptor.  
SOURCE Human cDNA to mRNA.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2112)  
Eukaryotes: mitochondrial eukaryotes; Metazoa: Chordata;  
Vertebrata: Eutheria; Primates; Catarrhini; Hominoidea; Homo.

**AUTHORS** Himmler, A., Maurer-Fogy, I., Krenke, M., Scheurich, P.,  
Pfleiderer, K., Lantz, M., Olsson, I., Hauptmann, R., Stratowa, C. and  
Adolf, G. R.

**TITLE** Molecular cloning and expression of human and rat tumor necrosis  
factor receptor chain (p60) and its soluble derivative, tumor  
necrosis factor-binding protein

**JOURNAL** DNA Cell Biol. 9, 705-715 (1990)

**MEDLINE** 91090841

**FEATURES**

**SOURCE** Location/Qualifiers

**sig\_peptide** 1..2112  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

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KONTVCTCHAGFLFLENVCSNCKKSLKLECKLCLPOLIENKGTEDSGTVLLPLVI  
FEGICLSLFLGLMYRYQRMKSKLSIVCGSKTEKGELEGTTRKPLAPSPSP  
PGFPTLGFSPVPSSTFTSSSTYTPGDCPNFAPRREVAAPYOGADPIATLASDPI  
PNPLQKWDSSAKRPOSIDTDPAITLYAVENVPPIRMKEFVRRLSLSHEDIRLELON  
GRCLREAOYSMLATWRRTPRRATLELLGRVLRMDLLGLCLEDIEALCGPALPPA  
PSLR"

**gene** 207..1574  
/gene="TNF receptor"  
mat\_peptide 294..1571  
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/product="tumor necrosis factor receptor"

**BASE COUNT** 435 a 632 c 589 g 456 t

**Query Match** 35.3%; Score 424; DB 27; Length 2112;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 327 GATAGTGTGTGTCGCCAAGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 386  
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Qy 345 GATAGTGTGTGTCGCCAAGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 404  
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Db 387 AAGTGCACAAAGAAACCTACTTGTACATGATGTCCAGGCCCGGCGCAGATACGGAC 446  
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Db 447 TCGAGGAGTGTGAGAGCGGCTCTCACCGCTTCAGAAACCACTCAGACCTGCTC 506  
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Qy 705 AAACAGAACCCGTGTGACCTGACATGACAGGTTCTTTCTTAAGAGAAAAAGAGTGTG 764  
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Db 747 TCTGT 752  
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Qy 765 TCTGT 770

**RESULT** 13  
**LOCUS** HSTNFR1A 2161 bp RNA PRI 18-JAN-1993

**DEFINITION** H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.  
**ACCESSION** X5513  
**VERSION** 937223  
**KEYWORDS** TNF-R gene; tumor necrosis factor receptor 1.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
Eukaryota; Eukaryota; Eukaryota; Eukaryota; Eukaryota; Eukaryota;  
Vertebrata; Vertebrata; Vertebrata; Vertebrata; Vertebrata; Vertebrata;  
Nophar.Y., Kemper.O., Brakebusch.C., Englemann.H., Zwang.R.,  
Aderka.D., Holtmann.H. and Wallach.D.

**TITLE** Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA  
for the type I TNF-R, cloned using amino acid sequence data of its  
soluble form, encodes both the cell surface and a soluble form of  
the receptor

**JOURNAL** EMBO J. 9 (10), 3269-3278 (1990)

**MEDLINE** 91006021

**FEATURES**

**source** Location/Qualifiers

**gene** 1..2161  
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256..1623  
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/product="tumor necrosis factor receptor type 1"  
/db\_xref="PID:937224"  
/db\_xref="SWISS-PROT:P19438"

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repeat\_region 634..756  
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**polyA\_site** 2161  
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**BASE COUNT** 459 a 642 c 604 g 456 t

**Query Match** 35.3%; Score 424; DB 27; Length 2161;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 376 GATAGTGTGTGTCGCCAAGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 435  
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Qy 345 GATAGTGTGTGTCGCCAAGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 404  
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Db 496 TCGAGGAGTGTGAGAGCGGCTCTCACCGCTTCAGAAACCACTCAGACACTGCTC 555  
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DB	AGTCTCCAAATGGCGAAGAAATGGGTGACGTGGAGATCTCTTTGCACTGAC	615
Db	556 AGTCTCCAAATGGCGAAGAAATGGGTGACGTGGAGATCTCTTTGCACTGAC	615
Qy	525 AGCTCTCCAAATGGCGAAGAAATGGGTGACGTGGAGATCTCTTTGCACTGAC	584
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Qy	585 CGGACACCGTGTGTGGGTGACAGAGAACAACGATACCGCATTTATGGAGTAAACCTT	644
Db	676 TTCAGTGTCTCAATTGACAGCCTGTGCTCAATTGAGGACCGTCTCTGACAGAG	735
Qy	645 TTCAGTGTCTCAATTGACAGCCTGTGCTCAATTGAGGACCGTCTCTGACAGAG	704
Db	736 AAACAGAACACCGTGTGACAGCCTGCATGAGGTCTTCTTAAGAGAAACGAGTGTG	795
Qy	705 AAACAGAACACCGTGTGACAGCCTGCATGAGGTCTTCTTAAGAGAAACGAGTGTG	764
Db	796 TCCTGT 801	
Qy	765 TCCTGT 770	
RESULT	14	
LOCUS	A43873 2175 bp DNA PAT 06-MAR-1997	
DEFINITION	Sequence 1 from Patent EP0657536.	
ACCESSION	A43873	
NID	92299022	
KEYWORDS	unidentified.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 2175)	
AUTHORS	Wallach,D., Brachebusch,C., Varfolomeev,E. and Balchin,M.	
TITLE	Proteases capable of shedding the soluble TNF-receptor and TNF-R derived peptides and antibodies against the proteases inhibiting the shedding	
JOURNAL	Patent: EP 0657536-A 1 14-JUN-1995;	
COMMENT	YEDA RES & DEV (IL)	
	Other publication ZA 9407962 951121	
	Other publication JP 7194376 950801	
	Other publication AU 7574294 950504	
	Other publication CA 2133872 950413.	
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BASE COUNT	474 a 641 c 604 g 456 t	
ORIGIN		
Query Match	35.3%; Score 424; DB 25; Length 2175;	
Best Local Similarity	99.8%; Pred. No. 0.00e+00;	
Matches	425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Db	376 GATAGTGTGTGCCCAAGAAATATATCCACCCCTCAAAATATTCGATTGCTGAC	435
Qy	345 GATAGTGTGTGCCCAAGAAATATATCCACCCCTCAAAATATTCGATTGCTGAC	404
Db	436 AAGTCCACAAAGAACTACTTGTACAAATGACTGTCCAGGCCGGGGCAGAGATCGAC	495

QY	405	AAAGTCCACAAAGAACTACTTGTACATGACTGTGTCCAGGCGCGGGACAGATACGGAC	464
DB	496	TGCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAAACACCTCAGACACTGTGCTC	555
QY	465	TGCAGGGAGTGTGAGAGGGGCTCTTTCACCGCTTCAGAAAAACACCTCAGACACTGTGCTC	524
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QY	525	AGCTGCTCCAAATGCGGAAGAAATGGGTGAGGTGAGATCTCTTGTGCACAGTGGAC	584
DB	616	CGGACACCGGTGTGGGTGTGCAGGAAGAACAGTACCGGCATTATTGGAGTGAACCTT	675
QY	585	CGGACACCGGTGTGGGTGTGCAGGAAGAACAGTACCGGCATTATTGGAGTGAACCTT	644
DB	676	TTCCAGTCTTCAATTTGACGCTCTGCTCTCAATGGAGACCGTGCACCTCTCCTGCGCAGAG	735
QY	645	TTCCAGTCTTCAATTTGACGCTCTGCTCTCAATGGAGACCGTGCACCTCTCCTGCGCAGAG	704
DB	736	AAACAGAACACCGGTGTGCACCTGCGCATGACAGATTCTTTCTTAAGAGAAAACGAGTGTGTC	795
QY	705	AAACAGAACACCGGTGTGCACCTGCGCATGACAGATTCTTTCTTAAGAGAAAACGAGTGTGTC	764
DB	796	TTCTGT 801	
QY	765	TTCTGT 770	
RESULT	15		
LOCUS	164751	2175 bp	DNA
DEFINITION	Sequence 1 from patent US 5665859.	PAT	26-SEP-1997
ACCESSION	164751		
NID	92481645		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2175)		
TITLE	Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.		
JOURNAL	Molecules influencing the shedding of the TNF receptor, their		
FEATURES	Preparation and their use		
source	Patent: US 5665859-A 1 09-SEP-1997;		
	Location/Qualifiers		
	1..2175		
BASE COUNT	474 a	641 c	604 g
ORIGIN		456 t	
	/organism="Unknown"		
Query Match	35.3%;	Score 424;	DB 25; Length 2175;
Best Local Similarity	99.8%;	Pred. No. 0.00e+00;	
Matches	425;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0

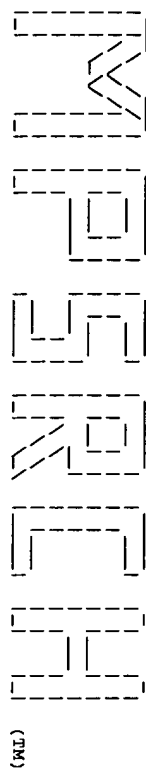
```

OY      645  TTCCAGTGCCTCAATGCGAGCCTCGCTCAATGGAGCGACCTCTCCTGCCAGGAG  704
Db      736  AACGAGAACCCGCTGTGCACCTGCCATGCGAGTTCTTTAAGAGAAACGAGTGTGTC  795
OY      705  AACGAGAACCCGCTGTGCACCTGCCATGCGAGTTCTTTAAGAGAAACGAGTGTGTC  764
Db      796  TCTGT  801
OY      765  TCTGT  770

```

Search completed: Wed May 6 13:18:35 1998  
 Job time : 1238 secs.

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(TM)

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MPsrch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:37:52 1998; Maspar time 155.56 Seconds  
891.677 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-3  
Description: (1-1202) from US08804166.seq  
Perfect Score: 1202  
N.A. Sequence: 1 CTCGAGATGGCTACAGTAA.....CCCCGATCCTCCACATTA 1202  
Comp: GAGCTCTACCGATGTCAT.....GGGGCTAGAGGGGTATT

Scoring table: TABLE default  
Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

## Database:

n-geneseg30  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.195; Variance 5.326; scale 1.727

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	424	35.3	608	4	Q24441	Encodes truncated TNF	1.67e-282
2	424	35.3	1334	1	Q06282	Plasmodium Tumour Necrosis	1.67e-282
3	424	35.3	1368	8	Q49932	Lambda-derived TNF-R	1.67e-282
4	424	35.3	2062	4	Q24440	Encodes TNF-alpha 55k	1.67e-282
5	424	35.3	2062	3	Q20973	TNF-alpha binding protein	1.67e-282
6	424	35.3	2088	2	Q10883	30kD TNF inhibitor protein	1.67e-282
7	424	35.3	2111	2	Q10955	Encodes human 55kD TN	1.67e-282
8	424	35.3	2141	1	Q06285	Human Tumour Necrosis	1.67e-282
9	424	35.3	2175	15	Q90513	P55 TNF-R gene.	1.67e-282
10	424	35.3	6889	18	T15931	DHFR/Inton (WTASD)	1.67e-282
11	422	35.1	2170	9	O50870	P55 Tumour necrosis f	4.91e-281
12	422	35.1	2176	2	Q12215	Type I TNF receptor.	4.91e-281
13	414	34.4	579	3	Q14800	Human chorionic gonad	3.68e-275
14	409	34.0	836	17	T03212	Single chain gonadotr	1.73e-271
15	409	34.0	836	17	T03243	Single chain gonadotr	1.73e-271

16	405	33.7	575	17	T03240	Human CG beta-subunit	1.49e-268
17	381	31.7	504	4	Q24445	Encodes truncated TNF	5.96e-251
18	315	26.2	743	17	T03219	Single chain gonadotr	1.09e-202
19	302	25.1	2771	31	T76770	Rat Fcgp1 gut-specific	3.27e-193
20	300	25.0	474	4	Q24442	Encodes truncated TNF	9.37e-192
21	301	25.0	2160	33	T62826	Human growth hormone	1.75e-192
22	294	24.5	336	6	Q41459	Human growth hormone	2.19e-187
23	283	23.5	426	2	N60524	Sequence encoding hum	2.20e-179
24	276	23.0	743	17	T03231	Single chain gonadotr	2.69e-174
25	276	23.0	743	17	T03233	Single chain gonadotr	2.69e-174
26	276	23.0	752	17	T03229	Single chain gonadotr	2.69e-174
27	274	22.8	744	17	T03221	Single chain gonadotr	2.69e-173
28	261	21.7	752	17	T03237	Single chain gonadotr	2.08e-163
29	255	21.2	477	4	Q24444	Encodes truncated TNF	4.58e-159
30	226	18.8	2173	1	Q06284	Rat Tumour Necrosis F	4.31e-138
31	209	17.4	525	1	Q03844	Bovine beta LH subun	7.56e-126
32	209	17.4	540	1	Q03851	Porcine beta LH subun	7.56e-126
33	206	17.1	2660	4	N30032	Sequence of gene for	1.08e-123
34	184	15.3	496	2	N60523	Sequence encoding dog	6.37e-108
35	179	14.9	611	1	Q03848	Equine beta LH subun	2.38e-104
36	169	14.1	462	4	Q24443	Encodes truncated TNF	3.19e-97
37	130	10.8	1027	2	Q10878	Partial sequence of c	1.15e-69
38	99	8.2	138	13	Q08319	Sequence encoding am	1.53e-49
39	84	7.0	1047	2	Q10572	LH-beta -5 to 41 frag	3.59e-48
40	84	7.0	1047	2	Q10572	Human Natriuretic pep	5.61e-38
41	77	6.4	1047	2	Q10572	Human Natriuretic pep	2.75e-33
42	72	6.0	114	6	Q34659	DNA encoding hCG beta	5.75e-30
43	71	5.9	651	2	N71239	Sequence encoding hum	2.63e-29
44	71	5.9	700	2	N60678	Sequence encoding pre	2.63e-29
45	71	5.9	3557	2	N60801	Human pro-growth horm	2.63e-29

## ALIGNMENTS

RESULT 1  
ID Q24441 standard; DNA; 608 BP.  
AC Q24441;  
DT 05-NOV-1992 (first entry)  
DE Encodes truncated TNF-alpha 55kD receptor (197 amino acids).  
KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
PN W09207076-A.  
PD 30-APR-1992.  
PE 18-OCT-1991: G01826.  
PR 18-OCT-1990: GB-022648.  
PA (CHAR-) CHARING CROSS SUNDLEY RES CENT.  
PI Brennan FM, Feldmann M, Gray PW, Turner MC;  
DR WPI: 92-167156/20.  
DR P-PSDB: R24080.  
PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for  
PT treating autoimmune disease, septic shock, HIV etc.  
PS Example: Fig 7; 43pp; English.  
CC This sequence encodes the designed TNF-alpha 55kD receptor  
CC derivative, as present in pTNFRcd. This was produced as described in  
CC Q24441. This derivative lacks the 81 carboxyl terminal residues of  
CC the cytoplasmic domain. The derivative could be used in the  
CC regulation of TNF-alpha mediated responses by binding and  
CC sequestering human TNF-alpha e.g. in the treatment of pulmonary  
CC diseases, septic shock, HIV infection, malaria, viral meningitis,  
CC graft versus host disease and autoimmune diseases, esp. rheumatoid  
CC arthritis.  
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
SQ Sequence 608 BP; 148 A; 159 C; 165 G; 136 T;  
Query Match 35.3%; Score 424; DB 4; Length 608;  
Best Local Similarity 99.8%; Pred. No. 1.67e-282;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 129 gatagtgctgtccccaagaataatataccaccctcaataatcgattgctgtacc 188

```

QY 345 GATAGTGTGTCCCAAGAAAATATATCCACCCTCAAAATATGATTGCTGTACC 404
DB 189 aagtgccacaaagaaacactactgtacaaatgtacagcccgaggagaaagaaac 248
QY 405 AAGTGCACAAAGAAACCTACTGTACATGACTGTCCAGCCCGGGGACAGATACGGAC 464
DB 249 tgcaggagtgtagagagcggtccctccacagcttcagaaacacactcagacatgcctc 308
QY 465 TGCAGGAGTGTGAGAGCGGCTCTTACCGGCTTCAGAAAACACCTCAGACACTGCCTC 524
DB 309 agctgtccaaatgcccgaagaaatggttcaggtgagatctctcttcgacagtgagac 368
QY 525 AGCTGCTCCAAATGCGAAAGAAATGGGTGAGTGGAGATCTCTTGTGACAGTGGAC 584
DB 369 cggagacacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 428
QY 585 CCGGACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
DB 429 ttccagtgctcaatgtcagcgcctgtcctcaatgtgagacggtgacactcctcagagag 488
QY 645 TTCAGTGTCTCAATGATGACGCTCTGCTCAATGGAGACCGTGACCTCTCTGCGAGAG 704
DB 489 aaacagaaacacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 548
QY 705 AAACAGAACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 764
DB 549 tccctgt 554
QY 765 TCCTGT 770

```

RESULT 2  
ID 006282 standard; DNA; 1334 BP.

```

AC 006282;
DT 29-JAN-1991 (first entry)
DE Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 213..1325
FT /product=TNF-BP
FT EP=393438-A.
FT PN 24-OCT-1990.
FT PE 06-APR-1990; 106624.
FT PR 21-APR-1989; DE-913101.
FT PR 21-JUN-1989; DE-920282.
FT PA (BOHR ) BOEHRINGER INGELHEIMINT.
FT PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;
FT DR P-PSDB; R07449.
FT PT DNA encoding TNF binding protein and TNF-receptor - used in
PS tumour treatment and to understand mechanism to TNF action
PS Disclosure: Fig 1(1-3); 51pp; German.
CC PTNF-BP15 is one of 30 positives clones in a screened cDNA library
CC from induced TNF-induced fibrosarcoma cells. A TNF-BP had been
CC isolated from the urine of patients with uremia and probes/primers
CC were constructed from the determined amino acid sequence.
CC To produce a vector expressing a soluble form of TNF-binding
CC protein, this plasmid was cut with XbaI, amplified by PCR and the
CC amplified DNA cut with BamHI and EcoRI.
CC The resulting 0.75 kb DNA fragment was inserted into pTZ19 alpha-19
CC (BRI) cut with the same enzymes to recover pTNF-BP. This was cut
CC with BamHI and EcoRI, and the recovered fragment inserted into
CC pAD-CMV1 (006883) to give the required plasmid pADTNF-BP.
CC See also 006282-006285.
SQ Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T;

```

Query Match 35.3%; Score 424; DB 1; Length 1334;  
Best Local Similarity 99.8%; Pred. No. 1.67e-282;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

DB 333 gatagtgtgttccccaagaaataatccaccctcaaaataattcgaattgcgtacc 392
QY 345 GATAGTGTGTGTCCCAAGAAAATATATCCACCCTCAAAATATGATTGCTGTACC 404
DB 393 aagtgccacaaagaaacactactgtacaaatgtacagcccgaggagaaagaaac 452
QY 405 AAGTGCACAAAGAAACCTACTGTACATGACTGTCCAGCCCGGGGACAGATACGGAC 464
DB 453 tgcaggagtgtagagagcggtccctccacagcttcagaaacacactcagacatgcctc 512
QY 465 TGCAGGAGTGTGAGAGCGGCTCTTACCGGCTTCAGAAAACACCTCAGACACTGCCTC 524
DB 513 agctgtccaaatgcccgaagaaatggttcaggtgagatctctcttcgacagtgagac 572
QY 525 AGCTGCTCCAAATGCGAAAGAAATGGGTGAGTGGAGATCTCTTGTGACAGTGGAC 584
DB 573 cggagacacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 632
QY 585 CCGGACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
DB 633 ttccagtgctcaatgtcagcgcctgtcctcaatgtgagacggtgacactcctcagagag 692
QY 645 TTCAGTGTCTCAATGATGACGCTCTGCTCAATGGAGACCGTGACCTCTCTGCGAGAG 704
DB 693 aaacagaaacacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 752
QY 705 AAACAGAACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 764
DB 753 tccctgt 758
QY 765 TCCTGT 770

```

RESULT 3  
ID 049932 standard; cDNA to mRNA; 1368 BP.

```

AC 049932;
DT 29-APR-1994 (first entry)
DE Lambda-derived TNF-R cDNA.
KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW IL-1; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW graft versus host disease; sepsis; inflammation; allergy;
KW Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1366
FT FT /product= hTNF-R
FT FT sig_peptide 1..120
FT FT /tag= b
FT FT mat_peptide 121..1363
FT FT /tag= c
FT PN WO9319777-A.
FT PD 14-OCT-1993.
FT PE 26-MAR-1993; U02938.
FT PR 30-MAR-1992; US-860710.
FT PA (IMMV ) IMMUNEX CORP.
FT PI Smith CA;
FT DR P-PSDB; RA2059.
FT PT New fusion protein tumour necrosis factor and human interleukin-1
PT receptor - useful in therapy, diagnosis and assays of e.g.
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS Disclosure: Page 57-59; 85pp; English.
CC The sequences given in 049931-32 encode human tumour necrosis factor
CC receptor (TNF-R) and the sequences in 049933-34 encode human
CC interleukin-1 receptor (IL-1R). These sequences were used in the
CC production of a fusion protein which conformed to one of the
CC formulae:
TNF-R-linker-TNF-R-linker-IL-1R

```



IL-1R-linker-TNF-R-linker-TNF-R or  
 CC TNF-R-linker-TNF-R  
 CC The linker may comprise 5-100 amino acids selected from Gly, Asp,  
 CC Ser, Thr and Ala. These linkers separate the individual moieties  
 CC by such a distance that each component of the fusion protein is  
 CC capable of folding into the secondary or tertiary structure required  
 CC for its biological activity. These fusion proteins may be used in  
 CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
 CC particularly in conditions in which both TNF and IL-1 play a causative  
 CC role. They may be used to treat cachexia, Rheumatoid arthritis,  
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
 CC cerebral malaria, allograft and xenograft rejection in graft verses  
 CC host disease, sepsis, septic shock, inflammation, allergies and  
 CC autoimmune dysfunctions.  
 SO Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T;  
 Query Match 35.3%; Score 424; DB 8; Length 1368;  
 Best Local Similarity 99.8%; Pred. No. 1,67e-282;  
 Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 121 gatagtggtgtcccaagaaatatatccaccccaataatcgttgcgtacc 180  
 Qy 345 GATAGTGTGTGCCCAAGAAATATATCCACCCCAAAATATATGATTGCTGTACC 404  
 Db 181 aagtgccacaaggaacctactgtacatgactgtccagggccgggagataagac 240  
 Qy 405 AAGTGCCACAAAGAACTACTGTATGATGATGTCAGGCCGGGCGAGATACGGAC 464  
 Db 241 tgcaggagtgtagagagcggtccctcaccgcttcagaaacacacctcagacactgc 300  
 Qy 465 TGCAGGAGATGTAGAGGCGGCTCTTTCACCGCTTCAGAAACACCTCAGACACTCC 524  
 Db 301 agctctcccaaatgcggaagaatgggtcaggtgagatcctcttcagacagtggac 360  
 Qy 525 AGCTCTCCAAATGCCGAAGAAGATGGGTGAGTGAATCTCTTTCAGACAGTGAC 584  
 Db 361 cggagacacgtgtgtggtgcgaggaagaaacagtaacgcatattggagtgtaaac 420  
 Qy 585 CGGAGACCGGTGTGTGCGTCGAGGAAGAACAGTACCGGCAATTATGGAGTGAAC 644  
 Db 421 ttcacagtgctcaatgtcagcctctcctcaatgtgacgcgtgcacctccctgcag 480  
 Qy 645 TTCACAGTCTTCATATGACAGCCTCTCCCTCAATGGAGACCGTGCACCTCTCC 704  
 Db 481 aaacagaaacacggtgtgcacctgtcagtgcaaggttcttcttaagagaaagag 540  
 Qy 705 AAACAGAAACACCGTGTGCACCTGCATGCAGGTTCTTCTTAAGAGAAACGAG 764  
 Db 541 tctctgt 546  
 Qy 765 TCCTGT 770  
 RESULT 4  
 ID Q24440 standard; DNA; 2062 BP.  
 AC Q24440.  
 DT 05-NOV-1992 (first entry)  
 DE Encodes TNF-alpha 55KD receptor.  
 KW tumor necrosis factor alpha; extracellular binding domain;  
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
 KW malaria; viral meningitis; graft versus host disease;  
 KW autoimmune disease; Rheumatoid arthritis.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 156..1517  
 FT /tag- a  
 FT /product- human TNF-alpha  
 FT mat\_peptide 1265..1267  
 FT /tag- b  
 FT /note- "3"  
 FT mat\_peptide 1265..1267  
 FT /tag- c  
 FT /codon- seq: "TGG", aa: Thr

mat\_peptide 1258..1260  
 FT /tag- d  
 FT /codon- Seq "AAG", aa: Leu  
 FT mat\_peptide 1433..1435  
 FT /tag- e  
 FT /codon- Seq: "GAC", aa: Asn  
 FT sig\_peptide 156..274  
 FT /tag- f  
 FT MO9207076-A.  
 PD 30-APR-1992.  
 PF 18-OCT-1991; G01826.  
 PR 18-OCT-1990; GB-022648.  
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.  
 PI Brennan FM, Feldmann M, Gray PW, Turner MJC;  
 DI WPT; 92-167156/20.  
 DR P-PSDB; R24000  
 PT New polypeptide capable of binding human TNF alpha - comprises  
 PT first three cysteine-rich subdomains of TNF alpha receptor for  
 PT treating autoimmune disease, septic shock, HIV etc.  
 PS Claim 4; Fig 1; 43pp; English.  
 CC This sequence encodes human TNF-alpha 55KD receptor. A placenta cDNA  
 CC library in gtl10 was screened with probe Q29236. Ten hybridising clones  
 CC were plaque purified and cDNA size determined by PAGE against an  
 CC Eco RI digested phage DNA. The inserts of two cDNA clones were then  
 CC sequenced. The coding region of the majority of the human TNF-alpha  
 CC 55KD receptor was isolated as an EcoRI fragment encoding 374 amino  
 CC acids, and cloned into a mammalian cell expression vector, resulting  
 CC in pTNFR. A derivative of the TNF-alpha receptor was produced by  
 CC engineering a termination codon just prior to the transmembrane  
 CC domain. PCR with primers Q29237,8 generated a 300bp  
 CC restriction fragment which was cloned into pTNFR, giving pTNFRcd.  
 CC DNA sequencing confirmed this contained the designed DNA sequence.  
 CC The TNF-alpha receptor expression plasmids were then transfected  
 CC into monkey COS-7 cells.  
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
 SO Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T;  
 Query Match 35.3%; Score 424; DB 4; Length 2062;  
 Best Local Similarity 99.8%; Pred. No. 1,67e-282;  
 Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 275 gatagtggtgtcccaagaaatatatccaccccaataatcgttgcgtacc 334  
 Qy 345 GATAGTGTGTGCCCAAGAAATATATCCACCCCAAAATATATGATTGCTGTACC 404  
 Db 335 aagtgccacaaggaacctactgtacaatgtcaggtccagggccgggagataagac 394  
 Qy 405 AAGTGCCACAAAGAACTACTGTATGATGATGTCAGGCCGGGCGAGATACGGAC 464  
 Db 395 tgcaggagtgtagagcggtctcctcaccgcttcagaaacacacctcagacactgc 454  
 Qy 465 TGCAGGAGTGTAGAGCGGCTCTTTCACCGCTTCAGAAACACCACTCAGACACTCC 524  
 Db 455 agctgtcccaatgtccgaagaatgggtcaggtggaatctctctgcacagtggac 514  
 Qy 525 AGCTGTCCAAATGCCGAAGAAGATGGGTGAGTGAATCTCTTTCGACAGTGAC 584  
 Db 515 cggagacacgtgtgtgtgcgaggaagaaacagtaacgcatattggagtgtaaac 574  
 Qy 585 CGGAGACCGGTGTGTGTCGAGGAAGAACAGTACCGGCAATTATGGAGTGAAC 644  
 Db 575 ttcacagtgctcaatgtcagcctctcctcaatgtggaacggtgcacctctcctgcag 634  
 Qy 645 TTCACAGTCTTCATATGACAGCCTCTCCATGGAGACCGTGCACCTCTCTCCAGAG 704  
 Db 635 aaacagaaacacggtgtgcacctgtcagtgcaaggttcttcttaagagaaagag 694  
 Qy 705 AAACAGAAACACCGTGTGCACCTGCATGCAGGTTCTTCTTAAGAGAAACGAGTGT 764  
 Db 695 tctctgt 700  
 Qy 765 TCCTGT 770

RESULT 5  
ID Q20973 standard; DNA; 2062 BP.  
AC Q20973;  
DT 11-MAY-1992 (first entry)  
DE TNF-alpha binding protein gene.  
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 155..1522  
FT /tag= a  
FT sig\_peptide 155..274  
FT /tag= b  
FT mat\_peptide 275..1522  
FT /tag= c  
FT misc\_feature 473..532  
FT /tag= d  
FT /note= "homologous to probe Q20974"  
FT misc\_feature 242..751  
FT /tag= e  
FT /note= "encodes the extracellular domain of human  
TNF alpha receptor"  
FT GB246568-A.  
PD 05-FEB-1992.  
PF 15-JUN-1990; 013410.  
PR 15-JUN-1990; GB-013410.  
PA (CHAR-) CHARING CROSS SUNLE.  
PI Feldman M, Gray P, Turner M, Brennan F;  
DR WPI: 92-043613/06.  
DR P-PSDB: R20787.  
PT New tumour necrosis factor alpha binding protein and polypeptide  
PT - useful in treating cachexia, sepsis and auto immune diseases  
PT e.g. rheumatoid arthritis  
PS Disclosure: Fig 1: 25pp; English.  
CC The sequence is that of DNA encoding tumour necrosis factor alpha  
CC binding protein which was obtd. from a human placental cDNA library  
CC in lambda g11 using a probe (Q20974). The DNA also encodes the  
CC extracellular domain of human TNF alpha receptor and as such it is  
CC useful for treating diseases where TNF alpha is involved as a  
CC causative agent, e.g. cachexia, sepsis and autoimmune diseases,  
CC specifically rheumatoid arthritis. See also Q20974.  
SQ Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;  
Query Match 35.3%; Score 424; DB 3; Length 2062;  
Best Local Similarity 99.8%; Pred. No. 1,67e-282;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 275 gatagtggtgtccccaagaaatatataccaccctcaaaataatcgattgtgtacc 334  
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 345 GATAGTGTGTCTCCCAAGAAATATATCCACCCTCAAAATATGCGATTGCTGTACC 404  
Db 335 aagtgccacaagaagaaacctctgtacaaatgactgtccagcccgaggagataagagac 394  
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 405 AAGTGCCACAAAGAACCTTACTTACAAATGACTGTCAGGCCCGGGGACGATACGGAC 464  
Db 395 tgcagggagtgtagagcggtccctccacgcgtccagaaacacacccctcagactgtcc 454  
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 465 TGCAGGAGAGTGTAGACGGCTCTTTACACCGCTTCAGAAACACCTTCAGACATGCTC 524  
Db 455 agctgtccaaatgcgaaagaaatggatcaggtgagatctctcttgcacagtgagac 514  
QY 525 AGCTGTCCAAATGCCAAAGAAATGGGTGAGTGGATCTCTTGTGACAGTGGAC 584  
Db 515 cgggacacccgtgtgtgctgtgagaaagaaacagtaacggcattatgtgagaaacctt 574  
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 585 CGGACACCGGTGTGCTGAGGAGAAACAGTACCGGCTTATTGAGAGAAACCTT 644  
Db 575 ttccagtgcttcaatgtcagacgtctcgtcctcaatggagacggtgcaacctctcctcagag 634  
QY 645 TTCAGAGTCTCAATTCAGAGCTCTGCTCATAATGGACCGTGCACCTCTCTGCGCAGAG 704  
Db 635 aaacagaacacccgtgtgtcaccctgcacatgcaggttcttctaagagaagaaacagtggtc 694

RESULT 6  
ID Q10883 standard; cDNA; 2088 BP.  
AC Q10883;  
DT 13-MAY-1991 (first entry)  
DE 30KD TNF inhibitor precursor gene in lambda-g110-7cinfnp.  
KW Tumour necrosis factor; inhibitor; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 171..1536  
FT /tag= a  
FT AU9058976-A.  
PD 24-JAN-1991.  
PF 16-JUL-1990; 058976.  
PR 18-JUL-1989; US-381080.  
PR 11-DEC-1989; US-450329.  
PR 07-FEB-1990; US-479661.  
PA (SYNE-) SYNERGEN INC.  
DR WPI: 91-073847/11.  
DR P-PSDB: R10986.  
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha  
PT and beta, useful as therapeutic agent.  
PS Disclosure: Fig 21; 142pp; English.  
CC The sequence encodes the entire 30 kD TNF inhibitor. The clone from  
CC which the sequence was obtd. was isolated from a cDNA library  
CC prepd. from RNA form U937 cells treated with PMA/PHA. The whole  
CC gene can be inserted into expression vectors for prepn. of TNF  
CC inhibitor for use in the treatment of inflammatory and degenerative  
CC diseases.  
SQ See also Q10878, Q10884 and Q10907.  
Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T;  
Query Match 35.3%; Score 424; DB 2; Length 2088;  
Best Local Similarity 99.8%; Pred. No. 1,67e-282;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 289 gatagtggtgtccccaagaaatatataccaccctcaaaataatcgattgtgtacc 348  
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 345 GATAGTGTGTCTCCCAAGAAATATATCCACCCTCAAAATATGCGATTGCTGTACC 404  
Db 349 aagtgccacaagaagaaacctctgtacaaatgactgtccagcccgaggagataagagac 408  
QY 405 AAGTGCCACAAAGAACCTTACTTACAAATGACTGTCAGGCCCGGGGACGATACGGAC 464  
Db 409 tgcagggagtgtagagcggtccctccacgcgtccagaaacacacccctcagactgtcc 468  
QY 465 TGCAGGAGAGTGTAGACGGCTCTTTACACCGCTTCAGAAACACCTTCAGACATGCTC 524  
Db 469 agctgtccaaatgcgaaagaaatggatcaggtgagatctctcttgcacagtgagac 528  
QY 525 AGCTGTCCAAATGCCAAAGAAATGGGTGAGTGGATCTCTTGTGACAGTGGAC 584  
Db 529 cgggacacccgtgtgtgctgtgagaaagaaacagtaacggcattatgtgagaaacctt 588  
QY 585 CGGACACCGGTGTGCTGAGGAGAAACAGTACCGGCTTATTGAGAGAAACCTT 644  
Db 589 ttccagtgcttcaatgtcagacgtctcgtcctcaatggagacggtgcaacctctcctcagag 648  
QY 645 TTCAGAGTCTCAATTCAGAGCTCTGCTCATAATGGACCGTGCACCTCTCTGCGCAGAG 704  
Db 649 aaacagaacacccgtgtgtcaccctgcacatgcaggttcttctaagagaagaaacagtggtc 708  
QY 705 AAGCAGACACCGGTGTGCTGAGGAGAAACAGTACCGGCTTATTGAGAGAAACGATGTGTC 764  
Db 709 tccctgt 714  
|||||

QY 765 TCCTGT 770

RESULT 7  
ID 010955 standard; cDNA; 2111 BP.  
AC 010955;  
DT 24-MAY-1991 (first entry)  
DE Encodes human 55kD TNF-binding protein.  
KW Tumour Necrosis Factor; binding proteins; septic shock;  
KW autoimmune glomerulonephritis; lymphokine; cytokine.  
FH Key Location/Qualifiers  
FT s1g\_peptide 187..273  
FT /tag- a  
FT mat\_peptide 274..1551  
FT /tag- b  
FT /product= 55kD TNF-BP  
FT EP-417563-A.  
PD 20-MAR-1991.  
PF 31-AUG-1990; 116707.  
PR 12-SEP-1989; CH-003319.  
PR 08-MAR-1990; CH-000746.  
PR 20-APR-1990; CH-001347.  
PA (HOFF) HOFFMANN-LA ROCHE AG.  
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
PI Schlaeger EJ;  
DR WPI: 91-081851/12.  
DR P-PSDB: R11082.  
PT Insoluble tumour necrosis factor binding proteins - and DNA  
PT encoding them, useful in pharmaceutical prods. and for antibody  
PT protn.  
PS Claim 4: Fig 1: 26pp; German.  
CC Partial amino acid sequences were determined for the 55 and 75kD  
CC TNF-BPs (see R11072-R11081) and oligonucleotide primers were  
CC synthesised based on these partial sequences. The primers were used  
CC to produce a cDNA fragment for use as a probe to screen a human  
CC plasmid cDNA bank constructed in lambda gill. Positive clones were  
CC identified and sequenced. DNA constructs comprising the TNF-BP coding  
CC sequence may also contain a fragment encoding a human Ig domain.  
CC Recombinant constructs are used to transform cells to confer  
CC improved TNF-binding properties.  
CC See also Q10956.  
SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;

Query Match 35.3%; Score 424; DB 2; Length 2111;  
Best Local Similarity 99.8%; Pred. No. 1.67e-282;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 307 gatagtgtgtccccaagaataatataccacccccaataatcgaattgtcttacc 366  
|||||  
QY 345 GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATATTCGATTTCCTGACC 404  
|||||  
DB 367 aagtgccacaagaagaaactactgttacaatgactgtccagccggggcagagtaacgac 426  
|||||  
QY 405 AAGTGCACAAAGGAAGCACTACTGTGTAATGACTGTCCAGGCCGGGGGAGATAGGAGAC 464  
|||||  
DB 427 tgcaggagatgtgagagcggtctcctcaccgcttcagaaacacacccacgacgtctc 486  
|||||  
QY 465 TGCAGGAGATGTGAGAGCGGCTCTTACCGCTTCAGAAAACACCACTCAGACACTGCTC 524  
|||||  
DB 487 agctgtccaatgtccgaagaagaatggttcaggtgagatctctcttcgcaagtgagac 546  
|||||  
QY 525 AGCTGCTCCAAATGCCGAAGAAATGGGTCAAGTGAAGTCTCTCTTTCACAGTGGAC 584  
|||||  
DB 547 cggagacacggtgtgtgtcgcaggaagaacacgtaacggatatttggatgaaacact 606  
|||||  
QY 585 CGGAGACCGGTGTGTGTGCGTCAGAGAAACCACTACCGGATATTGAGATGAACCTT 644  
|||||  
DB 607 ttccagtgttcaatgtcagcctctcctcaatgagacggtgacactctctctcagagag 666  
|||||  
QY 645 TTCAGTGTCTCAATGTGACCTCTCTCAATGAGGACCTGCACCTCTCTCCAGGAG 704  
|||||  
DB 667 aaacagaacacggtgtgcacctgcacgtgacgtttcttctaagagaacacgaggtgtgc 726  
|||||

QY 705 AAACAGAACCGGTGTGACCTGCATGCAGGTTCTTCTTAAGAGAAAACGAGTGTGC 764

DB 727 tcctgt 732  
|||||  
QY 765 TCCTGT 770

RESULT 8  
ID 006285 standard; DNA; 2141 BP.  
AC 006285;  
DT 29-JAN-1991 (first entry)  
DE Human Tumour Necrosis Factor-Receptor cDNA Insert.  
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KW lambdaTNF-R2; ratTNF-R8; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 213..1577  
FT /tag- a  
FT /label=hutnf-R  
FT EP-393438-R.  
PD 24-OCT-1990.  
PF 06-APR-1990; 106624.  
PR 21-APR-1989; DE-913101.  
PR 21-JUN-1989; DE-920282.  
PA (BOEH) BOEHRINGER INGELHEIMINT.  
PI Hauptmann R, Hümmler A, Maurer-Fogy I, Stratowa C;  
DR WPI: 90-321987/43.  
DR P-PSDB: R07451.  
PT DNA encoding TNF binding protein and TNF-receptor - used in  
PT tumour treatment and to understand mechanism to TNF action  
PS Disclosure: Fig 91(1-2): 51pp; German.  
CC ratTNF-R8 (006284) was used to screen the H5913T cDNA library.  
CC lambdaTNF-R2 encodes the complete human TNF-R2 and was used to  
CC construct a plasmid (pADTNF-R) expressing the product the same way  
CC as pADTNF-BP (see Q06282).  
CC See also Q06282-Q06285.  
SQ Sequence 2141 BP; 455 A; 633 C; 593 G; 460 T;

Query Match 35.3%; Score 424; DB 1; Length 2141;  
Best Local Similarity 99.8%; Pred. No. 1.67e-282;  
Matches 425; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 333 gatagtgtgtccccaagaataatataccacccccaataatcgaattgtcttacc 392  
|||||  
QY 345 GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATATTCGATTTCCTGACC 404  
|||||  
DB 393 aagtgccacaagaagaaactactgttacaatgactgtccagccggggcagagtaacgac 452  
|||||  
QY 405 AAGTGCACAAAGGAAGCACTACTGTGTAATGACTGTCCAGGCCGGGGGAGATAGGAGAC 464  
|||||  
DB 453 tgcaggagatgtgagagcggtctcctcaccgcttcagaaacacacccacgacgtctc 512  
|||||  
QY 465 TGCAGGAGATGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 524  
|||||  
DB 513 agctgtccaatgtccgaagaagaatggttcaggtgagatctctcttcgcaagtgagac 572  
|||||  
QY 525 AGCTGCTCCAAATGCCGAAGAAATGGGTCAAGTGAAGTCTCTTTCACAGTGGAC 584  
|||||  
DB 573 cggagacacggtgtgtgtcgcaggaagaacacgtaacggatatttggatgaaacact 632  
|||||  
QY 585 CGGAGACCGGTGTGTGTGCGTCAGAGAAACCACTACCGGATATTGAGATGAACCTT 644  
|||||  
DB 633 ttccagtgttcaatgtcagcctctcctcaatgagacggtgacactctctcagagag 692  
|||||  
QY 645 TTCAGTGTCTCAATGTGACCTCTCTCAATGAGGACCTGCACCTCTCTCCAGGAG 704  
|||||  
DB 693 aaacagaacacggtgtgcacctgcacgtgacgtttcttctaagagaacacgaggtgtgc 752  
|||||  
QY 705 AAACAGAACCGGTGTGACCTGCATGCAGGTTCTTCTTAAGAGAAAACGAGTGTGC 764  
|||||  
DB 753 tcctgt 758  
|||||  
QY 765 TCCTGT 770

ID	RESULT	9
AC	090513; standard; DNA; 2175 BP.	
DT	19-JAN-1996 (first entry)	
DE	p55 TNF-R gene.	
KM	p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;	
KW	epidermal growth factor receptor; EGF-R; protease; inhibitor;	
KM	phorbol myristate acetate; PMA; ss.	
HS	Homo sapiens.	
FT	Key	
FT	Location/Qualifiers	
FT	CDS	256..1623
FT	/*tag= a	
FT	/product= p55 TNF-R	
FT	misc.signal	2143..2149
FT	/*tag= b	
FT	/note= "possible poly-A signal"	
PN	AU94475742-A.	
PD	04-MAY-1995.	
PE	11-OCT-1994; 075742.	
PR	12-OCT-1993; 11-107268.	
PI	(YEDA ) YEDA RES & DEV CO LTD.	
PI	Backlin M, Brakebusch C, Varfolomeev E, Wallach D;	
DR	WPI: 95-1943442/26.	
DR	P-PSDB: R75084.	
PT	New protease capable of cleaving soluble tumour necrosis factor	
PT	(TNF) receptor - from cell-bound TNF- receptor, useful for	
PT	antagonising deleterious effects of TNF.	
PS	Disclosure; Fig 1; 40pp; English.	
CC	This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.	
CC	Expression of this receptor is regulated by shedding of the extracellular	
CC	receptor fragment. The p55 TNF-R can be shed in response to different	
CC	inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell	
CC	type. The only region of the receptor whose structure affects the	
CC	shedding response is the spacer region (see R75012) in the extracellular	
CC	domain. This region is located close to a site of cleavage of the	
CC	molecule, and links the Cys rich module to the transmembrane domain.	
CC	The spacer region of the encoded protein was used to create the chimeras	
CC	between human p55 TNF-R and murine epidermal growth factor receptor	
CC	(EGF-R) that are represented by R75007-11. This spacer region was	
CC	subjected to deletion mutations (R75013-25) and substitutions	
CC	(R75026-47). Of the spacer region, the most important residues are	
CC	Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most	
CC	important of these. The shedding of the receptor is independent of the	
CC	side chain identity of these residues, with the exception of a limited	
CC	dependence on the identity of Val 173. Mutations which alter the	
CC	conformation of the protein adversely effect the shedding process. The	
CC	mutations shown in R75013-47 were introduced in order to create an	
CC	inhibitor of a protease that is capable of cleaving the soluble TNF-R	
CC	from the cell bound TNF-R. Fragments of these inhibitors can be seen in	
CC	R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can	
CC	be used for enhancing TNF function.	
SQ	Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;	
DB	Query Match	35.3%; Score 424; DB 15; Length 2175;
DB	Best Local Similarity	39.8%; Pred. No. 1,67e-282;
DB	Matches 425; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	376 gatagtggtgtcccccagaagaatatatccaccctcaaaataatgtgattgtgtacc	435
OY	345 gatagtggtgtgtcccccagaagaatatatccaccctcaaaataatgtgattgtgtacc	404
DB	436 aagtgccacaaagaagaactactgttaaatgactgttcaggccggggcaggatacagac	495
OY	405 AAGTGCACAAAGAAGAACTACTGTGTACAAATGACGTCCAGGCCGGGGAGAGATACGAC	464
DB	496 tgcagagagatgtatagagcgctcccttcacgcgttcagaaaaacacctcagacactgtc	555
OY	465 TGCAGGAGATGTATAGACAGCGCTCTTTACCGCTTCAGAAAAACCACTCAGACACTGCCTC	524
DB	556 agctgtcccaaatgcccagaaggaaatgtgcagttggaatctcttcttgcaacgtgtac	615

Query Match	Score	DB	Length	Seq
Best Local Similarity 99.8%;				
Matches 425; Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0	
Db	1725	gtagtggtgtgtccccaagaaataataccaccctcaaaataatcgattgtgtgacc	1784	
Qy	345	GATATGTGTGTGTCGCCCAAGAAATATATCCACCCTCAAAATATATGATTTGCTGTATCC	404	
Db	1785	aagtgcccaaaaggaactactcttgcatactgctcaggtccggccggggcagataagagc	1844	
Qy	405	AAGTCCCAACAAAGGAACCTACTTGTATCATATACGTCCAGGCCCGGGGGCAGATACGGAC	464	
Db	1845	tgcagggaggtgtgaagggcttcctcaacgcgtccagaaacaccccaagcactgtgctc	1904	
Qy	465	TGCAGGGAGGTGTGAAGGCGGCTTTTACCCGCTTCAGAAAACCACTTCAGACACTGCTTC	524	
Db	1905	agctgtcccaaatgcccgaagaaatgggtcaggttggaatctctcttgacacagtgagac	1964	
Qy	525	AGCTGCTCCAAATGCGCAAGAAAGAAATGGGTCAAGGTGAGATCTCTTTCAGCAGTGGAC	584	
Db	1965	cgggaacccgtgtgtgtgtcaggaagaacagtaaccggcaattttgagtgaaacctc	2024	

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OY 585 CCGGACACCGTGTGTGGTGCAGAGAAACAGTACCGGATATTGAGTGAACACTT 644
DB 2025 ttccagtgcttcaatgtgacgctctgctcctcaatgtgacgctctcctccgacagag 2084
OY 645 TTCAGTGTCTCAATGTGACGCTCTGCTCAATGGACCGTCCACTCTCCGCCAGGAG 704
DB 2085 aaacagaacacgctgtgacgctcgcaggttctctctaagagaacagatgtgac 2144
OY 705 AAACGAAACACCGTGTGACCTGCAATGCAGGTTCTTCTTAAGAGAAACAGATGTGTC 764
DB 2145 tccgtgt 2150
OY 765 TCCTGT 770

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RESULT 11
ID 050870 standard; DNA; 2170 BP.
AC 050870;
DT 13-MAY-1994 (first entry)
DE P55 Tumour necrosis factor receptor coding sequence.
KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW effector protein; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 256..1623
FT /tag- a
FT /product- p55 Tumour necrosis factor receptor.
FT 10-NOV-1993.
FT 29-APR-1993: 106981.
FT 03-MAY-1992: IL-101769.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT Brakebusch C, Wallach D;
FT MPI; 93-353057/45.
FT P-PSDB; RA2197.
FT Modulating activity of tumour necrosis factor receptor - using
FT peptide(s), antihodies, etc. which interact with critical regions
FT of receptor or effector protein, for controlling auto-immune
FT disease, septic shock, etc.
FT Claim 2; Figure 1; 17pp; English.
FT Modification of the tumour necrosis factor receptor by mutation or
FT deletion modulates signal transduction and/or cleavage effected by
FT the receptor. This modulation of activity can also be achieved
FT using effector proteins which interact with the TNF receptor.
FT Molecules which interact with the TNF receptor or the effector
FT proteins can be used to treat or prevent diseases associated with
FT TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
FT rejection; graft vs. host disease or septic shock. They can also
FT be used to treat overdoses of exogenous TNF.
FT Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T;
SQ

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Query Match 35.1%; Score 422; DB 9; Length 2170;
Beat Local Similarity 99.5%; Pred. No. 4.91e-281;
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 376 gatagtggtgtccccaagaaataatataccacccccaataatcgaattgtgtacc 435
OY 345 GATAGTGTGTGCCCAAGAAATATATCCACCCCAAAATTCGATTTGCTGTACC 404
DB 436 aagtgcaacaagaagaaactactgtcaatgactgtcagggccggggaagatacgac 495
OY 405 AAGTGCACAAAGGAACCTACTTGTCAATGATGTCACGGCCGGGCAAGGATACGGAC 464
DB 496 tgcaggagtgtagagggcgctcctcaccgcttcagaaacacactcagacatgcctc 555
OY 465 TGCAGGAGATGTGAGAGCGGCTCTTCCACCGCTTCAGAAAACCACTCAGACCTGCC 524
DB 556 agctgtcacaatgtcgaagaagaatgggttcaggtgagatctctctgtcacaagtggac 615
OY 525 ACTGTCTCCAAATGCGGAAGAAATGGGTGACAGTGAAGATCTCTTGTGACAGTGGAC 584
DB 616 cgggaacacgctgtgtgtgcgcaggaagaaacagtaaccgcatattgtgagaaacct 675

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OY 585 CCGGACACCGTGTGTGGTGCAGAGAAACAGTACCGGATATTGAGTGAACACTT 644
DB 676 ttccagtgcttcaatgtgacgctctgctcctcaatgtgacgctctcctccgacagag 735
OY 645 TTCAGTGTCTCAATGTGACGCTCTGCTCAATGGACCGTCCACTCTCCGCCAGGAG 704
DB 736 aaacagaacacgctgtgacgctcgcaggttctctctaagagaacagatgtgac 795
OY 705 AAACGAAACACCGTGTGACCTGCAATGCAGGTTCTTCTTAAGAGAAACAGATGTGTC 764
DB 796 tccgtgt 801
OY 765 TCCTGT 770

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RESULT 12
ID Q12215 standard; DNA; 2176 BP.
AC Q12215;
DT 12-SEP-1991 (first entry)
DE Type I TNF receptor.
KW Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT terminator 244..246
FT /tag- a
FT /note- "In-frame termination codon"
FT CDS 256..1620
FT /tag- a
FT /product- type I TNF receptor
FT sig_peptide 256..318
FT /tag- b
FT mat_peptide 319..1620
FT /tag- c
FT misc_RNA 319..864
FT /tag- d
FT /label- soluble_domain
FT /note- "may be 2 codons shorter or a few codons
FT longer"
FT misc_feature 376..414
FT /tag- e
FT /note- "TBP-I derived sequence"
FT misc_feature 583..627
FT /tag- f
FT /note- "TBP-I derived sequence"
FT misc_feature 850..858
FT /tag- g
FT /note- "TBP-I derived sequence"
FT misc_RNA 889..957
FT /tag- h
FT /label- transmembrane_domain
FT repeat_unit 385..504
FT /tag- i
FT /number- 1
FT repeat_unit 505..633
FT /tag- j
FT /number- 2
FT repeat_unit 634..756
FT /tag- k
FT /number- 3
FT repeat_unit 757..858
FT /tag- l
FT /number- 4
FT POLYA_signal 2145..2150
FT /tag- m
FT EP-433900-A.
PD 26-JUN-1991.
PF 13-DEC-1990; 124133.
PF 13-DEC-1989; IL-092697.
PR 12-JUL-1990; IL-095064.
PA (YEDA ) YEDA RES & DEV CO LTD.
PA Wallach D, Nopnar Y, Kemper O, Engelmann H, Brakebusch C;
PI Aderka D;

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DR WPI: 91-186774/26.  
 PT Recombinant tumor necrosis factor binding protein I - prepd. by  
 PT transfecting eukaryotic cells with vector contg. deoxyribonucleic  
 PT acid encoding human type I TNF receptor or soluble domain  
 PS Disclosure: Fig 1(D): 30pp; English.  
 CC The Tumor Necrosis Factor Binding Protein I is the soluble form of  
 CC type I TNF-receptor and constitutes a fragment of the cell surface  
 CC form of this receptor, corresp. to its extracellular domain.  
 CC There is no characteristic poly(A) addition signal near the 3' end  
 CC of the cDNA. The sequence ACTAA (tag m) may serve as an  
 CC alternative to this signal, but with low efficiency.  
 CC See also Q1212-15.  
 SQ Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T;

Query Match 35.1%; Score 422; DB 2; Length 2176;  
 Best Local Similarity 99.5%; Pred. No. 4,91e-281;  
 Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 376 gatagtgtgtgtcccaagaagaatataccaccctcaaaatctcagtttcagttacc 435  
 QY 345 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATATGATTGCTGTACC 404

DB 436 aagtgccacaaagaaactacttgtacaatgactgtccagcccgaggcagatagcagac 495  
 QY 405 AAGTGCCACAAAGAACTACTGTACATAGCTGCCAGCCGCGGAGATACGAGAC 464

DB 496 tgcaggagagtgtagagcagcgtccctccacgcctcagaagaacacccctcagcagctc 555  
 QY 465 TGCAGGAGGTGAGAGAGGCGCTTTTCACGCTTCAGAAACACACTCAGACATGCTCTC 524

DB 556 agctgtcccaaatgcggaagaatgggtcaggtgagatcctctcttcagcagttgagac 615  
 QY 525 AGCTGTCCCAATGCCGAAGAAATGGGTGAGGTGAGATCTCTTCTTGACACAGTGAGAC 584

DB 616 cgggacacccgtgtgtgtgtgtgtaggaagaacagtaacggcattttgagatgaaacctt 675  
 QY 585 CGGACACCCGTGTGTGTGTGTCAGAGAAACAGTACCGGCTTATGTGAGTGAAGAAACCTT 644

DB 676 ttccagtgctcaattgcagcctctgcctcaattggagccgagccctctcctcagcagag 735  
 QY 645 TTCCAGTGCTCAATGCAAGCTCTGCTCAATGGACCGTGCACCTCTCCGCAAGAG 704

DB 736 aaacagaacacccgtgtgtgacatgcacatgagttctcttcttaagaagaacagatgtgtc 795  
 QY 705 AAACAGAACACCGTGTGTGACCTGCATGCAAGTTCCTTTTAAGAGAAAGAGATGTCTC 764

DB 796 tccctgt 801  
 QY 765 TCTGT 770

RESULT 13  
 ID 014800 standard: DNA; 579 BP.  
 AC 014800;  
 DT 11-FEB-1992 (first entry)  
 DE Human chorionic gonadotropin beta subunit analogue.  
 KW Glycoprotein hormone; hCGb'; fertility; immuno-castration;  
 KW immuno-contragestive; vaccine; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 26..523  
 FT /tag- a  
 FT mat\_peptide 86..520  
 FT /tag- b  
 FT sig\_peptide 26..85  
 FT /tag- c  
 FT polyA\_site 524..579  
 FT /tag- d  
 FT mutation 229  
 FT /tag- e  
 FT /note="c -> g"  
 FT mutation 232

FT /tag- f  
 FT /note="c -> g"  
 FT MO9116922-A.  
 PI 14-NOV-1991.  
 PD 07-MAY-1991.  
 PR 08-MAY-1990; US-520703.  
 PA (UINE-) UNIV MED NEW JERSEY.  
 PI Campbell RK, Moyle WR;  
 DR WPI: 91-353528/48.  
 PT Recombinant human chorionic gonadotropin (hCG) - for inducing fertility as  
 PT immuno-castration agents, for suppressing reproductive system  
 PS Example 3; Fig 4a; 94pp; English.  
 CC The sequence is an analogue of hCG beta subunit cDNA contg. two  
 CC silent mutations which eliminate restriction sites. It was prepd.  
 CC from the plasmid pKMB-hCG-beta, a construct contg. the hCG beta  
 CC subunit isolated from human placenta (Riddes and Goodman) in  
 CC plasmid pKMB, a derivative of pUC18 designed to facilitate cloning  
 CC of glycoprotein hormones. The sequence was used as the starting  
 CC construct for many mutants. (See R15061-R15125 and R15161-R15198).  
 SQ Sequence 579 BP; 128 A; 205 C; 151 G; 95 T;

Query Match 34.4%; Score 414; DB 3; Length 579;  
 Best Local Similarity 99.3%; Pred. No. 3.68e-215;  
 Matches 417; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 104 ccacggtgcgcccccatcaatctgcccacccctgtgtgtgagaaggggtgccccgtgtgc 163  
 QY 783 CCACGGTGCGCCCCCATCAATGACCACTGCTGTGAGAGAGAGGCTGCCGTGTGC 842

DB 164 atcaccttcaaacacacacatctgtgcggtactgtccacacatgacccggtgtcag 223  
 QY 843 ATCACCTTCAACACACACACTGTGCGGCTACTGCCCCACACATGACCCGGTGTCTCAG 902

DB 224 ggggtgtcccgccctgtcctcaggtgtgtgcaactacccgagatgtgccttgcagttcc 283  
 QY 903 GGGGTCTCCCGCCCGCTGCTCAAGTGTGTGCAATCCGCGATGTGCGCTTGAATGCC 962

DB 284 atcgggttccctgtcctcctcccgccggtgtgaaacccgtgtgtcttctcctagccgtgtcctc 343  
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DB 344 agctgtcaatgtgacatctccgcgcgcagcacacacatgactgtgcgggtgtcccaagacac 403  
 QY 1023 AGCTGTCAATGTGACATCTGCGCGCGACGACACACTACTCGGGGGTCCCAAGACAC 1082

DB 404 cccttgacctgtgtagcccccgcgtctccaggaactcctcttctcaaaagccctccccc 463  
 QY 1083 CCTTGAACCTGTGATGACCCCGCTTCCAGGACACTCTCTCAAAAGCCCTCCCCCC 1142

DB 464 agccttcaagcccatccgactcccggtgccccctcggaacaccccgatccctcccaataa 523  
 QY 1143 AGCCTTCAAGCCCATCCGACTCCCGGGCCCTCGGACACCCCGATCTCTCCCAATAA 1202

RESULT 14  
 ID T03212 standard: cDNA; 836 BP.  
 AC T03212;  
 DT 26-APR-1996 (first entry)  
 DE Single chain gonadotropin analogue 1 coding sequence.  
 KW Single chain gonadotropin; human chorionic gonadotropin; hCG;  
 KW alpha; beta; subunit; analogue; glycoprotein hormone; fertility;  
 KW inhibit; stimulate; increase; lutropin; luteinizing hormone; LH;  
 KW follicle stimulating hormone; FSH; vaccine; contraceptive; ds.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT CDS 33..830  
 FT /tag- a  
 FT /transl\_except- pos:240..242, aa:Arg  
 FT sig\_peptide 33..92  
 FT /tag- b  
 FT mat\_peptide 93..827

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FT /*tag- c
FT /label- Analogue-1
FT /note- "nucleotides 93..527 encode amino acids
FT 1-145 of hcg beta subunit; nucleotides
FT 528..551 encode a (Gly-Ser)4 linker and
FT nucleotides 552..827 encode amino acids
FT 1-92 of gonadotropin alpha-subunit"
FT misc.feature 1..26
FT
FT /*tag- d
FT /label- sticky-end
FT /note- "single-strand overhang. The complementary
FT strand also has a single-strand overhang at
FT its 5'-end; the sequence of the overhang is
FT 5'-TCCGATTAAGCTTGATGATGATCC-3'"
FT PN W09522340-A1.
PD 24-AUG-1995.
PF 17-FEB-1995; 02067.
PR 18-FEB-1994; US-199382.
PA (SENS-) SENSE-TEST.
PI MOyle WR:
PI WPI: 95-302553/39.
DR P-PSDB: R86247.
PT Methods for altering fertility in mammals, esp. humans - e.g.
PT stimulating fertility by reducing the activity and/or levels of
PT circulating glyco:protein hormones having lntropin activity
PS Example 12; Fig 6; 102pp; English.
CC Analogue 12 (human CG-beta(1-145)-linker-human CG-alpha(1-92)) is a
CC specific example of a single chain gonadotropin having a chorionic
CC gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-
CC subunit at the C-terminus, joined by a linker of 1-16 amino acids.
CC The analogue has luteinizing hormone (lutropin) activity and is
CC useful for inducing ovulation and increasing male fertility.
CC The sequences coding for analogue 1 were cloned from a human
CC placental cDNA library using strand overlap extension PCR.
SQ Sequence 836 Bp; 166 A; 282 C; 222 G; 166 T;
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Query Match 34.0%; Score 409; DB 17; Length 836;
Best Local Similarity 99.0%; Pred. No. 1,73e-271;
Matches 413; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 111 ccacggctgcgcgcacccaatgcaacccctgctgtgagaagaggagctgcccgtgtgc 170
Oy 783 CCACGGTGCCTCCGCCCATCAATGCGACCTGCTGTGAGAGAGAGGCTGCCCGTGTGC 842
Db 171 atcacccgtcaaacaccacccatctgtgcccgtactatgcccacacacacccggtgtgcag 230
Oy 843 ATCACCGTCAACACCACTGTGTGCGGCTACTGCCCCACCATGACCCCGTGTGCAG 902
Db 231 ggggtctcgcggcctgctcaggtgtgtgtaactaacgagatgtgctcaggttc 290
Oy 903 GGGGTCTCCCGCCCTGCTCAGGTGTGTGCACTACCGCATGTGCGCTGTGCAGTCC 962
Db 291 atccgctccctgtgctgcgcgcgcgcgtgtgaacccgctgtgtcccaagcgcgtgtc 350
Oy 963 ATCCGCTCCTGCTGCTGCGCGCGCGCGGTGAACCCGCTGTCTCTTACGTGTGCTCTC 1022
Db 351 agctgtcaatgtgactgtgcgcgcgcgcacacacacacacacacacacacacacac 410
Oy 1023 AGCTGTCAATGTGCACTGTGCGCGCGCGCATGACATGACGCGGGGTCCCAAGACAC 1082
Db 411 cccttacctgtatgaccccgctccaggaatctcttccccaagagccctccccc 470
Oy 1083 CCTTAACTGTATATACCCCGCTTCAGAGACTCTCTTCTCAAGAGGCGCTCCCGCC 1142
Db 471 agccttcaagccatccgcagactccggggcctcgtgacacaccccgatctcccca 527
Oy 1143 AGCCTTCAAGCCATCCGATCCGAGACTCCGGGGCGCTCGAGACACCCGATCTCCACAA 1199
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RESULT 15
ID T03243 standard; cDNA; 836 Bp.
AC T03243;
DT 08-MAY-1996 (first entry)
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DE Single chain gonadotropin analogue 1a coding sequence.
KW alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW inhibit; stimulate; increase; lutropin; luteinizing hormone; LH;
KW follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS Synthetic.
FH Key 33..830 Location/Qualifiers
FT CDS
FT /*tag- a
FT /transl_except- pos:240..242, aa:Arg
FT sig_peptide 33..92
FT /*tag- b
FT mat_peptide 93..827
FT /*tag- c
FT /label- Analogue-1a
FT /note- "nucleotides 93..527 encode amino acids
FT 1-145 of hcg beta subunit; nucleotides
FT 528..551 encode a (Gly-Ser)4 linker and
FT nucleotides 552..827 encode amino acids
FT 1-92 of gonadotropin alpha-subunit lacking
FT the glycosylation sites at amino acid
FT positions 52 and 78"
FT Misc.difference 705..707
FT /*tag- d
FT /note- "wild-type Asn 52 codon has been changed to a
FT Gln codon to remove a glycosylation site"
FT Misc.difference 783..785
FT /*tag- e
FT /note- "wild-type Asn 78 codon has been changed to a
FT Gln codon to remove a glycosylation site"
FT misc.feature 1..26
FT /*tag- f
FT /label- sticky-end
FT /note- "single-strand overhang. The complementary
FT strand also has a single-strand overhang at
FT its 5'-end; the sequence of the overhang is
FT 5'-TCCGATTAAGCTTGATGATGATCC-3'"
FT PN W09522340-A1.
PD 24-AUG-1995.
PF 17-FEB-1995; 02067.
PR 18-FEB-1994; US-199382.
PA (SENS-) SENSE-TEST.
PI MOyle WR:
PI WPI: 95-302553/39.
DR P-PSDB: R86259.
PT Methods for altering fertility in mammals, esp. humans - e.g.
PT stimulating fertility by reducing the activity and/or levels of
PT circulating glyco:protein hormones having lntropin activity
PS Example 23; Fig 18; 102pp; English.
CC Analogue 1a (human CG-beta(1-145)-linker-human CG-alpha(1-92) [N53Q,
CC N780]) is a specific example of a single chain gonadotropin having
CC a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a
CC CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino
CC acids. The analogue 1a was derived from analogue 1 by removing the
CC two glycosylation sites from the alpha-subunit. The analogue has
CC anti-luteinizing hormone (lutropin) activity and can be used for
CC facilitating ovulation, terminating pregnancy and reducing androgen
CC secretion. The present sequence codes for analogue 1a.
SQ Sequence 836 Bp; 166 A; 282 C; 222 G; 166 T;
```

```
Query Match 34.0%; Score 409; DB 17; Length 836;
Best Local Similarity 99.0%; Pred. No. 1,73e-271;
Matches 413; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Db 111 ccacggctgcgcgcacccaatgcaacccctgctgtgagaagaggagctgcccgtgtgc 170
Oy 783 CCACGGTGCCTCCGCCCATCAATGCGACCTGCTGTGAGAGAGAGGCTGCCCGTGTGC 842
Db 171 atcacccgtcaaacaccacacatctgtgcccgtactatgcccacacacacacacacac 230
Oy 843 ATCACCGTCAACACCACTGTGTGCGGCTACTGCCCCACCATGACCGCGTGTGCAG 902
Db 231 ggggtctcgcggcctgctcaggtgtgtgtaactaacgagatgtgctcaggttc 290
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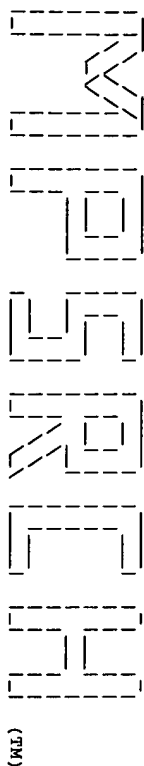
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QY 903 GGGGTCTCTCCCGCCGCTGCTGAGTGTGCACTACCGGATGTGCGCTTCGAGTCC 962
Db 291 atccggtccctggctggccgagcggtgagaccggtgtctctacgacgtgtgtctc 350
QY 963 ATCCGGCTCCCTGGCTGGCCGCGGCGGTGAACCCCGTGTCTCTACGCTGTGGCTCTC 1022
Db 351 agctgtcaatgtgactctgacgacgagcaaccactgactgagggtgtcccaaggaccac 410
QY 1023 AGCTGTCAATGTGCACTGTGCGCGGCGGCACTGACTGCGGGGTGCCAAGACCAAC 1082
Db 411 cccttgacctgtgtgagcccgcttcgaaggactctctctcaaaaggccctccccc 470
QY 1083 CCCTTGACCTGTGTGATGACCCCGCTTCAGGACTCTCTTCTCAAAAGGCCCTCCCCCC 1142
Db 471 agccttccaaagccatcccgactcccgaggccctcggaacaccccgatctctcccca 527
QY 1143 AGCCTTCCAAAGCCATCCCGACTCCCGGGGCCCTGGAGACCCCGATCTCTCCACAA 1199

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Search completed: Wed May 6 13:40:33 1998  
 Job time : 161 secs.





(TM)

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Distribution rights by Oxford Molecular Ltd

MPearch\_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 13:18:57 1998; Masparr time 1103.82 Seconds

Tabular output not generated. 1323.848 Million cell updates/sec

Title: >US-08-804-166-3

Description: (1-1202) from US08804166.seq

Perfect Score: 1202

N.A. Sequence: 1 CTCGAGATGGCTACAGATTA.....CCCCATCTCCACACATTA 1202

Comp: GAGCTCTACGATGTCATTT.....GGGGCTAGAGAGGTGTATT

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

emb1-est

1:em\_est1 2:em\_est2 3:em\_est3 4:em\_est4 5:em\_est5

6:em\_est6 7:em\_est8 8:em\_gss 9:em\_est13

genbank-est

10:gb\_est1 11:gb\_est2 12:gb\_est3 13:gb\_est4 14:gb\_est5

15:gb\_est6 16:gb\_est7 17:gb\_est8 18:gb\_est9 19:gb\_est10

20:gb\_est11 21:gb\_est12 22:gb\_est13 23:gb\_est14 24:gb\_est15

25:gb\_est16 26:gb\_est17 27:gb\_est18 28:gb\_est19 29:gb\_est20

Statistics: Mean 11.212; Variance 2.135; scale 5.252

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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3	382	31.8	533.13	N29730	yw78h03.s1 Homo sapien	0.00e+00
4	381	31.7	564.13	N32604	yw95d03.s1 Homo sapien	0.00e+00
5	379	31.5	442.13	N32233	yw81f08.s1 Homo sapien	0.00e+00
6	379	31.5	473.13	N27302	yw71f12.s1 Homo sapien	0.00e+00
7	379	31.5	548.13	N30036	yw80b11.s1 Homo sapien	0.00e+00
8	377	31.4	566.13	N30831	yw70b04.s1 Homo sapien	0.00e+00
9	373	31.0	563.13	N31955	yw89a07.s1 Homo sapien	0.00e+00
10	371	30.9	473.25	AA400910	zc71h09.s1 Soares test	0.00e+00
11	372	30.9	479.13	N30684	yw77b04.s1 Homo sapien	0.00e+00
12	365	30.4	446.13	N31616	yw84a02.s1 Homo sapien	0.00e+00
13	363	30.2	526.28	AA644163	af62d08.s1 Soares NHM	0.00e+00

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c	16	345	28.7	419.16	H93774	yw60b03.s1 Soares plac	0.00e+00
c	17	341	28.5	403.13	N26397	yw76g11.s1 Homo sapien	0.00e+00
c	18	335	27.0	441.13	N30741	yw74b04.s1 Homo sapien	0.00e+00
c	19	322	26.8	422.11	R23214	yh28a03.s1 Homo sapien	0.00e+00
c	20	319	26.5	515.13	N30608	yw72c07.s1 Homo sapien	0.00e+00
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c	29	288	24.0	386.16	H94451	yw59g08.s1 Soares plac	0.00e+00
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c	32	278	23.1	329.13	H87156	yw15b04.s1 Homo sapien	0.00e+00
c	33	276	23.0	311.10	T47334	y10e11.s1 Homo sapien	0.00e+00
c	34	269	22.4	284.13	H93656	yw58a11.s1 Homo sapien	0.00e+00
c	35	267	22.2	303.13	H86993	yw15b10.s1 Homo sapien	0.00e+00
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c	42	228	19.0	341.12	T29543	EST83815 Homo sapiens	0.00e+00
c	43	222	18.5	244.16	H94107	yw58b09.s1 Soares plac	0.00e+00
c	44	217	18.1	255.11	R63352	y107b10.s1 Homo sapien	0.00e+00
c	45	214	17.8	275.10	T47316	y10c02.s1 Homo sapien	0.00e+00

## ALIGNMENTS

RESULT	LOCUS	1	N32759	601 bp	mRNA	EST	10-JAN-1996
DEFINITION			yw91b05.s1 Homo sapiens CDNA clone 259569 3' similar to gb:U00117				
ACCESSION			N32759				
KEYWORDS			CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);				
SOURCE			human clone-259569 primer-m13 -40 forward library-Soares placenta				
			8to9weeks 2NBP8CO9W vector-pRT30 (pharmacia) with a modified				
			polylinker host-DH10B (ampicillin resistant) Raitel-Not I				
			Raitel2-Eco RI two placentae: one from 8 weeks and another from 9				
			weeks post conception. 1st strand cDNA was primed with a Not I -				
			oligo(dT) primer				
			[5'-TGTTACCAATCTGAGTGGAGGCGCGCATTTTCTTTTCTTTT-3']				
			double-stranded cDNA was size selected, ligated to Eco RI adaptors				
			(Pharmacia), digested with Not I and cloned into the Not I and Eco				
			RI sites of a modified pRT30 vector (Pharmacia). Library				
			constructed by Bento Soares and M. Fatima Boudado.				
ORGANISM			Homo sapiens				
			Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;				
			Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;				
			Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;				
			Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.				
REFERENCE			1 (bases 1 to 601)				
AUTHORS			Hillier, L., Clark, N., Dubugue, T., Elliston, K., Hawkins, M.,				
			Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,				
			Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,				
			Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and				
			Wilson, R.				
TITLE			The WashU-Merck EST Project				
JOURNAL			Unpublished (1995)				
COMMENT			Contact: Wilson RK				
			WashU-Merck EST Project				
			Washington University School of Medicine				
			4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence stops: 387  
Source: IMAGE Consortium, LNLN  
This clone is available royalty-free through LNLN; contact the  
IMAGE Consortium (infoimage.lnl.gov) for further information.  
Location/Qualifiers  
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BASE COUNT 112 a 154 c 219 g 110 t 6 others  
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CP 1202 TTATGTGGAGATCGGGGTGTCCGAGGCCCGCGAGTGGGCTTGAAGGCT 1143  
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Db 77 GGGGGAGAGGCGCTTTGAGAGAGAGAGTCTCTGAGAGCGGGGCTATCAGAGTCAAGGG 136  
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CP 1142 GGGGGAGAGGCGCTTTGAGAGAGAGAGTCTCTGAGAGCGGGGCTATCAGAGTCAAGGG 1083  
|||||  
Db 137 GTGTCTCTGGAGACCC-GCAGTCAGTGTGTCTGCGGGCGGAGTGCATTTGACAGCT 195  
|||||  
CP 1082 GTGTCTCTGGAGACCCCGCGAGTGTGTCTGCGGGCGGAGTGCATTTGACAGCT 1023  
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Db 196 GAGAGCCAGCGGTGAGAGACCCAGGGGTTACAGCGCGCGGAGCCAGAGAGCGGAT 255  
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CP 1022 GAGAGCCAGCGGTGAGAGACCCAGGGGTTACAGCGCGCGGAGCCAGAGAGCGGAT 963  
|||||  
Db 256 GGACTCGAAGCGCATATGCGGTAGTTGCACACCACTGAGGAGCGCGGAGAGACCC 315  
|||||  
CP 962 GGACTCGAAGCGCATATGCGGTAGTTGCACACCACTGAGGAGCGCGGAGAGACCC 903  
|||||  
Db 316 TTGCAGCAGCGGGTATGAGTGGGAGGAGGAGAGTGGTGTGAGAGGAT 375  
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CP 902 CTGCAGCAGCGGGTATGAGTGGGAGGAGGAGAGTGGTGTGAGAGGAT 843  
|||||  
Db 376 GCACAGCGGGAGCGGCTCTCTCCACAGCAGGAGGATGAGGAGCGGAGCGGATG 435  
|||||  
CP 842 GCACAGCGGGAGCGGCTCTCTCCACAGCAGGAGGATGAGGAGCGGAGCGGATG 783  
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RESULT 2  
LOCUS N30276 537 bp mRNA EST 05-JAN-1996

DEFINITION yw69d04.s1 Homo sapiens cDNA clone 257479 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.

ACCESSION N30276  
NID g1148796  
KEYWORDS EST.  
SOURCE human clone-257479 primer-m13 -40 forward library-Soares placenta  
289weeks 2NDHPto3W vector-pT73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) RstIcl-Not I  
RstIcl-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTTACCAATCTGAGTGGAGCGCGGATTTTCTTTTCTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library  
constructed by Bento Soares and M. Fatima Bonaldo.  
Homo sapiens  
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostoma; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 537)

AUTHORS Hillier, L., Clark, N., Dubuque, J., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rife, L., Rife, L., Rife, L., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The Mashu-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

CONTACT: Wilson RK  
Mashu-Merck EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence stops: 313  
Source: IMAGE Consortium, LNLN  
This clone is available royalty-free through LNLN; contact the  
IMAGE Consortium (infoimage.lnl.gov) for further information.  
Location/Qualifiers  
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CP 1202 TTATGTGGAGATCGGGGTGTCCGAGGCCCGCGAGTGGGCTTGAAGGCT 1143  
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Db 77 GGGGGAGAGGCGCTTTGAGAGAGAGAGTCTCTGAGAGCGGGGCTATCAGAGTCAAGGG 136  
|||||  
CP 1142 GGGGGAGAGGCGCTTTGAGAGAGAGAGTCTCTGAGAGCGGGGCTATCAGAGTCAAGGG 1083  
|||||  
Db 137 GTGTCTCTGGAGACCC-GCAGTCAGTGTGTCTGCGGGCGGAGTGCATTTGACAGCT 195  
|||||  
CP 1082 GTGTCTCTGGAGACCCCGCGAGTGTGTCTGCGGGCGGAGTGCATTTGACAGCT 1023  
|||||  
Db 196 GAGAGCCAGCGGTGAGAGACCCAGGGGTTACAGCGCGCGGAGCCAGAGAGCGGAT 254  
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CP 1022 GAGAGCCAGCGGTGAGAGACCCAGGGGTTACAGCGCGCGGAGCCAGAGAGCGGAT 964  
|||||  
Db 255 TGACTCGAAGCGCATATGCGGTAGTTGCACACCACTGAGGAGCGCGGAGAGACCC 314  
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CP 963 TGACTCGAAGCGCATATGCGGTAGTTGCACACCACTGAGGAGCGCGGAGAGACCC 904  
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Db 315 CCCGCGAGCAGCGGGTATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374  
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CP 903 CC-TGCACAGCAGCGGGTATGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 845  
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Db 375 ATGCACAGCGGGAGCGGCTCTCTCCACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 434  
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CP 844 ATGCACAGCGGGAGCGGCTCTCTCCACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG 785  
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Db 435 GGCNAAGC 442  
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CP 784 GGACCAGC 777  
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RESULT 3  
LOCUS N29730 593 bp mRNA EST 05-JAN-1996

DEFINITION yw78d03.s1 Homo sapiens cDNA clone 258389 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.

ACCESSION N29730  
NID g1148250  
KEYWORDS EST.  
SOURCE human clone-258389 primer-m13 -40 forward library-Soares placenta

8to9weeks 2Nbp8to9w vector-pT7J3D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) RstIeI-Not I RstIe2-Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 (5'-TGTACCAATCTGAAGTGGAGCGCGCGCATTTT-TTTT-TTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.

## ORGANISM

Homo sapiens  
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 593)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasks, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished (1995)

## TITLE

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 368  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Location/Qualifiers  
 1..593  
 source  
 /organism="Homo sapiens"  
 /clone="258389"

## FEATURES

BASE COUNT 109 a 151 c 216 g 111 t 6 others  
 ORIGIN

Query Match 31.8%; Score 382; DB 13; Length 593;  
 Best Local Similarity 96.7%; Pred. NO. 0.00e+00;

Matches 414; Conservative 0; Mismatches 10; Indels 4; Gaps 4;

Db 18 TTATTTGGAGAGATGGGGTGTCCGAGGCGCCCGGAGTCCGGATGGGCTTGAAGGCT 77  
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 Cp 1202 TTATTTGGAGAGATGGGGTGTCCGAGGCGCCCGGAGTCCGGATGGGCTTGAAGGCT 1143  
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 Db 78 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCGAAGCGGGGGTTCATCAGAGTCAAGG 137  
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 Cp 1142 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCGAAGCGGGGGTTCATCAGAGTCAAGG 1083  
 |||||||  
 Db 138 GTGTCTCTTGGAGCCCG-CAAGTCAAGTGTGTCTGCGCGCCGAGAGTCCAGATTGACAGCT 196  
 |||||||  
 Cp 1082 GTGTCTCTTGGAGCCCG-CAAGTCAAGTGTGTCTGCGCGCCGAGAGTCCAGATTGACAGCT 1023  
 |||||||  
 Db 197 GAGAGCAGCGGCTAGAGAGCAAGCGGGGTTCAGCGCGCGNG-CAGCCAGGAGCGCGAT 255  
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 Cp 1022 GAGAGCAGCGGCTAGAGAGCAAGCGGGGTTCAGCGCGCGNG-CAGCCAGGAGCGCGAT 963  
 |||||||  
 Db 256 GAGCTCGAAGCGGACATCGCGGTAGTTGACACACCACTGAGGAGCGGCGCAAGCCACC 315  
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 Cp 962 GAGCTCGAAGCGGACATCGCGGTAGTTGACACACCACTGAGGAGCGGCGGAGGAGACCCC 903  
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 Db 316 CTCACAGACCGGGGTATGTTGGGGAGTAGCGGACAGATGTTGTTGACGGTGA 375  
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 Cp 902 CTCACAGACCGGGGTATGTTGGGGAGTAGCGGACAGATGTTGTTGACGGTGA 844  
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 Db 376 TGACACAGGGGCGGCGCTCTTCTCCACAGCCAGCANGTGTGACATTGATGGGCGGACCGT 435  
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Cp 843 TGACACAGGGGCGGACCGCTCTCTCCACAGCAGCGGT-GGCAATTGATGGGCGGACCGG 785  
 Db 436 GGCCAGC 443  
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 Cp 784 GGACGAGC 777

RESULT 4  
 LOCUS N32604 564 bp mRNA EST 10-JAN-1996

## DEFINITION

yw95d03.s1 Homo sapiens cDNA clone 259973 3' similar to gb:J00117  
 CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.

## ACCESSION

N32604  
 NID  
 G1153003

## KEYWORDS

EST.

## SOURCE

human clone-259973 primer-m13 -40 forward library-Soares placenta  
 8to9weeks 2Nbp8to9w vector-pT7J3D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) RstIeI-Not I RstIe2-Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 (5'-TGTACCAATCTGAAGTGGAGCGCGCGCATTTT-TTTT-TTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.

## ORGANISM

Homo sapiens  
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 564)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasks, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished (1995)

## TITLE

The WashU-Merck EST Project

## COMMENT

Contact: Wilson RK  
 WashU-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 High quality sequence stops: 364  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 Location/Qualifiers  
 1..564  
 source  
 /organism="Homo sapiens"  
 /clone="259973"

## FEATURES

BASE COUNT 103 a 148 c 206 g 99 t 8 others  
 ORIGIN

Query Match 31.7%; Score 381; DB 13; Length 564;  
 Best Local Similarity 96.5%; Pred. NO. 0.00e+00;  
 Matches 410; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

Db 17 TTATTTGGAGAGATGGGGTGTCCGAGGCGCCCGGAGTCCGGATGGGCTTGAAGGCT 76  
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 Cp 1202 TTATTTGGAGAGATGGGGTGTCCGAGGCGCCCGGAGTCCGGATGGGCTTGAAGGCT 1143  
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 Db 77 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCGAAGCGGGGTTCATCAGAGTCAAGG 136  
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 Cp 1142 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCGAAGCGGGGTTCATCAGAGTCAAGG 1083  
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 Db 137 GTGTCTCTTGGAGCCCG-CAAGTCAAGTGTGTCTGCGCGCCGAGAGTCCAGATTGACAGCT 195  
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CP	1082	GTGGCCCTTGGAGCCCCCGCAGTCAGTGTGCTGTGGGGGGAGAGTGCACATTGACAGCT	1023
Db	196	GAGAGCCACGGGCGGTAAGAGGACACGAGGGGTTACGGCCCGCGGGACCCAAAGGAGACGGAT	255
CP	1022	GAGAGCCACAGCGTAGGAGAGCACCGGGGTTACCGCCGGGGGAGCGACAGGAGACCCGGAT	963
Db	256	GGACTCGAAGCGCACATGCGGGTAGTTGCACACCACCTGAGGCGAGGCGCGGACAGACCCC	315
CP	962	GGACTCGAAGCGCACATGCGGGTAGTTGCACACCACCTGAGGCGAGGCGGGGAGAGACCCC	903
Db	316	CTTGACGACGCGGGGTCAATGGTGGGGGACGATGC - GGCACAGATGGTGTGTTGACGGTGA	374
CP	902	CT - GCGACGACCGGGGTCAATGGTGGGGGACGATGC - GGCACAGATGGTGTGTTGACGGTGA	844
Db	375	TGCACACGGGGCAGCGCCTCTTCTCCACAGCCAGGAGGTGGCATTTGATGGGCGGACCGCTG	434
CP	843	TGCACACGGGGCAGCGCCTCTTCTCCACAGCCAGGAGGTGGCATTTGATGGGCGGACCGCTG	784
Db	435	GCCNA 439	
CP	783	GACCA 779	

RESULT	5				
LOCUS	N32233	442 bp	mrna	EST	10-JAN-1996
DEFINITION	y816f8.s1 Homo sapiens cDNA clone 258663 3' similar to gp:J00117				
DESCRIPTION	CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN)).				

ACCESSION	N32223
NID	g1152632
KEYWORDS	EST.
SOURCE	human clone-258663 primer-m3 -40 forward library-Soures placenta

**SOURCE**  
human clone#2586b3 primer-m13 -40 forward library-Soares placenta  
80c9weeks 2NDPR6105W vector-PT7373 (Pharmacia) with a modified  
polylinker host-DH10 (ampicillin resistant) Rstel+Not I  
Rstle+Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTCACCATCTCGAGTGGAGGCGCGCGCATTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapted  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library  
constructed by Benito Soares and M. Fatima Bonaldo.

ORGANISM

Homo sapiens  
Eukaryotae: Metazoa: Eumetazoa: Bilateria: Coelomata:  
Deuterostomata: Chordata: Vertebrata: Gnathostomata: Osteichthyes:  
Sarcopterygii: Chosonata: Tetrapoda: Amniota: Mammalia: Theria:  
Eutheria: Archonta: Primates: Catarrhini: Hominiidae: Homo:  
1 (bases 1 to 442)

REFERENCE

AUTHORS  
Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucabst, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifeikin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Weterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	

**FEATURES**

Contact: Wilson RK  
Mashu-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel.: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu

High quality sequence stops: 364  
Source: IMAGE Consortium, LML

This clone is available royalty-free through LML; contact the  
IMAGE Consortium ([inf@image.lml.gov](mailto:inf@image.lml.gov)) for further information.  
Location/Qualifiers

source	1. .442				
	/organism="Homo sapiens"				
	/clone="258663"				
mrna	<1. .5442				
BASE COUNT	85 a	110 c	174 g	68 t	5 others

ORIGIN	
Query Match	31.5%; Score 379; DB 13; Length 442;
Best Local Similarity	94.6%; Pred. No. 0.00e+00;
Matches 402; Conservative	0; Mismatches 22; Indels 1; Gaps 1;

Db 17 TTATTGTGGAGATCCGGGCTGTCCGAGGGCCCCGGAGTCGGGATGCACTTGGAAAGCT 76  
|||||  
Cp 1202 TTATTGTGGAGATCCGGGCTGTCCGAGGGCCCCGGAGTCGGGATGCGCTTGGAAAGCT 1143

Db 77 GGGGGGAGGGCCCTTTTGAGGAAGAAGATCCTGGAAACCGGGGGTCATCAACAGGTCAAAGG 136  
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Cp 1142 GGGGGGAGGGCCCTTTTGAGGAAGAAGATCCTGGAAACCGGGGGTCATCAACAGGTCAAAGG 1083  
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Db 137 GTGGTCCTTGGGACCCCGCAAGTCAGTTGGTGTGCGGCGGAGAGTGCACATTGACAGC 196  
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CP 1082 GTGTGCTTTGGGACCCCGCAGTAGT-GGTGTGCGCGCGGAGAGTGCACATTGACAGC 1024

D6 197 TGAGAGCCACGGCGTAGGAGACACGGGGTTCACGCCCMGGCAGCCANGGAGCCGGA 256  
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CP 1023 TGAGAGCCACGCCTAGGAGACACGGGGTTCACGCCCMGGCAGCCANGGAGCCGGA 964

Db	257	TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACTGAGCGAGGCGCNCAAGACAC	316
Dp	257		
Cp	963	TGGACTCGAAGCGCACATCGCGGTAGTTGCACACCACTGAGCGAGGCGCGGAGGACCC	904

Db 317 CCTGCAGCACC GGGT CATGTG GGGGAGTAA CCGGCACAGATGGTGTGACGGTNA 376  
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 Cp 903 CCTGCAGCACC GGGT CATGTG GGGGAGTAA CCGGCACAGATGGTGTGACGGTGA 844  
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377 TGCACACGGGGCAGCCCTCTCTCCACAGCAGCAGGTGGCATTTGATGGGGCGGCANCGT 436

[illegible]

	op	100	Shen's 772
RESULT	6	N07J003	472 ha
LOCUS			-BWA
			MOM
			90-080-100E

LOCUS	121302	4/3 UP	11K1NA	BS1	45-DEC-1993
DEFINITION	yw71fi2.s1 Homo sapiens cDNA clone 257711 3' similar to qb:J00117				
DESCRIPTION	CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN)..				
ORIGIN	CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN)..				

ACCESSION	N21302
NUM	g1141650
KEYWORDS	EST.
SOURCE	human clone-257711 primer-m13 -40 forward library=Scars placenter

ORGANISM Homo sapiens

**REFERENCE**  
**AUTHORS**  
Eulatyrotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Saccopterygii; Chonadata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Carnivori; Homiidae; Homo. 1 (bases 1 to 473)  
Hillier, L., Clark, N., Dubouche, T., Elliston, R., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Riklin, L., Rohlfs, T., Soares, M., Tan, F., Tsvetakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK

WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 225  
Source: IMAGE Consortium, LNLN  
This clone is available royalty-free through LNLN; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

## FEATURES

Source  
1. .473  
/organism="Homo sapiens"  
/clone="257711"

BASE COUNT 87 a 122 c 182 g 76 t 6 others

## ORIGIN

Query Match 31.5%; Score 379; DB 13; Length 473;  
Best Local Similarity 95.5%; Pred. No. 0.00e+00;  
Matches 402; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

Db 18 TTATGTGGAGAGATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 77  
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Cp 1202 TTATGTGGAGAGATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 1143  
Db 78 GGGGGAGGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 137  
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Cp 1142 GGGGGAGGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083  
Db 138 GTGTCTTGGAGT 197  
Cp 1082 GTGTCTTGGAGT 1023  
Db 198 GAGAGCCAGGGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256  
Cp 1022 GAGAGCCAGGGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 963  
Db 257 GGACTCGAAGGCGCATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 316  
Cp 962 GGACTCGAAGGCGCATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 903  
Db 317 TTGACAGCAGGGGCTGATGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 376  
Cp 902 CTGACAGCAGGGGCTGATGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 844  
Db 377 TGCACAGCAGGGGCGCCGCTTCTCCACAGCCAGGGGTGGCATTTGATGGGCGCACCGTN 436  
Cp 843 TGCACAGCAGGGGCGCCGCTTCTCTCCACAGCCAGGGGTGGCATTTGATGGGCGCACCGTG 784  
Db 437 G 437  
Cp 783 G 783

RESULT 7  
LOCUS N30036 548 bp mRNA EST 05-JAN-1996  
DEFINITION yw80b11.s1 Homo sapiens cDNA clone 258525 3' similar to gb:J00117  
CHORIGONADOTROBIN BETA CHAIN PRECURSOR (HUMAN);.  
ACCESSION N30036  
NID g1148556  
KEYWORDS EST.  
SOURCE human clone-258525 primer-m13 -40 forward library=Soares placenta  
8to9weeks 2NDHP109W vector=PT73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant). Raitel-Not I  
Raitel-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTACCAATCTGAAGTGGAGCGCCGCGATTTTATTTTATTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library

## ORGANISM

constructed by Bento Soares and M. Fatima Bonaldo.

Homo sapiens

Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

1 (bases 1 to 548)

## AUTHORS

Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, B., Rong, F., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and  
Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 333  
Source: IMAGE Consortium, LNLN  
This clone is available royalty-free through LNLN; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

## FEATURES

Source  
1. .548  
/organism="Homo sapiens"  
/clone="258525"

BASE COUNT 99 a 143 c 206 g 93 t 7 others

## ORIGIN

Query Match 31.5%; Score 379; DB 13; Length 548;  
Best Local Similarity 96.9%; Pred. No. 0.00e+00;  
Matches 410; Conservative 0; Mismatches 9; Indels 4; Gaps 4;

Db 18 TTATGTGGAGAGATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 77  
|||||  
Cp 1202 TTATGTGGAGAGATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 1143  
Db 78 GGGGGAGGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 137  
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Cp 1142 GGGGGAGGGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083  
Db 138 GTGTCTTGGAGT 196  
Cp 1082 GTGTCTTGGAGT 1023  
Db 197 GAGAGCCAGGGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256  
Cp 1022 GAGAGCCAGGGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964  
Db 257 GGACTCGAAGGCGCATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 316  
Cp 962 GGACTCGAAGGCGCATCGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 904  
Db 317 CTTGACAGCAGGGGCTGATGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 376  
Cp 903 CTTGACAGCAGGGGCTGATGGGGTGTCCGAGGGCCCGGAGTGGGATGGAGGCT 846  
Db 377 GATGACAGCAGGGGCGCCGCTTCTCCACAGCCAGGGGTGGCATTTGATGGGCGCACCG 436  
Cp 845 GATGACAGCAGGGGCGCCGCTTCTCTCCACAGCCAGGGGTGGCATTTGATGGGCGCACCG 786  
Db 437 TGG 439  
Cp 785 TGG 783

RESULT 8  
LOCUS N30831 566 bp mRNA EST 05-JAN-1996

DEFINITION yw70b04.s1 Homo sapiens cDNA clone 257551 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.  
ACCESSION N30831  
NID g1149351  
KEYWORDS EST.  
SOURCE human clone-257551 primer-m13 -40 forward library-Soares placenta  
8to9weeks 2NbpP8to9w vector-pt73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) Raitel-Not I  
Raitel2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[3'-TGTTACCAATCTGAGTGGAGCGCGCGCATTTTCTTTTCTTTT-3']  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia) library  
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 566)  
Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merk EST Project  
Unpublished (1995)

TITLE JOURNAL  
COMMENT

ORGANISM Contact: Wilson RK  
WashU-Merk EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 400  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source 1..566  
/organism="Homo sapiens"  
/clone="257551"

BASE COUNT mRNA  
ORIGIN 103 a 148 c 209 g 100 t 6 others

Query Match 31.4%; Score 377; DB 13; Length 566;  
Best Local Similarity 96.4%; Pred. No. 0.00e+00;  
Matches 407; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

Db 17 TTTTGTGGAGAGATGGGGTGTCCAGAGGCCCCGGAGTGGGATGACTGGAAGGCT 76  
|||  
Cp 1202 TTTTGTGGAGAGATGGGGTGTCCAGAGGCCCCGGAGTGGGATGACTGGAAGGCT 1143  
|||  
Db 77 GGGGGAGAGGCGCTTGGAGAGAGAGTCTCGAAGCGGGGCTCATCAGAGTCAAGG 136  
|||  
Cp 1142 GGGGGAGAGGCGCTTGGAGAGAGAGTCTCGAAGCGGGGCTCATCAGAGTCAAGG 1083  
|||  
Db 137 GTGTGCTTGTGGG-CGCCCGAGTCACTGTGCTGCGGCGGACAGTGCACATTTGACAGCT 195  
|||  
Cp 1082 GTGTGCTTGTGGGAGAGAGTCACTGTGCTGCGGCGGACAGTGCACATTTGACAGCT 1023  
|||  
Db 196 GAGAGCCAGCGCTTAGAGAGACAGGGGTTACAGCGCGGCGGACAGCCAGGAGCCGGA 255  
|||  
Cp 1022 GAGAGCCAGCGCTTAGAGAGACAGGGGTTACAGCGCGGCGGACAGCA-GGAGCGCGGA 964  
|||  
Db 256 TGAGCTCGAAGCGCAATAGCGGGGTAGTTGACACCACTGAGGCGAGGGCGGACACCC 315  
|||  
Cp 963 TGAGCTCGAAGCGCACATGCGGG-TAGTTGACACCACTGAGGCGAGGGCGGAGGAGCC 905  
|||

Db 316 CCTGCAGCAGCGGGGTCAATGGTGGGACAGTAGCGGTCAACAGATGGTGGTACGGTG 375  
|||  
Cp 904 CCTGCAGCAGCGGGGTCAATGGTGGGACAGTAGCGGTCAACAGATGGTGGTACGGTG 845  
|||  
Db 376 ATGCACAGCGGGGAGCGCCCTCTTCTCCACAGCCAGGATGGATGGGCGGACCGT 435  
|||  
Cp 844 ATGCACAGCGGGGAGCGCCCTCTTCTCCACAGCCAGGATGGATGGGCGGACCGT 785  
|||  
Db 436 GG 437  
||  
Cp 784 GG 783

RESULT 9  
LOCUS N31955 563 bp mRNA EST 10-JAN-1996

DEFINITION yw89a07.s1 Homo sapiens cDNA clone 259380 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.  
ACCESSION N31955  
NID g1152354  
KEYWORDS EST.  
SOURCE human clone-259380 primer-m13 -40 forward library-Soares placenta  
8to9weeks 2NbpP8to9w vector-pt73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) Raitel-Not I  
Raitel2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[3'-TGTTACCAATCTGAGTGGAGCGCGCGCATTTTCTTTTCTTTT-3']  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia) library  
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 563)  
Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merk EST Project  
Unpublished (1995)

TITLE JOURNAL  
COMMENT

ORGANISM Contact: Wilson RK  
WashU-Merk EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 335  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source 1..563  
/organism="Homo sapiens"  
/clone="259380"

BASE COUNT mRNA  
ORIGIN 101 a 148 c 208 g 103 t 3 others

Query Match 31.0%; Score 373; DB 13; Length 563;  
Best Local Similarity 97.0%; Pred. No. 0.00e+00;  
Matches 416; Conservative 0; Mismatches 7; Indels 6; Gaps 6;

Db 17 TTTTGTGGAGAGATGGGGTGTCCAGAGGCCCCGGAGTGGGATGACTGGAAGGCT 76  
|||  
Cp 1202 TTTTGTGGAGAGATGGGGTGTCCAGAGGCCCCGGAGTGGGATGACTGGAAGGCT 1143  
|||

Db 77 GGGGGAGGGGCTTTGAGAGAGAGAGCTGGAAGCGGGGGTCATCACAGGCAAGG 136  
|||||  
Cp 1142 GGGGGAGGGGCTTTGAGAGAGAGAGCTGGAAGCGGGGGTCATCACAGGCAAGG 1083  
Db 137 GTGCTCTTGGAGCCCG-CCAGTCAGTTGGTGTGCGCGGCGAGAGTCACATTGACAGC 195  
|||||  
Cp 1082 GTGCTCTTGGAGCCCGCGAGTCAGT-GGTGCGCGGCGGCGAGAGTCACATTGACAGC 1024  
Db 196 TGAGAGCCAGCGGCTTGAAGAGACCGGGGTTCAAGCCGCGGCGCAAGCCAGAGAGCCG 255  
|||||  
Cp 1023 TGAGAGCCAGCGGCT-AGGAGACCACCGGGGTTCAAGCCGCGGCGGCGAGCA-GGAGCCG 966  
Db 256 GATGAGCTGAGAGCGACATCGGGGCTGTGACACACCACTGAGGCGGCGGCAAG-AC 314  
|||||  
Cp 965 GATGAGCTGAGAGCGACATCGGGGCTGTGACACCACTGAGGCGGCGGCGGAGAC 906  
Db 315 CCC-TGCAGCAGCGGCTCATGTGTGGGCGAGTAGCCGCGACAGATGGTGTGACGCT 373  
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Cp 905 CCCCTGAGACCGCGGTCTATGGTGGGCGAGTAGCCGCGACAGATGGTGTGACGCT 846  
Db 374 GATGACACAGCGGGGCGAGCCCTCTCTTCACACAGCCAGGGTGCAATGATGGGCGGCGACCG 433  
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Cp 845 GATGACACAGCGGGGCGAGCCCTCTCTTCACACAGCCAGGGTGCAATGATGGGCGGCGACCG 786  
Db 434 TGGCCAGC 442  
|||  
Cp 785 TGGACCGC 777

RESULT 10  
LOCUS AA400910 473 bp mRNA EST 12-ANG-1997

DEFINITION  
z71h09.s1 Soares testis NHT Homo sapiens cDNA clone 727841 3'  
similar to gb:J00117 CHORIOGNADOTROPIN BETA CHAIN PRECURSOR  
(HUMAN).  
AA400910  
NID 52054783  
KEYWORDS  
EST.  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;  
Homo.  
1 (bases 1 to 473)  
REFERENCE  
AUTHORS  
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,  
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,  
Moore,B., Schellenberg,K., Steppe,M., Tan,F., Theising,B.,  
White,Y., Wylie,T., Waterston,R. and Wilson,R.  
WashU-Merck EST Project 1997  
Unpublished (1997)

TITLE  
JOURNAL  
COMMENT

CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LNLN; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 640 Std Error: 0.00  
Seq primer: -41m13 fwd. RT from Amersham  
High quality sequence stop: 392.  
Location/Qualifiers  
1. 473  
/organism="Homo sapiens"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker. Site\_1: Not I. Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5'.  
TGTTACCAATCTGAAGTGGAGCGGCGCCCAATTTTTTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73D vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo.  
/db\_xref="taxon:9606"  
/clone="727841"  
/clone\_lib="Soares testis NHT"  
/sex="male"  
/lab\_host="DH10B"  
/db\_xref="GDB:5924752"  
complement(<1..>473)  
BASE COUNT 84 a 120 c 190 g 78 t 1 others  
ORIGIN

Query Match 30.9%; Score 371; DB 25; Length 473;  
Best Local Similarity 97.6%; Pred. No. 0.00e+00;  
Matches 405; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

Db 20 TTAATGGGAGGATGGGGTGTCTGAGGGGCGGAGTCGGGATGGGCTTGAAGGCT 79  
|||||  
Cp 1202 TTAATGGGAGGATGGGGTGTCTGAGGGGCGGAGTCGGGATGGGCTTGAAGGCT 1143  
Db 80 GGGGGAGGGGCTTTGAGAGAGAGAGAGCGCTGAAAGCGGGGTCATCAGAGTCAAGG 139  
|||||  
Cp 1142 GGGGGAGGGGCTTTGAGAGAGAGAGTCTGGAAGCGGGGTCATCAGAGTCAAGG 1083  
Db 140 GTGGCTCTTGGAGCCCG-CCAGTCAGTGTGTGCGGCGGCGAGATGACAGCT 198  
|||||  
Cp 1082 GTGGCTCTTGGAGCCCGCGAGTCAGTGTGCGGCGGCGAGATGACAGCT 1023  
Db 199 GAGAGCCAGCGGCTTGAAGAGAGAGAGAGCGGTCAGCGGCGGCGG-CAGCAGAGAGCGCGAT 257  
|||||  
Cp 1022 GAGAGCCAGCGGCTTGAAGAGAGAGAGAGCGGTCAGCGGCGGCGGCGAGAGCGGAT 963  
Db 258 GAGCTGAGAGCGGAGATCGGGGAGTGTGACACACCACTGAGGAGAGCGGCGGAG-ACCCC 316  
|||||  
Cp 962 GAGCTGAGAGCGGAGATCGGGGAGTGTGACACACCACTGAGGAGAGCGGCGGAGAGCCCC 903  
Db 317 -TGCAGCAGCGGGGTCATGTGTGGGCGAGTAGC-GGCACAGATGTGTGTGACGCTGAT 374  
|||||  
Cp 902 CTCAGACAGCGGGGTCATGTGTGGGCGAGTAGCAGGCGGCGAGATGTGTGTGACGCTGAT 843  
Db 375 GCACAGCGGGGAGCCCTCTCTTCACACAGCCAGGGTGCAATGATGGGCGGCGAC 429  
|||||  
Cp 842 GCACAGCGGGGAGCCCTCTCTTCACACAGCCAGGGTGCAATGATGGGCGGCGAC 788

RESULT 11  
LOCUS N30684 479 bp mRNA EST 05-JAN-1996

DEFINITION  
yw77h04.s1 Homo sapiens cDNA clone 258295 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN).  
N30684  
NID 51149204  
KEYWORDS  
SOURCE  
EST.  
human clone-258295 primer-m13 -40 forward library-Soares placenta  
8to9weeks 2NBP8to9w vector-pT73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) Rsite1-Not I  
Rsite2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-GTTACCAATCTGAAGTGGAGCGGCGCGCATTTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73D vector (Pharmacia). Library  
constructed by Bento Soares and M. Fatima Bonaldo.  
Homo sapiens  
Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 479)  
REFERENCE  
AUTHORS  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

**TITLE** POLMAN, M., HULTMAN, M., KUCSBA, T., LE, M., LENNON, G., MATTE, M., PARSONS, J., RIFKIN, L., ROHLFING, T., SOARES, M., TAN, F., TREVASKIS, E., WATERSTON, R., WILLIAMSON, A., WOHLDMANN, P. and WILSON, R.  
**JOURNAL** The Washu-Merck EST Project  
**COPIES** Unpublished (1995)



RESULT 13  
LOCUS AA644163 526 bp mRNA EST 27-OCT-1997  
DEFINITION af62d08.s1 Soares NHMPu S1 Homo sapiens cDNA clone 1046607 3' similar to gb:J00117 CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);  
ACCESSION AA644163  
NID 92569381  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 526)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project unpublished (1997)  
TITLE JOURNAL  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: -40m13 fwd. Et from Amersham  
High quality sequence stop: 335.  
Location/Qualifiers  
1. 526  
/organism="Homo sapiens"  
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."  
/db\_xref="taxon:9606"  
/clone="1046607"  
/clone\_lib="Soares NHMPu S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"  
BASE COUNT 100 a 140 c 201 g 85 t  
ORIGIN  
Query Match 30.2%; Score 363; DB 28; Length 526;  
Best Local Similarity 96.7%; Pred. No. 0.00e+00;  
Matches 407; Conservative 0; Mismatches 8; Indels 6; Gaps 6;  
DB 16 TTATGTGGAGATCGGGGTGTCGAGAGCCCGGAGTCCGATGACTTGAAGGCT 75  
CP 1202 TTATGTGGAGATCGGGGTGTCGAGAGCCCGGAGTCCGATGACTTGAAGGCT 1143  
DB 76 GGCAGAGAGGCGCTTAAAGAGAGAGTCTGAAGCGGGGTCATCAGAGTCAAGG 135  
CP 1142 GGGGAGAGGCGCTTGAAGAGAGAGTCTGAAGCGGGGTCATCAGAGTCAAGG 1083  
DB 136 GTGTCTCTTGGAGCCGACAGTCACTGTGCTGCGCGCGCAGAGTGCACATTGACGCT 195  
CP 1082 GTGTCTCTTGGAGCCGACAGTCACTGTGCTGCGCGCGCAGAGTGCACATTGACGCT 1023  
DB 136 GAGAGCCAGCGGCTAGAGAGACCAAGGCGTTCAAGCGCGCGG-CAGCCAGGAGCCGAT 254

CP 1022 GAGAGCCAGACGCTAGAGAGACACGCGGCTTCACGCGCGCGGCGGAGGAGCCGAT 963  
DB 255 GGAATCGAAGCGCACATCGCGGTAGTTCACACACCACTGAGCAGGCGGCGG-AGGACCCC 313  
CP 962 GGACTCGAAGCGCACATCGCGGTAGTTCACACACCACTGAGCAGGCGGAGAGGAGCC 903  
DB 314 -TGACGACGCGGGTCACTGTGCGGCACTAGC-GGCACAGATGTGTGTGTGACGCTAT 371  
CP 902 CTGACGACGCGGGTCACTGTGCGGCACTAGC-CGCACAGATGTGTGTGTGACGCTAT 843  
DB 372 GGCACGCGGCGAGCCCTCTTCACACAGCAGGCGGTCATTGAGGCGCGG-ACCGTG 430  
CP 842 G-CACACGCGGCGAGCCCTCTTCACACAGCAGGCGGTCATTGAGGCGCGGCGG 784  
DB 431 G 431  
CP 783 G 783  
RESULT 14  
LOCUS AA232905 400 bp mRNA EST 06-NOV-1997  
DEFINITION z146c04.s1 Soares NHMPu S1 Homo sapiens cDNA clone 666438 3' similar to gb:J00117 CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);  
ACCESSION AA232905  
NID 91855917  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 400)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheilenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-Merck EST Project 1997 unpublished (1997)  
TITLE JOURNAL  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 834 Std Error: 0.00  
Seq primer: -41m13 fwd. Et from Amersham  
High quality sequence stop: 361.  
Location/Qualifiers  
1. 400  
/organism="Homo sapiens"  
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."  
/db\_xref="taxon:9606"  
/clone="666438"  
/clone\_lib="Soares NHMPu S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"





Dh 61 tdcrcceasgftsaenhlrhclscskcrkemgqvaisctvdrtvcgcrknqyrhywse 120  
| | | | |  
Qy 61 tdcrcceasgftsaenhlrhclscskcrkemgqvaisctvdrtvcgcrknqyrhywse 120  
| | | | |  
Dh 121 nlfcgfnscslngtvlhslscqekqntvctchagfflrenecvscagaprcrpnatlay 180  
| | | | |  
Qy 121 nlfcgfnscslngtvlhslscqekqntvctchagfflrenecvscagaprcrpnatlay 180  
| | | | |  
Dh 181 ekegpcvctvnttcaagcprmtvlgvlpalpqvvcnrvdrvfesrlrjpcgcrqvnv 240  
| | | | |  
Qy 181 ekegpcvctvnttcaagcprmtvlgvlpalpqvvcnrvdrvfesrlrjpcgcrqvnv 240  
| | | | |  
Dh 241 vsvyavalscgaalcrsttcdgprkdhplctcdprfcdssaskappslpsarlpgps 300  
| | | | |  
Qy 241 vsvyavalscgaalcrsttcdgprkdhplctcdprfcdssaskappslpsarlpgps 300  
| | | | |  
Dh 301 dtlplpq 307  
| | | | |  
Qy 301 dtlplpq 307  
| | | | |

## RESULT 2

ID W33360 standard; Protein: 336 AA.  
AC W33360; (first entry)  
DE TBP(20-190)/hCG-beta fusion protein.  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW beta subunit; hCG-beta.  
OS Homo sapiens.  
PN W09730161-A1.  
PD 21-AUG-1997.  
PE 20-FEB-1997; US-02315.  
PR 20-FEB-1996; US-011936.  
PS (ISTE ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chappel SC, Jameson BA;  
DR WPI: 97-425036/39.  
DR N-PSDB: T94007.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PT hormone, especially FSH, for inducing follicular maturation  
PS Example; Pages 39-40; 60pp; English.  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotropin-beta subunit  
CC (hCG-beta) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.  
SQ Sequence 336 AA;

Query Match 86.4%; Score 2022; DB 26; Length 336;  
Best Local Similarity 91.4%; Pred. No. 4,776-191;

Matches 307; Conservative 0; Mismatches 0; Indels 29; Gaps 1;

Dh 1 srtslilaflgllcplwldesadavcpqgkylyhpqnsicctckhkytlylndcpqpgqd 60  
| | | | |  
Qy 1 srtslilaflgllcplwldesadavcpqgkylyhpqnsicctckhkytlylndcpqpgqd 60  
| | | | |  
Dh 61 tdcrcceasgftsaenhlrhclscskcrkemgqvaisctvdrtvcgcrknqyrhywse 120  
| | | | |  
Qy 61 tdcrcceasgftsaenhlrhclscskcrkemgqvaisctvdrtvcgcrknqyrhywse 120  
| | | | |  
Dh 121 nlfcgfnscslngtvlhslscqekqntvctchagfflrenecvscagaprcrpnatlay 180  
| | | | |  
Qy 121 nlfcgfnscslngtvlhslscqekqntvctchagfflrenecvscagaprcrpnatlay 180  
| | | | |  
Dh 181 lenyktedsglttagagprcrpinaatlavekegpcvctvnttcaagcprmtvlgvlp 240  
| | | | |

Qy 165 -----AGAGRCRPNATLAVEKEGCPVCTVNTTICAGCPTMTRVLGVL 211  
| | | | |  
Dh 241 palpqvvcnrvdrvfesrlrjpcgcrqvnvsvyavalscgaalcrsttcdgprkdhpl 300  
| | | | |  
Qy 212 palpqvvcnrvdrvfesrlrjpcgcrqvnvsvyavalscgaalcrsttcdgprkdhpl 271  
| | | | |  
Dh 301 cddprfcdssaskappslpsarlpgpsdtlplpq 336  
| | | | |  
Qy 272 cddprfcdssaskappslpsarlpgpsdtlplpq 307  
| | | | |

## RESULT 3

ID W33357 standard; Protein: 256 AA.  
AC W33357;  
DE TBP(20-161)/hCG-alpha fusion protein.  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW alpha subunit; hCG-alpha.  
OS Homo sapiens.  
PN W09730161-A1.  
PD 21-AUG-1997.  
PE 20-FEB-1997; US-02315.  
PR 20-FEB-1996; US-011936.  
PS (ISTE ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chappel SC, Jameson BA;  
DR WPI: 97-425036/39.  
DR N-PSDB: T94007.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PT hormone, especially FSH, for inducing follicular maturation  
PS Example; Pages 32-33; 60pp; English.  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotropin-alpha subunit  
CC (hCG-alpha) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.  
SQ Sequence 256 AA;

Query Match 56.4%; Score 1321; DB 26; Length 256;  
Best Local Similarity 98.8%; Pred. No. 1,848-119;

Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Dh 1 srtslilaflgllcplwldesadavcpqgkylyhpqnsicctckhkytlylndcpqpgqd 60  
| | | | |  
Qy 1 srtslilaflgllcplwldesadavcpqgkylyhpqnsicctckhkytlylndcpqpgqd 60  
| | | | |  
Dh 61 tdcrcceasgftsaenhlrhclscskcrkemgqvaisctvdrtvcgcrknqyrhywse 120  
| | | | |  
Qy 61 tdcrcceasgftsaenhlrhclscskcrkemgqvaisctvdrtvcgcrknqyrhywse 120  
| | | | |  
Dh 121 nlfcgfnscslngtvlhslscqekqntvctchagfflrenecvscagaprcrpnatlay 180  
| | | | |  
Qy 121 nlfcgfnscslngtvlhslscqekqntvctchagfflrenecvscagaprcrpnatlay 180  
| | | | |

## RESULT 4

ID W33359 standard; Protein: 285 AA.  
AC W33359;  
DE TBP(20-190)/hCG-alpha fusion protein.  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW alpha subunit; hCG-alpha.  
OS Homo sapiens.  
PN W09730161-A1.  
PD 21-AUG-1997.  
PE 20-FEB-1997; US-02315.  
PR 20-FEB-1996; US-011936.

PA (ISTR) ARS APPLIED RES SYSTEMS HOLDING NV.  
 PI Campbell RK, Chapel SC, Jameson BA;  
 DR WPI: 97-425036/39.  
 DR N-PSDB: T94021.  
 PT Hybrid dimeric protein comprising two co-expressed units - each  
 PT based on receptor or ligand and a subunit of a heterodimeric  
 PT hormone, especially FSH, for inducing follicular maturation  
 PS Example: Pages 37-38; 60pp: English.  
 CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
 CC acid sequences, each consisting of a homodimeric or heterodimeric  
 CC receptor chain or ligand, with ligand-receptor binding activity,  
 CC bound directly or via a peptide linker to a subunit of a  
 CC heterodimeric protein hormone capable of forming a heterodimer with  
 CC the hormone's other subunits. The fusion protein, e.g. the  
 CC thrombopoietin (TPO)/human chorionic gonadotropin-alpha subunit  
 CC (hCG-alpha) fusion protein denoted by the present sequence,  
 CC significantly increases the biological activity of the hormone  
 CC component, reducing the requirement for hormone itself and the  
 CC number of injections needed.  
 SO Sequence 285 AA;

Query Match 55.1%; Score 1289; DB 26; Length 285;  
 Best Local Similarity 98.8%; Pred. No. 3.29e-116;  
 Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 strslalafgllclpwlgsasdvcpqgkyihpnnslcctckhgtlylndcpqpgd 60  
 QY 1 strslalafgllclpwlgsasdvcpqgkyihpnnslcctckhgtlylndcpqpgd 60  
 Db 61 tdrecesgftasenhlfhncfscskcrkcmgqvslscvtdidvcgrkngryhws 120  
 QY 61 tdrecesgftasenhlfhncfscskcrkcmgqvslscvtdidvcgrkngryhws 120  
 Db 61 tdcrcesgftasenhlfhncfscskcrkcmgqvslscvtdidvcgrkngryhws 120  
 QY 61 tdcrcesgftasenhlfhncfscskcrkcmgqvslscvtdidvcgrkngryhws 120  
 Db 121 nlfqfncclngtlhscqekntvctchagffilrenecvscs 165  
 QY 121 nlfqfncclngtlhscqekntvctchagffilrenecvscs 165  
 QY 121 nlfqfncclngtlhscqekntvctchagffilrenecvscs 165

RESULT 5  
 ID R27496 standard; protein: 161 AA.  
 AC R27496;  
 DT 09-MAR-1993 (first entry)  
 DE Native 30 kD TNF inhibitor.  
 KM Tumour necrosis factor; ethylene glycol; pharmacokinetic;  
 KM adult respiratory distress syndrome; rheumatoid arthritis;  
 KM septic shock; pulmonary fibrosis; spacer.  
 OS Homo sapiens.  
 PN MO9216221-A.  
 PD 01-OCT-1992.  
 PF 13-MAR-1992: 002122.  
 PR 15-MAR-1991: US-669862.  
 PR 17-JAN-1992: US-822296.  
 PA (SYND) SYNERGEN INC.  
 PI Armes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;  
 DR WPI: 92-348933/42.  
 PT New ethylene glycolated polypeptide(s) with improved  
 PT pharmacokinetic properties - for treating e.g. TNF and IL-1  
 PT mediated diseases, e.g. adult respiratory distress syndrome,  
 PT rheumatoid arthritis, septic shock etc.  
 PS Claim 54; Fig 2; 100pp: English.  
 CC The sequence shows a native 30 kD TNF inhibitor which may be  
 CC modified to contain at least one non-native cysteine residue, pref.  
 CC at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is  
 CC joined to a non-peptidic polymer, pref. monomethoxy PEG via  
 CC this-ether bonds. Two such TNF inhibitor moieties may be linked via  
 CC non-peptidic spacer. The modified polypeptides show improved  
 CC pharmacokinetic properties, i.e. increased mol. wt. hence reduced  
 CC clearance rate following s.c. or systemic administration, increased  
 CC sol. of native TNF inhibitors, and reduced antigenicity. The  
 CC polypeptides may be used for treatment of TNF mediated diseases such  
 CC as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid  
 CC arthritis, inflammatory bowel disease and septic shock. The same  
 CC method may be applied to the interleukin-1 receptor antagonist

CC IL-1ra. See also R27495.  
 SQ Sequence 161 AA;  
 Query Match 48.0%; Score 1124; DB 5; Length 161;  
 Best Local Similarity 99.3%; Pred. No. 1.82e-99;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 dsvcpqgkyihpnnslcctckhgtlylndcpqpgdtdcrecesgftasenhlfhcl 60  
 QY 23 dsvcpqgkyihpnnslcctckhgtlylndcpqpgdtdcrecesgftasenhlfhcl 82  
 Db 61 scskcrkcmgqvslscvtdidvcgrkngryhwsenlfqfncslclngtlhscqe 120  
 QY 83 scskcrkcmgqvslscvtdidvcgrkngryhwsenlfqfncslclngtlhscqe 142  
 Db 121 kntvctchagffilrenecvscs 143  
 QY 143 kntvctchagffilrenecvscs 165

RESULT 6  
 ID R24080 standard; protein: 199 AA.  
 AC R24080;  
 DT 05-NOV-1992 (first entry)  
 DE Truncated TNF-alpha 55kD receptor.  
 KM tumour necrosis factor alpha; extracellular binding domain;  
 KM treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
 KM malaria; viral meningitis; graft versus host disease;  
 KM autoimmune disease; rheumatoid arthritis.  
 OS Homo sapiens.  
 PN WO9207076-A.  
 PD 30-APR-1992.  
 PF 18-OCT-1991: G01826.  
 PR 18-OCT-1990: GB-022648.  
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.  
 PI Brennan FM, Feldmann M, Gray PM, Turner MJC;  
 DR WPI: 92-167156/20.  
 DR N-PSDB: Q24441.  
 PT New polypeptide capable of binding human TNF alpha - comprises  
 PT first three cysteine-rich subdomains of TNF alpha receptor for  
 PT treating autoimmune disease, septic shock, HIV etc.  
 PS Example: Fig 7; 43pp: English.  
 CC This sequence is a truncated TNF-alpha receptor derivative, as encoded  
 CC in pNFRect. This was produced as described in Q24440.  
 CC This derivative lacks the 81 carboxyl terminal residues of the  
 CC cytoplasmic domain. The derivative could be used in the  
 CC regulation of TNF-alpha mediated responses by binding and  
 CC sequestering human TNF-alpha e.g. in the treatment of pulmonary  
 CC diseases, septic shock, HIV infection, malaria, viral meningitis,  
 CC graft versus host disease and autoimmune diseases, esp. rheumatoid  
 CC arthritis.  
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
 SQ Sequence 199 AA;

Query Match 48.0%; Score 1124; DB 4; Length 199;  
 Best Local Similarity 99.3%; Pred. No. 1.82e-99;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvcpqgkyihpnnslcctckhgtlylndcpqpgdtdcrecesgftasenhlfhcl 100  
 QY 23 dsvcpqgkyihpnnslcctckhgtlylndcpqpgdtdcrecesgftasenhlfhcl 82  
 Db 101 scskcrkcmgqvslscvtdidvcgrkngryhwsenlfqfncslclngtlhscqe 160  
 QY 83 scskcrkcmgqvslscvtdidvcgrkngryhwsenlfqfncslclngtlhscqe 142  
 Db 161 kntvctchagffilrenecvscs 183  
 QY 143 kntvctchagffilrenecvscs 165

RESULT 7  
 ID R70108 standard; protein: 309 AA.

AC R70108; (first entry)  
DE 10-NOV-1995 (first entry)  
DE TNF-R-GBP fusion protein.  
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;  
KW GBP 130; GBP: glycoprotein binding peptide homologue; glycoprotein A;  
KW tumour necrosis factor receptor; TNF-R.  
OS Chimeric Homo sapiens.  
OS Chimeric Plasmodium falciparum.  
FH Key Location/Qualifiers  
FT misc\_difference 230..269  
FT /label=repeat\_region  
FT /note="can be repeated n times, where n is a real  
FT number"  
PN WO9506737-A.  
PD 09-MAR-1995.  
PF 01-SEP-1994; G01900.  
PR 03-SEP-1993; GB-018350.  
PR 23-AUG-1994; GB-017021.  
PA (PREN/) PRENDERGAST K F.  
PI Prendergast KF;  
DR WPI: 95-115452/15.  
PT New hybrid peptide(s) for binding cytokine(s) - comprising a  
PT malaria parasite peptide capable of binding a red blood cell and  
PT a receptor peptide.  
PS Example A: Page 54-55; 93pp; English.  
CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples  
CC of these hybrid peptides. R70108 is a fusion of tumour necrosis factor  
CC and glycoprotein binding protein (GBP) homologue (GBP). The  
CC use of cytokine receptors not normally found on RBCs means that the  
CC cytokine can bind harmlessly to the RBC without deleterious effect.  
CC The RBC protects the hybrid peptides from excretion from the kidney, and  
CC due to steric hindrance prevents the cytokines binding to a receptor in  
CC another cell. GBP 130 or GBP are the pred. malaria parasite peptides  
CC used, others include BSA 175 (175 kDa erythrocyte binding antigen), PMMSA  
CC (pre major merozoite surface antigen) and the Duffy binding receptor  
CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to  
CC pref. glycoprotein A, B and C, sialo glycoproteins, found on the surface  
CC of RBCs. The hybrid peptides are thus used to lower the levels of free  
CC cytokines in the circulation to reduce pathological damage.  
SQ Sequence 309 AA;  
Query Match 48.0%; Score 1124; DB 13; Length 309;  
Best Local Similarity 99.3%; Pred. No. 1.82e-99;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 20 dsvcpqgkyihpnmnsicctckhkytylyndcpqpgdtdcrecsagfssenhlncl 79  
QY 23 DSVCPQGYIHPNMNSICTCKHKTLYLNDPQPGDTRDRECSGSGFTASENHLRCL 82  
DB 80 scskcrkmgvvelsscvtddtvcgrkngryhwsenlfqfncslclngtvhlsqce 139  
QY 83 SCSKCRKMGVVELSSCVTDRTVCGCRKNQRYHWSENLFCFCNCSLCLNGTVHLSQCE 142  
DB 140 kntvctchagfflrenecvscs 162  
QY 143 KNTVCTCHAGFFLRENECVSCA 165  
RESULT 8  
ID R07449 standard; protein; 371 AA.  
AC R07449;  
DE 29-JAN-1991 (first entry)  
DE Tumour Necrosis Factor-Binding Protein from P1NF-BP15 cDNA.  
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KW P1NF-BP15; infectious disease; parasitic disease; cachexia;  
KW autoimmune disease; shock.  
OS Homo sapiens.  
PN EP-393438-A.  
PD 24-OCT-1990.

PF 06-APR-1990; 106624.  
PR 21-APR-1989; DE-913101.  
PR 21-JUN-1989; DE-920282.  
PA (BOEH) BOEHRINGER INGELHEIMINT.  
PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;  
DR WPI: 90-321987/43.  
DR N-PSDB: 006282.  
PT DNA encoding TNF binding protein and TNF-receptor - used in  
PT tumour treatment and to understand mechanism to TNF action  
PS Disclosure: Fig 1(1-3); 51pp; German.  
CC Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of  
CC e.g. COS7 cells. The expressed proteins are useful  
CC prophylactically and therapeutically to control disorders which  
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
CC respiratory distress syndrome etc., or side effects of treatment with  
CC TNF-alpha). They can also be used as diagnostic reagents for  
CC assaying TNF and in study of TNF-receptor interactions.  
CC See also 006282-006285.  
SQ Sequence 371 AA;  
Query Match 48.0%; Score 1124; DB 2; Length 371;  
Best Local Similarity 99.3%; Pred. No. 1.82e-99;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 41 dsvcpqgkyihpnmnsicctckhkytylyndcpqpgdtdcrecsagfssenhlncl 100  
QY 23 DSVCPQGYIHPNMNSICTCKHKTLYLNDPQPGDTRDRECSGSGFTASENHLRCL 82  
DB 101 scskcrkmgvvelsscvtddtvcgrkngryhwsenlfqfncslclngtvhlsqce 160  
QY 83 SCSKCRKMGVVELSSCVTDRTVCGCRKNQRYHWSENLFCFCNCSLCLNGTVHLSQCE 142  
DB 161 kntvctchagfflrenecvscs 183  
QY 143 KNTVCTCHAGFFLRENECVSCA 165  
RESULT 9  
ID R70107 standard; protein; 451 AA.  
AC R70107;  
DE 10-NOV-1995 (first entry)  
DE TNF-R-GBP 130 fusion protein.  
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;  
KW GBP 130; GBP: glycoprotein binding peptide homologue; glycoprotein A.  
OS Chimeric Homo sapiens.  
OS Chimeric Plasmodium falciparum.  
PN WO9506737-A.  
PD 09-MAR-1995.  
PF 01-SEP-1994; G01900.  
PR 03-SEP-1993; GB-018350.  
PR 23-AUG-1994; GB-017021.  
PA (PREN/) PRENDERGAST K F.  
PI Prendergast KF;  
DR WPI: 95-115452/15.  
PT New hybrid peptide(s) for binding cytokine(s) - comprising a  
PT malaria parasite peptide capable of binding a red blood cell and  
PT a receptor peptide.  
PS Example A: Page 53-54; 93pp; English.  
CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples  
CC of these hybrid peptides. R70107 is a fusion of tumour necrosis factor  
CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
CC and glycoprotein binding protein (GBP) 130. The use of cytokine  
CC receptors not normally found on RBCs means that the cytokine can bind  
CC harmlessly to the RBC without deleterious effect. The RBC protects the  
CC hybrid peptides from excretion from the kidney, and due to steric  
CC hindrance prevents the cytokines binding to a receptor in another cell.  
CC GBP 130 or GBP (GBP homologue) are the pred. malaria parasite peptides  
CC used, others include BSA 175 (175 kDa erythrocyte binding antigen),  
CC PMMSA (pre major merozoite surface antigen) and the Duffy binding

CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on  
CC the surface of RBCs. The hybrid peptides are thus used to lower  
CC the levels of free cytokines in the circulation to reduce pathological  
CC damage.  
SQ Sequence 451 AA;

Query Match 48.0%; Score 1124; DB 13; Length 451;  
Best Local Similarity 99.3%; Pred. No. 1.82e-99;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 20 dsvcpqgkylhpnmslctckhkgtylndcpqpgdtdccceesgfsfassenhlrhcl 79  
|||  
QY 23 DSVCPQGXTHPQNNISICTCKHKGTYLNDGPGQDTCRCESGFSFASSENHLRHCL 82  
|||  
Db 80 scskckremgqvaisctvdrtdvcgcrknqyrhysenlfgcfncslcngtvhscqe 139  
|||  
QY 83 SCSCKRKEMGOVEISSCTVDRTVCCGCRKNQYRHYSENLFGCFNCSLCLNGTVHLSQOE 142  
|||  
Db 140 kqntvctchagfflrenevcs 162  
|||  
QY 143 KQNTVCTCHAGFFLRENECVSCA 165  
|||

RESULT 10  
ID R42059 standard; Protein: 455 AA.

AC R42059;  
DT 29-APR-1994 (first entry)  
DE Lambda derived TNF-R.  
KW Human: tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
pulmonary fibrosis; silicosis; allograft; xenograft; rejection;  
KW graft verses host disease; sepsis; inflammation; allergy;  
KW autoimmune dysfunction.  
OS Homo sapiens.  
FH Lambda-gt10-7cutfp.  
FT Key Location/Qualifiers  
FT peptide 1..40  
FT protein /note="Signal peptide"  
FT 41..455  
FT /note="Mature hTNF-R"  
PN MO9319777-A.  
PD 14-OCT-1993.  
PE 26-MAR-1993; 002938.  
PR 30-MAR-1992; US-860710.  
PA (IMMUNEX ) IMMUNEX CORP.  
PI Smith CA;  
DR WPI: 93-336592/42.  
N-PSDB: Q49932.  
PT New fusion protein tumour necrosis factor and human interleukin-1  
receptor - useful in therapy, diagnosis and assays of e.g.  
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.  
PS Disclosure: Page 57-59; 85pp; English.  
CC The sequences given in R42058-59 represent human tumour necrosis  
factor receptor (TNF-R) and the sequences in R42060-61 represent  
human interleukin-1 receptor (IL-1R). These sequences were used in  
CC the production of a fusion protein which conformed to one of the  
CC formulae:  
CC TNF-R-linker-TNF-R-linker-IL-1R  
CC IL-1R-linker-TNF-R-linker-TNF-R or  
CC TNF-R-linker-TNF-R  
CC The linker may comprise 5-100 amino acids selected from gly, Asp,  
CC Ser, Thr and Ala. These linkers separate the individual moieties  
CC by such a distance that each component of the fusion protein is  
CC capable of folding into the secondary or tertiary structure required  
CC for its biological activity. These fusion proteins may be used in  
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
CC particularly in conditions in which both TNF and IL-1 play a causative  
CC role. They may be used to treat cachexia, rheumatoid arthritis,  
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
CC cerebral malaria, allograft and xenograft rejection in graft verses  
CC host disease, sepsis, septic shock, inflammation, allergies and

CC autoimmune dysfunctions.  
SQ Sequence 455 AA;

Query Match 48.0%; Score 1124; DB 8; Length 455;  
Best Local Similarity 99.3%; Pred. No. 1.82e-99;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvcpqgkylhpnmslctckhkgtylndcpqpgdtdccceesgfsfassenhlrhcl 100  
|||  
QY 23 DSVCPQGXTHPQNNISICTCKHKGTYLNDGPGQDTCRCESGFSFASSENHLRHCL 82  
|||  
Db 101 scskckremgqvaisctvdrtdvcgcrknqyrhysenlfgcfncslcngtvhscqe 160  
|||  
QY 83 SCSCKRKEMGOVEISSCTVDRTVCCGCRKNQYRHYSENLFGCFNCSLCLNGTVHLSQOE 142  
|||  
Db 161 kqntvctchagfflrenevcs 183  
|||  
QY 143 KQNTVCTCHAGFFLRENECVSCA 165  
|||

RESULT 11  
ID R10986 standard; Protein: 455 AA.

AC R10986;  
DT 13-MAY-1991 (first entry)  
DE 30kd TNF inhibitor precursor.  
KW Tumour necrosis factor; inhibitor.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT cleavage\_site 40..41  
FT note=" cleavage gives active protein "  
PN AU9058976-A.  
PD 24-JUN-1991.  
PE 16-JUL-1990; 058976.  
PR 18-JUL-1989; US-381080.  
PR 11-DEC-1989; US-450329.  
PR 07-FEB-1990; US-479661.  
PA (SYNE-) SYNERGEN INC.  
DR WPI: 91-073847/11.  
N-PSDB: Q10883.  
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha  
PT and -beta, useful as therapeutic agent.  
PS Disclosure: Fig 21; 142pp; English.  
CC The sequence comprises the entire 30 kD TNF inhibitor. The clone  
CC from which the sequence was deduced was isolated from a cDNA  
CC library prep. from RNA form U937 cells treated with PMA/PMA.  
CC The whole gene can be inserted into expression vectors for prepn.  
CC of TNF inhibitor for use in the treatment of inflammatory and  
CC degenerative diseases. The active protein is claimed (Claim 8).  
CC See also R10984 and R11001.  
SQ Sequence 455 AA;

Query Match 48.0%; Score 1124; DB 2; Length 455;  
Best Local Similarity 99.3%; Pred. No. 1.82e-99;  
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 dsvcpqgkylhpnmslctckhkgtylndcpqpgdtdccceesgfsfassenhlrhcl 100  
|||  
QY 23 DSVCPQGXTHPQNNISICTCKHKGTYLNDGPGQDTCRCESGFSFASSENHLRHCL 82  
|||  
Db 101 scskckremgqvaisctvdrtdvcgcrknqyrhysenlfgcfncslcngtvhscqe 160  
|||  
QY 83 SCSCKRKEMGOVEISSCTVDRTVCCGCRKNQYRHYSENLFGCFNCSLCLNGTVHLSQOE 142  
|||  
Db 161 kqntvctchagfflrenevcs 183  
|||  
QY 143 KQNTVCTCHAGFFLRENECVSCA 165  
|||

RESULT 12  
ID R20787 standard; Protein: 455 AA.  
AC R20787;  
DT 11-MAY-1992 (first entry)  
DE TNF-alpha binding protein.

Accession	Protein	Location/Qualifiers
KM	Tumour necrosis factor alpha; autoimmune diseases; cachectin;	
KW	extracellular domain.	
OS	Homo sapiens.	
FT	Key	
FT	peptide	1..40
FT	peptide	/note= "signal peptide"
FT	peptide	41..455
FT	domain	/note= "mature peptide"
FT	domain	30..199
FT	domain	/note= "extracellular domain"
FT	domain	212..234
FT	modified_site	/note= "transmembrane domain"
FT	modified_site	145..147
FT	modified_site	/note= "potential N-glycosylation site"
FT	modified_site	151..153
FT	modified_site	/note= "potential N-glycosylation site"
PN	GB2246569-A.	
PD	05-FEB-1992.	
PD	15-JUN-1990.	013410.
PR	15-JUN-1990; GB-013410.	
PA	(CHAR-) CHARING CROSS SUNLE.	
PI	Feldman M, Gray P, Turner M, Brennan F;	
DR	WPI: 92-043613/06.	
DR	N-PSDB: 020973.	
PT	New tumour necrosis factor alpha binding protein and polypeptide	
PT	- useful in treating cachexia, sepsis and autoimmune diseases	
PT	e.g. Rheumatoid arthritis	
PS	Disclosure; Fig 1; 25pp; English.	
CC	The amino acid sequence is that of tumour necrosis factor alpha	
CC	binding protein which contains the extracellular domain of human TNF	
CC	alpha receptor. It is soluble and can be used in the regulation of	
CC	TNF-mediated responses by binding and sequestering the cytokine. It	
CC	can therefore be used therapeutically to treat disorders such as	
CC	cachexia, sepsis and autoimmune diseases, specifically rheumatoid	
CC	arthritis.	
SO	Sequence 455 AA;	
Query Match	48.0%; Score 1124; DB 4; Length 455;	
Best Local Similarity	99.3%; Pred. No. 1.82e-99;	
Matches 142; Conservative	1; Mismatches 0; Indels 0; Gaps 0;	
Db	41 dsavppgkyihppqnsicctctchxytyjyndcpqpgdtdcreesgsfssenhhlcl 100	
OY	23 DSVCPQGYTHPNPNNSICCTCKHKGTYLYNCCPBPQDPTDCESSSFASSENHLRHL 82	
Db	101 scsckrckmgvvelssctvdrtvcgcrkngyryhwsenlfqcfncslcngtvhlsacge 160	
OY	83 SCSCKRCKMGVVELSSCTVDRTVCGCRKNQRYRHSBNLFCPCNCSLCINGTVHLSQCE 142	
Db	161 kqntvctchagffireneccvas 183	
OY	143 KQNTVCTCHAGFFIRENECVSCA 165	
RESULT 13		
ID	R75084 standard; Protein; 455 AA.	
AC	R75084;	
DT	19-JAN-1996 (first entry)	
DE	p55 TNF-R.	
KW	p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;	
KW	epidermal growth factor receptor; EGF-R; protease; inhibitor;	
OS	phorbol myristate acetate; PMA.	
OS	Homo sapiens.	
FT	Key	
FT	peptide	Location/Qualifiers
FT	peptide	41..53
FT	modified_site	/note= "N terminus of soluble p55 TNF-R"
FT	modified_site	54..56
FT	modified_site	/note= "glycosylation site"
FT	modified_site	145..147
FT	modified_site	/note= "glycosylation site"
FT	modified_site	161..163
FT	peptide	/note= "glycosylation site"
FT	peptide	193..210

Query Match	Best Local Similarity	Matches 142; Conservative	48.0%; Score 1124; DB 14; Length 455;
DB	41 dsyvpqgkylhpnqnslocckkxkqlylyndcpqpggdicrcceagsgfssenhrlhcl 100		
OY	23 DSVCPQGRYIHPPNNSSICCTKCHGRTILYNDCEPQGDITCRCESSGFSASEHRLHCL 82		
DB	101 scskrkemqveisactvdtdtcgcrkqzhryhysenlfqfncalcjngvtvlhsqce 160		
OY	83 SCSCKRKMGMVEISSCTVDREDTVCGRKNQRYRWSENLFCQFNCSLCJNGVTHLSQCE 142		
DB	161 kqntvctchagfltrnecyscs 183		
OY	143 KQNTVCTCHAGFLTRNECVSCA 165		
RESULT 14			
ID	R07451 standard; protein; 455 AA.		
AC	R07451;		
DT	26-JAN-1991 (first entry)		
DE	Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.		
FW	Tumour necrosis factor binding protein; TNF- $\beta$ ; TNF-receptor;		
IN	Infectious disease; parasitic disease; cachexia;		
FW	autoimmune disease; shock; lambdaTNF-R2; ratTNF-R8.		



OS Homo sapiens.  
 PN EP-393438-A.  
 PD 24-OCT-1990.  
 PF 06-APR-1990; 106624.  
 PR 21-APR-1989; DE-913101.  
 PR 21-JUN-1989; DE-920282.  
 PA (BOEH) BOEHRINGER INGELHEIMINT.  
 PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;  
 DR WPI: 90-321987/43.  
 DR N-PSDB: Q06285.  
 PT DNA encoding TNF binding protein and TNF-receptor - used in  
 PT tumour treatment and to understand mechanism to TNF action  
 PS Disclosure: Fig 91(1-2): 51pp; German.  
 CC rATNF-R8 (Q06284) was used to screen the H913T cDNA library.  
 CC LambdaTNF-R2 encodes the complete human TNF-R2 and was used to  
 CC construct a plasmid (pADTNF-R) expressing the product the same way  
 CC as pADTNF-BP (see Q06282). The expressed proteins are useful  
 CC prophylactically and therapeutically to control disorders which  
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
 CC respiratory distress syndrome etc., or side effects of treatment with  
 CC TNF-alpha). They can also be used as diagnostic reagents for  
 CC assaying TNF and in study of TNF-receptor interactions.  
 CC See also Q06282-Q06285.  
 CC Sequence 455 AA;  
 SQ

Query Match 48.0%; Score 1124; DB 2; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 1,82e-99;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 41 dsvcpqgkyihpqnmsicctckhkgtylyndcpqpgqdtcrecsqsfstasenhrlhcl 100  
 |||||||  
 QY 23 DSVCPQGXIHQNNNSICCTCKHKGTYLYNDCPGQDTCRECSGSGSTASENHLRCL 82  
 |||||||

DB 101 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfncslclngtvhlsce 160  
 |||||||  
 QY 83 SCSKCRKEMGVEISSCTVDRTVCGCRKNQYRHYSENLFQCFNCSLCLNGTVHLSCE 142  
 |||||||

DB 161 kqntvctchagfflrenevscs 183  
 |||||||  
 QY 143 KQNTVCTCHAGFFLRENECVSCA 165  
 |||||||

RESULT 15  
 ID R11082 standard; Protein: 455 AA.  
 AC R11082;  
 DT 24-MAY-1991 (first entry)  
 DE Human 55kD TNF-binding protein.  
 KW Tumour Necrosis Factor; binding proteins; septic shock;  
 KW autoimmune glomerulonephritis; lymphokine; cytokine.  
 FH key Location/Qualifiers  
 FT modified\_site 54  
 FT modified\_site 145 /label= putative N-glycosylation site  
 FT modified\_site 151 /label= putative N-glycosylation site  
 FT modified\_site 270 /label= putative N-glycosylation site  
 FT region 212..230 /label= transmembrane region  
 FT peptide 1..28 /label= signal peptide  
 FT  
 PN EP-41563-A.  
 PD 20-MAR-1991.  
 PD 31-AUG-1990; 116707.  
 PR 12-SEP-1989; CH-003319.  
 PR 08-MAR-1990; CH-000746.  
 PR 20-APR-1990; CH-001347.  
 PA (HOFF) HOFFMANN-LA ROCHE AG.  
 PI Brockschhaus M, Demblie Z, Gentz R, Lesslauer W, Lotscher H;  
 PI Schlaeger EJ;  
 DR WPI: 91-081851/12.

DR N-PSDB: Q10955.  
 PT Insoluble tumour necrosis factor binding proteins - and DNA  
 PT encoding them, useful in pharmaceutical prods. and for antibody  
 PT prodn.  
 PS Claim 1; Fig 1; 26pp; German.  
 CC Partial amino acid sequences were determined for the 55 and 75kD  
 CC TNF-BPs (see R11072-R11081) and oligonucleotide primers were  
 CC synthesised based on these partial sequences. The primers were used  
 CC to produce a cDNA fragment for use as a probe to screen a human  
 CC placental cDNA bank constructed in lambda gt11. Positive clones were  
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding  
 CC sequence may also contain a fragment encoding a human Ig domain.  
 CC Recombinant constructs are used to transform cells to confer  
 CC improved TNF-binding properties.  
 CC See also Q10956.  
 CC Sequence 455 AA;  
 SQ

Query Match 48.0%; Score 1124; DB 2; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 1,82e-99;  
 Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 41 dsvcpqgkyihpqnmsicctckhkgtylyndcpqpgqdtcrecsqsfstasenhrlhcl 100  
 |||||||  
 QY 23 DSVCPQGXIHQNNNSICCTCKHKGTYLYNDCPGQDTCRECSGSGSTASENHLRCL 82  
 |||||||

DB 101 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfncslclngtvhlsce 160  
 |||||||  
 QY 83 SCSKCRKEMGVEISSCTVDRTVCGCRKNQYRHYSENLFQCFNCSLCLNGTVHLSCE 142  
 |||||||

DB 161 kqntvctchagfflrenevscs 183  
 |||||||  
 QY 143 KQNTVCTCHAGFFLRENECVSCA 165  
 |||||||

Search completed: Wed May 6 08:57:56 1998  
 Job time : 99 secs.

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23-42	#disulfide_bonds\
45-60	#disulfide_bonds\
63-78	#disulfide_bonds\
66-86	#disulfide_bonds\
88-104	#disulfide_bonds\
107-119	#disulfide_bonds\
110-127	#disulfide_bonds\
129-140	#disulfide_bonds\
143-156	#disulfide_bonds\
146-152	#disulfide_bonds\
SUMMARY	#length 158 #molecular-weight 17827 #checksum 5022
Query Match	48.0%; Score 1124; DB 5; Length 158;
Best Local Similarity	99.3%; Pred. No. 2,76e-207;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Db	2 DSVCPQGRKTHQNNNSICTCKHKGTYLYNDGPGDPDDRCRCESGSPFASNNHRLHCL 61
Oy	23 DSVCPQGRKTHQNNNSICTCKHKGTYLYNDGPGDPDDRCRCESGSPFASNNHRLHCL 82
Db	62 SCSCRKREKGVYEISSCTVDRDPTVCGCRKNQYRHYSENLFQCFNCSLCLNGTVHLSQCE 121
Oy	83 SCSCRKREKGVYEISSCTVDRDPTVCGCRKNQYRHYSENLFQCFNCSLCLNGTVHLSQCE 142
Db	122 KONTVCTCHAGFFLRNECVSCS 144
Oy	143 KONTVCTCHAGFFLRNECVSCA 165
RESULT 2	GQHUT1 #type complete
ENTRY	
TITLE	tumor necrosis factor receptor type 1 precursor - humanALTERNATE_NAMES
CONTAINS	tumor necrosis factor alpha inhibitor; tumor necrosis factor
ORGANISM	blinding protein 1 (TNF blocking factor)
DATE	#formal_name Homo sapiens #common_name man
	30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
	24-Oct-1997
ACCESSIONS	A38208; A34899; A36555; C36555; A38281; S12057;
REFERENCE	J70758; A60231; A38258; A60594; A35010; JC2404
#authors	Fuchs, P.; Strohl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.
#journal	Genomics (1992) 13:219-224
#title	Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and
	localization to chromosome 12p13.
#accession	A38208
#molecule_type	DNA
#residues	1-455 #label FUC
##cross-references	GB:M75864; GB:M75865; GB:M75866; NID:g339748;
PID:g339750	
REFERENCE	
#authors	A34899
#journal	Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
#title	M.; Tschuch, H.; Lesslauer, W.
	Cell (1990) 61:351-359
	Molecular cloning and expression of the human 55 kd tumor
	necrosis factor receptor.
##cross-references	MUID:90235284
#accession	A34899
#molecule_type	mRNA
#residues	1-455 #label LOE
##cross-references	GB:M58286; GB:M33480; NID:g339753; PID:g339754
##experimental_source	Placenta
#note	part of this sequence, including the amino end of the
	mature protein, confirmed by protein sequencing
REFERENCE	
#authors	A34900
#journal	Schall, T.U.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
#title	Wong, G.H.W.; Gatanaga, T.; Ganger, G.A.; Lentz, R.; Raab,
	H.; Kohr, W.J.; Goeddel, D.V.
	Cell (1990) 61:361-370
	Molecular cloning and expression of a receptor for human
	tumor necrosis factor.
##cross-references	MUID:90235285

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#accession A34900
##molecule-type mRNA
##residues 1-455 ##label SCH
##cross-references GB:M35294; NID:g339744; PID:g339745
REFERENCE
#authors Himmler, A.; Maurer-Fogy, I.; Kroecken, M.; Scheurich, P.;
Pflanzmayer, K.; Lantz, M.; Olson, I.; Hauptmann, R.;
Stratowa, C.; Adolf, G.R
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
#accession A36555
##molecule-type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:g339755; PID:g339756
#accession C36555
##molecule-type protein
##residues 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;
107-128;162-167,'X',169-201 ##label H12
#note the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
receptor
REFERENCE
#authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
##molecule-type mRNA
##residues 1-455 ##label GRA
##cross-references GB:M37764
#note the authors translated the codon TGG for residue 371 as
Thr. AAG for residue 372 as Leu, and GAC for residue
427 as Asn
REFERENCE
#authors Noplat, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang
R.; Aderka, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs).
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
#cross-references MUID:91006021
#accession S12057
##molecule-type mRNA
##residues 1-455 ##label NOP
##cross-references EMBL:X5513; NID:g37223; PID:g37224
#note parts of soluble TNF binding protein 1, including its
amino and carboxyl ends, were confirmed by protein
sequencing
REFERENCE
#authors Kemper, O.; Wallach, D.
#journal Gene (1993) 134:209-216
#title Cloning and partial characterization of the promoter for the
human p55 tumor necrosis factor (TNF) receptor.
#accession J70758
##molecule-type DNA
##residues 1-13 ##label KEM
REFERENCE
#authors Seclinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
J.M.
#journal Eur. J. Immunol. (1990) 20:1167-1174
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal
amino acid sequence and evidence for anti-inflammatory and
immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
##molecule-type protein
##residues 41-45,'X',45-53,'X',55-57 ##label SEC

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REFERENCE      A38258
#authors       Gatanga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III,
               J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
               R.S.; Granger, G.A.
#journal       Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
#title         Purification and characterization of an inhibitor (soluble
               tumor necrosis factor receptor) for tumor necrosis factor
               and lymphotoxin obtained from the serum ultrafiltrates of
               human cancer patients.
#cross-references MIMD:91062364
#accession     A38258
#molecule-type protein
#residues      41-60 #label GAT
#experimental_source cancer patient serum
REFERENCE      A60594
#authors       Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
               Grubb, A.; Adolf, G.
#journal       Eur. J. Haematol. (1989) 42:270-275
#title         Isolation and characterization of a tumor necrosis factor
               binding protein from urine.
#accession     A60594
#molecule-type protein
#residues      41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 #label OLS
#experimental_source renal failure patient urine
REFERENCE      A35010
#authors       Engelmann, H.; Novick, D.; Wallach, D.
#journal       J. Biol. Chem. (1990) 265:1531-1536
#title         Two tumor necrosis factor-binding proteins purified from
               human urine. Evidence for immunological cross-reactivity
               with cell surface tumor necrosis factor receptors.
#cross-references MIMD:90110215
#accession     A35010
#molecule-type protein
#residues      41-45 #label ENG
#experimental_source normal urine
REFERENCE      JC2404
#authors       Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal       Biotechol. Biochem. (1994) 58:2266-2268
#title         Amino acid sequence of natural tumor necrosis factor alpha
               inhibitor purified from human urine.
#accession     JC2404
#molecule-type protein
#residues      41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201
               #label KAJ
#experimental_source urine
COMMENT        This protein is one of two known receptors for both TNF-alpha
               (cachectin) and TNF-beta (lymphotoxin).
GENETICS
#gene          GDB:TNR1
#cross-references GDB:125913; OMIM:191190
#map_position  12p13.2-12p13.2
#introns       13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
               receptor repeat homology
               duplication: glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
#domain        #domain signal sequence #status predicted #label SIG\
1-21            #product tumor necrosis factor receptor type 1 #status
22-455          predicted #label MAT\
30-211          #domain extracellular #status predicted #label EX\
41-201          #product TNF binding protein 1 (tumor necrosis factor
               alpha inhibitor) #status experimental #label TBP1\
44-82           #domain NGF receptor repeat homology #label NG1\
84-126          #domain NGF receptor repeat homology #label NG2\
127-167         #domain NGF receptor repeat homology #label NG3\
168-196         #domain NGF receptor repeat homology #label NG4\
212-234         #domain transmembrane #status predicted #label MEM\
235-455         #domain intracellular #status predicted #label INT\
54,145,151     #binding_site carbohydrate (Asn) (covalent) #status
               predicted
SUMMARY        #length 455 #molecular-weight 50494 #checksum 153
Query Match    48.0%; Score 1124; DB 1; Length 455;

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Best Local Similarity 99.3%; Pred. No. 2,76e-207;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 41 DSVCPQGYIHPNNSICCTCKHKTLYNDCCPGGQDTCRECESSGFTASENHLRCL 100
Oy 23 DSVCPQGYIHPNNSICCTCKHKTLYNDCCPGGQDTCRECESSGFTASENHLRCL 82
Db 101 SCSKCKEMGVEISSCVDVDTVGCGKKNQYRHWSENMLQCFCNSCLNGTVHLSQOE 160
Oy 83 SCSKCKEMGVEISSCVDVDTVGCGKKNQYRHWSENMLQCFCNSCLNGTVHLSQOE 142
Db 161 KONTVCTCHAGFFLENECVSCS 183
Oy 143 KONTVCTCHAGFFLENECVSCA 165

RESULT 3
ENTRY 1EXTA #type complete
TITLE tumor necrosis factor receptor extracellular domain, chain A
PDB-TITLE extracellular domain of the 55kDa tumor necrosis factor
ORGANISM receptor, crystallized at pH 7.7 in p 21 21 21.
#note #formal_name Homo sapiens #common_name man
        expressed in Escherichia coli, the construct contains
        residues 12 to 172 of the mature sequence of the entire
        receptor. residue 11 is mutated to met as a result of the
        expression system
REFERENCE      A65560
#authors       Nalsmith, J.H.; Sprang, S.R.
#submission    submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
REFERENCE      TN026248
#authors       Nalsmith, J.H.; Devine, T.O.; Brandhuber, B.J.; Sprang, S.R.
#journal       J. Biol. Chem. (1995) 270:13303
#title         Crystallographic evidence for dimerization of unliganded
               tumor necrosis factor receptor.
REFERENCE      TN026249
#authors       Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
               K.; Nalsmith, J.H.; Sprang, S.R.
#journal       J. Mol. Biol. (1994) 239:332
#title         Two crystal forms of the extracellular domain of type 1 tumor
               necrosis factor receptor.
REFERENCE      A40737
#authors       Banner, D.W.; D'Arcy, A.; Jones, W.; Gentz, R.; Schoenfeld,
               H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal       Cell (1993) 73:431-445
#title         Crystal structure of the soluble human 55 kd TNF
               receptor-human TNFbeta complex: implications for TNF
               receptor activation.
COMMENT        Resolution: 1.85 angstroms
               Determination: X-ray diffraction
               R-value: no refinement
               binding protein; cytokine; signalling protein
KEYWORDS
FEATURE
#region        #region helix (right hand 3-10)\
66-68          #region helix (right hand 3-10)\
141-143        #region helix (right hand alpha)\
151-154        #region beta sheet\
7-9,17-19     #region beta sheet\
131-134,137-140 #region beta sheet\
25-29,39-42   #region beta sheet\
71-74,83-85   #region beta sheet\
90-96,99-104  #region beta sheet\
111-115,124-127 #region beta sheet\
3-17          #disulfide_bonds\
18-31         #disulfide_bonds\
21-40         #disulfide_bonds\
43-58         #disulfide_bonds\
61-76         #disulfide_bonds\
64-84         #disulfide_bonds\
86-102        #disulfide_bonds\
105-117       #disulfide_bonds\
108-125       #disulfide_bonds\
127-138       #disulfide_bonds\

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141-154 #disulfide\_bonds\  
144-150 #disulfide\_bonds  
SUMMARY #length 160 #molecular-weight 18065 #checksum 2297

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Best Local Similarity 99.3%; Pred. No. 5,286-206;  
Matches 141; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 SVCPOGKIYHPNNNSICTCKHKGTYLYNDGPGPGDTCRCESGSGFTASENHLRHCLCS 60  
OY 24 SVCPOGKIYHPNNNSICTCKHKGTYLYNDGPGPGDTCRCESGSGFTASENHLRHCLCS 83

Db 61 CSKCKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 120  
OY 84 CSKCKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 143

Db 121 NTVCTCHAGFFLRENECVSCS 142  
OY 144 NTVCTCHAGFFLRENECVSCA 165

RESULT 4 INCFB #type complete  
ENTRY

TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
chain B - hu

ALTERNATE\_NAMES stnfr1; type 1 receptor  
ORGANISM #formal name Homo sapiens #common name man  
#note expressed in Escherichia coli, residue 11 is mutated to met  
as a result of the expression system

REFERENCE A6195  
#authors Naismith, J.H.; Sprang, S.R.  
#submission Submitted to the Brookhaven Protein Data Bank, October 1994  
#cross-references PDB:1NCF

REFERENCE TN029041  
#authors Rodwell, L.E.; Brandhuber, B.; Devlane, T.Q.; Eck, M.J.; Hale,  
K.; Naismith, J.H.; Sprang, S.R.  
#journal J. Mol. Biol. (1994) 239:332  
#title Two crystal forms of the extracellular domain of type 1 tumor  
necrosis factor receptor.  
A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
#journal Cell (1993) 73:431-445  
#title Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
binding protein; cytokine; signalling protein

KEYWORDS

FEATURE 2-16  
17-30 #disulfide\_bonds\  
20-39 #disulfide\_bonds\  
42-57 #disulfide\_bonds\  
60-75 #disulfide\_bonds\  
63-83 #disulfide\_bonds\  
85-101 #disulfide\_bonds\  
104-116 #disulfide\_bonds\  
107-124 #disulfide\_bonds\  
126-137 #disulfide\_bonds\  
SUMMARY #length 142 #molecular-weight 16046 #checksum 1225

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Best Local Similarity 99.3%; Pred. No. 3,786-205;  
Matches 140; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 VCPGKIYHPNNNSICTCKHKGTYLYNDGPGPGDTCRCESGSGFTASENHLRHCLCS 60  
OY 25 VCPGKIYHPNNNSICTCKHKGTYLYNDGPGPGDTCRCESGSGFTASENHLRHCLCS 84

Db 61 SKCKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 120  
OY 85 SKCKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 144

Db 121 NTVCTCHAGFFLRENECVSCS 141  
OY 145 NTVCTCHAGFFLRENECVSCA 165

RESULT 5 1TNRR #type complete  
ENTRY

TITLE tumor necrosis factor receptor type 1 (p55 extracellular  
#formal name Homo sapiens #common name man  
recombinant form expressed in Baculovirus Sf9  
A52442  
REFERENCE  
#authors Banner, D.W.  
#submission Submitted to the Brookhaven Protein Data Bank, May 1994  
#cross-references PDB:1TNRR  
A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
#journal Cell (1993) 73:431-445  
#title Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
TN034093  
#authors D'Arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;  
Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;  
Lesslauer, W.  
#journal J. Mol. Biol. (1993) 229:555  
#title Crystallization and preliminary analysis of tnf-beta and a  
tnf-beta-55 kd tnf receptor complex.  
Resolution: 2.85 angstroms  
Determination: X-ray diffraction  
Complex(lymphokineRECEPTOR)

KEYWORDS

FEATURE 1-15  
16-29 #disulfide\_bonds\  
19-38 #disulfide\_bonds\  
41-56 #disulfide\_bonds\  
59-74 #disulfide\_bonds\  
62-82 #disulfide\_bonds\  
84-100 #disulfide\_bonds\  
103-115 #disulfide\_bonds\  
106-123 #disulfide\_bonds\  
125-136 #disulfide\_bonds\  
SUMMARY #length 139 #molecular-weight 15746 #checksum 5235

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Best Local Similarity 100.0%; Pred. No. 3,176-203;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CPOGKIYHPNNNSICTCKHKGTYLYNDGPGPGDTCRCESGSGFTASENHLRHCLCS 60  
OY 26 CPOGKIYHPNNNSICTCKHKGTYLYNDGPGPGDTCRCESGSGFTASENHLRHCLCS 85

Db 61 KCKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 120  
OY 86 KCKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEK 145

Db 121 TVCTCHAGFFLRENECVSC 139  
OY 146 TVCTCHAGFFLRENECVSCA 164

RESULT 6 INCFB #type complete  
ENTRY

TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
chain A - hu

ALTERNATE\_NAMES stnfr1; type 1 receptor

ORGANISM	#formal_name Homo sapiens #common_name man
#note	expressed in Escherichia coli, residue 11 is mutated to met as a result of the expression system
REFERENCE	A66195
#authors	Naismith, J.H.; Sprang, S.R.
#submission	submitted to the Brookhaven Protein Data Bank, October 1994
#cross-references	PDB:1NCF
REFERENCE	TN029039
#authors	Rodeseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale, K.; Naismith, J.H.; Sprang, S.R.
#journal	J. Mol. Biol. (1994) 239:332
#title	Two crystal forms of the extracellular domain of type I tumor necrosis factor receptor.
REFERENCE	A40737
#authors	Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld, H.O.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal	Cell (1993) 73:431-445
#title	Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for TNF receptor activation.
COMMENT	Resolution: 2.25 angstroms
COMMENT	Determination: X-ray diffraction
COMMENT	R-value: no refinement
KEYWORDS	binding protein; cytokine; signalling protein
FEATURE	
5-19	
20-33	#disulfide_bonds\
23-42	#disulfide_bonds\
45-60	#disulfide_bonds\
63-78	#disulfide_bonds\
66-86	#disulfide_bonds\
88-104	#disulfide_bonds\
107-119	#disulfide_bonds\
110-127	#disulfide_bonds\
129-140	#disulfide_bonds
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Best Local Similarity	100.0%; Pred. No. 9,90e+202;
Matches 139; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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OY	23 DSVCPQGXIIHONNSICTCKHKGYLYNDGPGPDDRCPCSGSFASPNHLRHCL 82 
Db	62 SCSCRKEKGQVEISSCTYDRDTCVCGCRKNQRYHYSENLFQCFNCSLCINGVHLSCE 121 
OY	83 SCSCRKEKGQVEISSCTYDRDTCVCGCRKNQRYHYSENLFQCFNCSLCINGVHLSCE 142 
Db	122 KONTVCTCHAGFFLRENEC 140 
OY	143 KONTVCTCHAGFFLRENEC 161 
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DATE	21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
ACCESSIONS	I37412
REFERENCE	I37412
#authors	Talmadge, K.; Yamvakopoulos, N.C.; Fiddes, J.C.
#journal	Nature (1984) 307:37-40
#title	Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone.
#cross-references	MUID:84093590
#accession	I37412
#status	preliminary; translated from GB/EMBL/DDBJ
#molecule_type	DNA
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##cross-references	EMBL:X00265; NID:g31119
GENETICS	

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44.0%;	Score 1030;	DB 2:	Length 145;			
Pred. No. 3.16e-187;						
41/3	#superfamily pituitary glycoprotein hormone beta chain					
CLASSIFICATION	#length 145	#checksum 2358				
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Qy	169	PRCRRINATLVEKGCVCITVNTTICAGTCGPTMTRYLQGVLPALPOLVVCNRYDVFRES	228			
Db	67	IRLPECPCGVNPVSYANALSCQALCRSRITDCGGPDHPLTCDPFDQSSSSKAPP	126			
Qy	229	IRLPECPCGVNPVSYANALSCQALCRSRITDCGGPDHPLTCDPFDQSSSSKAPP	288			
Db	127	SLPSPRLPGSPDPTILPQ	145			
Qy	289	SLPSPRLPGSPDPTILPQ	307			
RESULT	8					
ENTRY	KTUDB	#type complete				
TITLE	Chorionodotrofin beta chain precursor - humanALTRRNATE_NAMES					
ORGANISM	Homo sapiens					
DATE	23-Oct-1981					
ACCESSIONS	A93230; I69972; I55224; I70007; I70008; A92303; A92181; A92142; PC1016; A61097; B56873; A01502					
REFERENCE	A93230 Fiddes, J.C.; Goodman, H.M.					
#authors	Fiddes, J.C.; Goodman, H.M.					
#journal	Nature (1980) 286:684-687					
#title	The CDNA for the beta-subunit of human chorionic gonadotropin suggests evolution of a gene by readthrough into the 3'-untranslated region.					
#cross-references	MIM:112134					
#accession	A93230					
#molecule_type	mRNA					
#residues	1-165					
#cross-references	GB:J00117; GB:M8559; GB:M54563; NID:g180436; PID:g180437					
REFERENCE	I55224					
#authors	Pollicastro, P.; Ovit, C.E.; Hoshina, M.; Fukuoaka, H.; Boothby, M.R.; Bolme, I.					
#journal	J. Biol. Chem. (1983) 258:11492-11499					
#title	The beta subunit of human chorionic gonadotropin is encoded by multiple genes.					
#cross-references	MIM:8408141					
#accession	I69972					
#status	translated from GB/EMBL/DBJ					
#molecule_type	DNA					
#residues	1-165					
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#note	clone CG-beta-e					
#accession	I55224					
#status	translated from GB/EMBL/DBJ					
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#residues	1-23, 'M', 25-136, 'A', 138-165					
#cross-references	GB:K03183; NID:g180442; PID:g180444					
#note	clone CG-beta-a					
REFERENCE	I55250					
#authors	Pollicastro, P.F.; Daniels-McQueen, S.; Carle, G.; Bolme, I.					
#journal	J. Biol. Chem. (1986) 261:5907-5916					
#title	A map of the hCG beta-LH beta gene cluster.					
#cross-references	MIM:86195987					
#accession	I55250					
#status	preliminary; translated from GB/EMBL/DBJ					
#molecule_type	DNA					
#residues	1-5					
#cross-references	GB:M13504; NID:g180419; PID:g463088					
#note	CG-beta-3 gene					
#accession	I70007					

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##residues    1-5 ##label PO4
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##note        CG-beta-6 gene
#accession    I70008
##status      preliminary; translated from GB/EMBL/DBJ
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##residues    1-5 ##label RPS
##cross-references GB:M13503; NID:g180432; PID:g463090
##note        CG-beta-7 gene
#accession    A92303
#authors      Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
#journal      J. Biol. Chem. (1981) 256:1816-1823
#title        The amino acid sequences of the prepeptides contained in the
              alpha and beta subunits of human choriongonadotropin.
#cross-references MIM:81117268
#accession    A92303
##molecule_type protein
##residues    1-20 ##label BIR
##note        the identity of the residue at position 19 could not be
              determined
#accession    A92181
#authors      Morgan, F.J.; Birken, S.; Canfield, R.E.
#journal      J. Biol. Chem. (1975) 250:5247-5258
#title        The amino acid sequence of human chorionic gonadotropin. The
              alpha subunit and beta subunit.
#cross-references MIM:75211304
#accession    A92181
##molecule_type protein
##residues    21-165 ##label MOR
#accession    A92142
#authors      Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
#journal      J. Biol. Chem. (1973) 248:6810-6827
#cross-references MIM:74011267
#accession    A92142
##molecule_type protein
##residues    21-22,'O',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
              ##label CAR
#accession    PC1016
#authors      Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.;
              Wang, Y.
#journal      Chinese Biochem. J. (1990) 6:558-562
#title        The immunological characteristics of the enzymatic fragments
              of human chorionic gonadotropin beta-subunit.
#accession    PC1016
##molecule_type protein
##residues    21-165 ##label SHI
##note        article in Chinese with English abstract
#accession    A61097
#authors      Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.;
              Agosto, G.M.; Krichevsky, A.; Valtukaitis, J.L.; Canfield,
              R.E.
#journal      Endocrinology (1988) 123:572-583
#title        Structure of the human chorionic gonadotropin beta-subunit
              fragment from pregnancy urine.
#accession    A61097
##molecule_type protein
##residues    26-32,'X',34-49,'X',51-60,75-112 ##label B12
##note        this material from pregnancy urine lacks stialic acid in
              its carbohydrate and has been processed further from
              the mature form into two chains linked by disulfide
              bonds
#accession    A56873
#authors      Kaidana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
#journal      Br. J. Cancer (1993) 67:686-692
#title        Characterisation of USP and its relationship with beta-core
              fragment.
#cross-references MIM:93229246
#accession    B56873
##molecule_type protein
##residues    26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',
              78-91,'G',93-102 ##label KAR

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##experimental_source urine
##note        sequence modified after extraction from NCBI backbone
              this material was designated urinary gonadotropin
              peptide (peak 2)
#accession    A44674
#authors      Laphorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
              J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaac,
              N.W.
#journal      Nature (1994) 369:455-461
#title        Crystall structure of human chorionic gonadotropin.
              annotation; X-ray crystallography, 3.0 angstroms; correction
              of disulfide bonds
#contents
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#gene         GDB:CGB
##cross-references GDB:119055; OMIM:118860
#map_position 19q13.3-19q13.3
#introns      5/3; 61/3
#note         the choriongonadotropin beta chain locus contains six genes
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              #superfamily pituitary glycoprotein hormone beta chain
              glycoprotein; hormone; pituitary
#CLASSIFICATION
#KEYWORDS     #domain signal sequence #status experimental #label SIG\
              #product choriongonadotropin beta chain #status
              experimental #label MAT\
#FEATURES
#1-20         #disulfide_bonds #status experimental\
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              experimental\
              #binding_site carbohydrate (Ser) (covalent) #status
              predicted\
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              experimental
141,147,152,158 #length 165 #molecular_weight 17739 #checksum 6523
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              169 PCRPRINATLAVKRGCPVCTVNTTICAGTCPTTRVLQGVLPALPOVVCYRVDVRES 228
#Db          87 IRLPGCPGVNVYVYAVALSCQALCRSTDCGPRDHPRTCDPRDSSSKAPP 146
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              229 IRLPGCPGVNVYVYAVALSCQALCRSTDCGPRDHPRTCDPRDSSSKAPP 288
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              289 SUPSPRLPGSPDTPILPQ 307
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#DATE        21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
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#REFERENCE   I37231
#authors     Talmadge, K.; Vamvakopoulos, N.C.; Fildes, J.C.
#journal     Nature (1984) 307:37-40
#title       Evolution of the genes for the beta subunits of human
              chorionic gonadotropin and luteinizing hormone.
#cross-references MIM:84093590
#accession   I37231
##status     preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues   1-145 ##label RPS
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#introns     41/3

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[illegible]

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#residues  1-454  ##label  ROT
#cross-references  EMBL:X57796; NID:g54848; PID:g54849
REFERENCE
#authors  Bebo, B.F.
#journal  Immunogenetics (1994) 39:450-451
#title  Nucleotide sequence of the TNF type I receptor from a mouse endothelium cell line.
#cross-references  MIMD:94245292
#accession  I54532
#status  translated from GB/EMBL/DBJ
#molecule_type  mRNA
#residues  1-454  ##label  RRS
#cross-references  GB:L26349; NID:g430732; PID:g430733
COMMENT  This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
1-29
30-454
30-212
44-82
84-126
127-167
168-204
213-235
236-454
54,151,202
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#product tumor necrosis factor receptor type 1 #status predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#domain NGF receptor repeat homology #label NG1\
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#domain intracellular #status predicted #label INT\
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Matches 101; Conservative 23; Mismatches 19; Indels 0; Gaps 0;
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OY 23 DSVCPGKRIHPQNNISICTCKHKGTLYVNCPPGDDTCRECESSFTASEHNLHCL 82
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 101 SCKTKCKREMSQVEISPCQADKDYVCGCKENQFQYLTETHFQCVDCSPCENGVTYTPCKE 160
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OY 83 SCSCCKREMGVEISSCVYDRDYVCGCKRNKRHYWSENLFOCFNCISLCLNGTHTLSCQE 142
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Db 161 TONTVNCNAGFPLRESQVPCS 183
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OY 143 KONTVCTCHAGFPLENDCVSCA 165
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RESULT 14
ENTRY
GQRTT1 #type complete
TITLE tumor necrosis factor receptor type 1 precursor - ratCONTAINS
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 05-Sep-1997
ACCESSIONS B36555
REFERENCE A36555
#authors Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
Pitzemmler, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
Stratowa, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
derivative, tumor necrosis factor-binding protein.
#cross-references MIMD:91090841
#accession B36555
#molecule_type mRNA
#residues 1-461 ##label HIM
#cross-references GB:M63122; NID:g207361; PID:g207362

```

COMMENT This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS

FEATURE

1-79 #domain signal sequence #status predicted #label SIG\

30-461 #product tumor necrosis factor receptor type 1 #status predicted #label MAT\

30-211 #domain extracellular #status predicted #label EXT\

30-201 #product tumor necrosis factor binding protein #status predicted #label TBP\

44-82 #domain NGF receptor repeat homology #label NG1\

84-126 #domain NGF receptor repeat homology #label NG2\

127-167 #domain NGF receptor repeat homology #label NG3\

168-204 #domain NGF receptor repeat homology #label NG4\

212-234 #domain transmembrane #status predicted #label MEM\

235-461 #domain intracellular #status predicted #label INT\

54,151,201 #binding\_site carbohydrate (Asn) (covalent) #status predicted

SUMMARY #length 461 #molecular-weight 50969 #checksum 1617

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QY 23 DSVCPGKTIHPNNNSICTCKHGYLYNDPCGPGDITDCRECSGSEFTASSENHLRHCL 82

Db 101 SCTCKREMEFQVEISPCAKMDFTVCGKKNQFORYISETHFOCVDSPCFNGTVPDCKE 160

QY 83 SCCKCKREKMGQVETISCTYDRDVTVCCKKNQYHWSENLFCQFCSLCLNGTVHLSQCE 142

Db 161 KONTVCNCHAGFLSGNECTPCS 183

QY 143 KONTVCTCHAGFLRENECVSCA 165

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ORGANISM #formal\_name Homo sapiens #common\_name man

REFERENCE #authors A66957

#submission Jjiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N. submitted to the Brookhaven Protein Data Bank, December 1996

REFERENCE #cross-references PDB:1XUL

#authors Jjiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N.

#journal Structure (London) (1996) 3:1341

#title Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions structure.

REFERENCE TNO32626

#authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.; Hendrickson, W.A.

#journal Structure (London) (1994) 2:545

#title Structure of human choriionic gonadotropin at 2.6 a resolution from mad analysis of the selenomethionyl protein.

COMMENT Resolution: not applicable

KEYWORDS Determination: theoretical model

KEYWORDS complex; glycoprotein hormone receptor glycoprotein; hormone; phosphorylation; receptor

FEATURE

97-101,26-39,9-17 #region beta sheet\

54-59,86-91 #region beta sheet\

61-67,78-84 #region beta sheet\

8-56 #disulfide\_bonds\

22-71 #disulfide\_bonds\

25-109 #disulfide\_bonds\

33-87 #disulfide\_bonds\

37-89 #disulfide\_bonds\

92-99 #disulfide\_bonds\

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QY 169 PRCPINATLAVEKECCPVCTIVNTTICAGYCPMTNRVLQGVLPALPQVYCNRYRFEES 228

Db 66 IRLPGCPRGVNPVSYAVALSCQCALCRSTDDGSPKDHPLTCD 110

QY 229 IRLPGCPRGVNPVSYAVALSCQCALCRSTDDGSPKDHPLTCD 273

Search completed: Wed May 6 08:55:58 1998

Job time : 34 secs.

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 RX MEDLINE; 90110215.  
 RA ENGELMANN H., NOVICK D., WALLACH D.;  
 RL J. BIOL. CHEM. 265:1531-1536(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
 RX MEDLINE; 93258809.  
 RA BANNER D.W., D'ARCY A., JAMES W., GENTZ R., SCHOENFELD H.-J.,  
 RL BROGER C., LOETSCHER H., LESSLAUER W.,  
 RL CELL 73:431-445(1993).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE; 97094982.  
 RA NAIMSMITH J.H., DEVINE T.O., RHONO H., SPRANG S.R.;  
 RL STRUCTURE 4:1251-1262(1996).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS.  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; X55313; G37224; -;  
 DR EMBL; M33394; G339745; -;  
 DR EMBL; M58286; G339754; -;  
 DR EMBL; M63121; G339756; -;  
 DR EMBL; M75866; G339750; -;  
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 DR EMBL; M75865; G339750; JOINED.  
 DR EMBL; M60275; G339760; -;  
 DR EMBL; A21522; G579600; -;  
 DR PIR; A34899; G0HUT1.  
 DR PIR; A35010; A35010.  
 DR PIR; S12057; S12057.  
 DR PIR; A38208; A38208.  
 DR PDB; 1TNR; 31-JUL-94.  
 DR PDB; 1NCF; 07-DEC-95.  
 DR PDB; 1EXT; 11-JAN-97.  
 DR MIM; 191190; -;  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KM RECEPTOR, TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;  
 KW 3D-STRUCTURE.  
 FT SIGNAL 1 21  
 FT CHAIN 22 455  
 FT CHAIN 41 291  
 FT DOMAIN 22 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 455  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
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 FT DOMAIN 356 441  
 FT DISULFID 44 58  
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 FT DISULFID 102 117  
 FT DISULFID 105 125

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 Db 41 DSVCPQGYIHPNNSICTCKHGTLYNDPCPGQDPTDCRECSGSFTASENHLRCL 100  
 QY |||||  
 Db 23 DSVCPQGYIHPNNSICTCKHGTLYNDPCPGQDPTDCRECSGSFTASENHLRCL 82  
 QY |||||  
 Db 101 SCSCKRKMGEYIISCTVDYDTCGCKRKNRYHWSNLFQCFNCSICLNGYHLSQCE 160  
 QY |||||  
 QY 83 SCSCKRKMGEYIISCTVDYDTCGCKRKNRYHWSNLFQCFNCSICLNGYHLSQCE 142  
 Db 161 KONTVCCHAGFLRENECVCS 183  
 QY |||||  
 QY 143 KONTVCCHAGFLRENECVCS 165  
 RESULT 2  
 ID CGHB\_HUMAN STANDARD; PRT; 165 AA.  
 AC P01233;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DE 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPIN BETA  
 DE SUBUNIT).  
 GN CGB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 81012134.  
 RA FIDDES J.C., GOODMAN H.M.;  
 RL NATURE 286:684-687(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 84093590.  
 RA TAIMADGE K., VAYANAKOPOULOS N.C., FIDDES J.C.;  
 RL NATURE 307:37-40(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 84008141.  
 RA POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,  
 RL J. BIOL. CHEM. 258:11492-11499(1983).  
 RN [4]  
 RP SEQUENCE OF 1-20.  
 RX MEDLINE; 81117268.  
 RA BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;  
 RL J. BIOL. CHEM. 256:1816-1823(1981).  
 RN [5]  
 RP SEQUENCE OF 21-165.  
 RX MEDLINE; 75211304.  
 RA MORGAN F.J., BIRKEN S., CANFIELD R.E.;  
 RL J. BIOL. CHEM. 250:5247-5258(1975).  
 RN [6]  
 RP PRELIMINARY SEQUENCE OF 21-165.  
 RX MEDLINE; 74011267.  
 RA CARLSEN R.B., BAHL O.P., SWAMINATHAN N.;  
 RL J. BIOL. CHEM. 248:6810-6827(1973).

RP SEQUENCE OF 1-5 FROM N.A.  
 RX MEDLINE; 86195987.  
 RA POLICISTRO P.F., DANIELS-MCQUEEN S., CARLE G., BOIME I.;  
 RL J. BIOL. CHEM. 261:5907-5916(1986).  
 RN (8)  
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
 RX MEDLINE; 81215630.  
 RA MISE T., BAH L O P.  
 RL J. BIOL. CHEM. 256:6587-6592(1981).  
 RN (9)  
 RP DISULFIDE BONDS.  
 RX MEDLINE; 90094415.  
 RA SACCUBO BEEBE J., MOUNTJOY K., KRZESICKI R.F., PERINI F.,  
 RA RUDDON R.W.;  
 RL J. BIOL. CHEM. 265:312-317(1990).  
 RN (10)  
 RP STRUCTURE OF CARBOHYDRATES.  
 RX MEDLINE; 92314469.  
 RA WEISSHAR G., HIYAMA J., RENNICK A.G.C.;  
 RL GLYCOBIOLOGY 1:393-404(1991).  
 RN (11)  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE; 94261179.  
 RA LATHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,  
 RA CARFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;  
 RL NATURE 369:455-461(1994).  
 CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT  
 ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC -1- TISSUE SPECIFICITY: PLACENTA.  
 CC -1- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.  
 DR EMBL; J00117; G180437; -;  
 DR EMBL; M13504; G463088; -;  
 DR EMBL; M13505; G463089; -;  
 DR EMBL; M13503; G463090; -;  
 DR EMBL; K03189; G180453; -;  
 DR EMBL; K03187; G180453; JOINED.  
 DR EMBL; K03186; G180453; JOINED.  
 DR PIR; A01502; KTHUB.  
 DR PDB; 1HCN; 30-SEP-94.  
 DR PDB; 1HRP; 01-NOV-94.  
 DR MIM; 118860; -;  
 DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE; PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 DR KW HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.  
 FT SIGNAL 1 20  
 FT CHAIN 1 165  
 FT DISULFID 29 77 CHORIOGONADOTROPIN BETA CHAIN.  
 FT DISULFID 43 92  
 FT DISULFID 46 130  
 FT DISULFID 54 108  
 FT DISULFID 58 110  
 FT DISULFID 113 120  
 FT CARBOHYD 33 33  
 FT CARBOHYD 50 50  
 FT CARBOHYD 141 141  
 FT CARBOHYD 147 147  
 FT CARBOHYD 152 152  
 FT CARBOHYD 158 158  
 FT VARIANT 137 137  
 FT SEQUENCE 165 AA; 17739 MM; FRIID802 CR32;  
 D -> A (IN GENE 6).  
 Query Match 44.0%; Score 1030; DB 1; Length 165;  
 Best Local Similarity 100.0%; Pred. No. 8,926-219;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps

Db	87	IRLGCPRGVNPNVSVAVNVALSCGALCRSTTCGGCKHPLTCCDDPRDSSSSKAPP	146
Oy	229	IRLGCPRGVNPNVSVAVNVALSCGALCRSTTDCGGKHPHPLTCCDDPRDSSSSKAPP	288
Db	147	SLPSPSRLLPGSPDPIPLPQ	165
Oy	289	SLPSPSRLLPGSPDPIPLPQ	307
RESULT	3	STANDARD;	PRT; 461 AA.
ID	TNR1_PIG		
AC	PS0555;		
DT	01-OCT-1996 (REL. 34, CREATED)		
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)		
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).		
GN	TNR1.		
OS	SUS SCROFA (PIG).		
OC	EUAROTIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; ARTIODACTYLA.		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE-KIDNEY;		
RX	MEDLINE; 96011645.		
RA	SUTER B., PAULI U.H.;		
RL	GENE 163;263-266(1995).		
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD		
CC	RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING		
CC	AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)		
CC	PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE		
CC	SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE		
CC	PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).		
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO		
CC	HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS		
CC	PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY		
CC	WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING		
CC	PROTEINS SUCH AS TRAF6, RIP AND POSSIBLY FADD, ARE RECRUITED TO		
CC	TNR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX		
CC	ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND		
CC	NF-KAPPA B SIGNALING (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.		
DR	EMBL; U19994; G1141753; -.		
DR	PROSITE; PS00652; TNFR_NGFR.1; 3.		
DR	PROSITE; PS50050; TNFR_NGFR.2; 2.		
DR	PROSITE; PS50017; DEATH_DOMAIN: 1.		
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.		
FT	SIGNAL	1	21
FT	CHAIN	22	461
FT	DOMAIN	22	210
FT	TRANSMEM	211	233
FT	DOMAIN	234	461
FT	DOMAIN	43	195
FT	REPEAT	43	82
FT	REPEAT	83	125
FT	REPEAT	126	166
FT	REPEAT	167	195
FT	DOMAIN	362	447
FT	DISULFID	44	58
FT	DISULFID	59	72
FT	DISULFID	62	81
FT	DISULFID	84	99
FT	DISULFID	102	117
FT	DISULFID	105	125
FT	DISULFID	127	143
FT	DISULFID	146	158
FT	DISULFID	149	166
FT	DISULFID	168	179
FT	DISULFID	182	190
FT	DISULFID	185	194
FT	CARBOHYD	54	54
FT	CARBOHYD	86	86
FT	CARBOHYD	145	145

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FT CARBOHYD 151 151 POTENTIAL.
SQ SEQUENCE 461 AA; 50696 MW; 8E2C350A CRC32;
Query Match
Best Local Similarity 80.3%; Score 955; DB 1; Length 461;
Matches 114; Conservative 16; Mismatches 12; Indels 0; Gaps 0;
Db 41 ESLCPQKXSHPNONSICCTCKCHKGYLLANDLGPGLDTCRECDNGTFTASENHLTCL 100
Oy 23 DSVCPQKXIHPNONSICCTCKCHKGYLLANDLGPGLDTCRECDNGTFTASENHLTCL 82
Db 101 SCSKRSKMSQVEISPCYVDRTVCGCRNORYKRWSETLFQCLNCSLCPNQTQVLPCL 160
Oy 83 SCSKRSKMSQVEISPCYVDRTVCGCRNORYKRWSETLFQCLNCSLCPNQTQVLPCL 142
Db 161 KODTICNCHSGFELDKECVSC 182
Oy 143 KONTVCTCHAGFFLENECVSC 164
RESULT 4
ID CGHB_PAPAN STANDARD; PRT; 165 AA.
AC P07434.
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPIN BETA SUBUNIT).
GN CGB.
OS PARIO ANDEBIS (OLIVE BABOON).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 87106851.
RA CRAWFORD R.J., TREGAR G.W., NIALL H.D.;
RL GENE 46:161-169(1986).
CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC -1- SUBUNIT: HETEROIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- TISSUE SPECIFICITY: PLACENTA.
CC -1- THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
DR EMBL: M14966; G176573; -.
DR PIR: A25808; KTBAB.
DR HSSP: P01333; 1HCN.
DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT CHAIN 1 20 BY SIMILARITY.
FT SIGNAL 21 165 CHORIOGONADOTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 BY SIMILARITY.
FT CARBOHYD 50 50 BY SIMILARITY.
FT CARBOHYD 141 141 BY SIMILARITY.
FT CARBOHYD 147 147 BY SIMILARITY.
FT CARBOHYD 152 152 BY SIMILARITY.
SQ SEQUENCE 165 AA; 17592 MW; 78987D30 CRC32;
Query Match
Best Local Similarity 81.3%; Score 857; DB 1; Length 165;
Matches 113; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
Db 27 PLCPRIINATLAERACPCVTVNTTICAGCPTPMARIVQAVLPVPVQVYCYREVRES 86
Oy 169 PRCRINATLAERACPCVTVNTTICAGCPTPMARIVQAVLPVPVQVYCYREVRES 228

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Db 87 IRLPCPPGVDPVMSVPYALSCALCRSTSDCGPDKHPLTCDPMLQAASSSKDPP 146
Oy 229 IRLPCPPGVDPVMSVPYALSCALCRSTSDCGPDKHPLTCDPMLQAASSSKDPP 288
Db 147 SPSPSRLLPEAGTFFLPQ 165
Oy 289 SPSPSRLLPEAGTFFLPQ 307
RESULT 5
ID TNRI_MOUSE STANDARD; PRT; 454 AA.
AC P25118.
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN TNFR1 OR TNFR-1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91187885.
RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA WONG G.H., CHEN E.Y., GOEDEL D.Y.;
RA PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91246168.
RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL MOL. CELL. BIOL. 11:3020-3026(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91285014.
RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA GRAY P.W., FELDAMANN M., FOXWELL B.M.J.;
RL EUR. J. IMMUNOL. 21:1649-1656(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE-SPLEEN.
RC MEDLINE: 92039815.
RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RL IMMUNOGENETICS 34:338-340(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94245292.
RA BEBO B.F., LINTHICUM D.S.;
RL IMMUNOGENETICS 39:450-451(1994).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93156721.
RA ROTHE J., BLUTHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RL MOL. IMMUNOL. 30:165-175(1993).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DR EMBL: M59377; G202097; -.

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DR EMBL: X59238; G53579; -
DR EMBL: X57796; G54849; -
DR EMBL: L26349; G430733; -
DR EMBL: M76656; G202102; -
DR EMBL: M88067; G202102; JOINED.
DR EMBL: M76655; G202102; JOINED.
DR PIR: A38634; GOMSP1.
DR PIR: S16677; S16677.
DR PIR: S19021; S19021.
DR HSP: P19438; 1TNR.
DR MGD: MGI:98781; 1TNR.
DR PROSITE: PS00652; TNR_NGFR_1; 3.
DR PROSITE: PS0050; TNR_NGFR_2; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
KM SIGNAL 1 21
FT CHAIN 1 21
FT DOMAIN 22 454
FT TRANSMEM 213 235
FT DOMAIN 236 454
FT DOMAIN 43 186
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT DOMAIN 356 441
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHYD 34 54
FT CARBOHYD 151 151
FT CARBOHYD 202 202
FT CONFLICT 394 394
SQ SEQUENCE 454 AA; 50129 MM; 486ECC09 CRC32;

Query Match 35.98; Score 841; DB 1; Length 454;
Best Local Similarity 70.6%; Pred. No. 7.59e-172;
Matches 101; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

Db 41 DNLCPGKTYAHKNNISICCTCKHKGTYLVSDCPSPGQDYVCECEKGTFTASQNYLRQCL 100
QY 23 DSVCPGKTYIHPONNSICCTCKHKGTYLVSDCPSPGQDYVCECEKGTFTASQNYLRQCL 82
Db 101 SCCTCKREKMFQVETISPCQADKDTVCCKENQFQRYLSETHFQCVDSPCFNGTYTPCKE 160
QY 83 SCCTCKREKMFQVETISPCQADKDTVCCKENQFQRYLSETHFQCVDSPCFNGTYTPCKE 160
QY 83 SCCTCKREKMFQVETISPCQADKDTVCCKENQFQRYLSETHFQCVDSPCFNGTYTPCKE 160
Db 161 TQNTVCHAGGFLRESECVCS 183
QY 143 KQNTVCHAGGFLRESECVCSA 165

RESULT 6
ID TNR1_RAT STANDARD; PRT; 461 AA.
AC P22934;
DT 01-AUG-1991 (REL. 19, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNR-R1) (P55).
GN TNR1 OR TNR-1.
OS RATIUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
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RP SEQUENCE FROM N.A.
RX HEMLINE: 91090841.
RA HANMER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA LANTZ M., OLSSON I., HAUTMANN R., STRATOWA C., ADOLF G.R.;
RL DNA CELL BIOL. 9:705-715(1990).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAF6, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M63122; G207362; -
DR PIR: B36555; B36555.
DR HSP: P19438; 1TNR.
DR PROSITE: PS00652; TNR_NGFR_1; 3.
DR PROSITE: PS0050; TNR_NGFR_2; 3.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.
KM SIGNAL 1 21
FT CHAIN 1 21
FT DOMAIN 22 455
FT TRANSMEM 212 234
FT TRANSMEM 235 461
FT DOMAIN 43 196
FT DOMAIN 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT REPEAT 167 196
FT DOMAIN 363 448
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
SQ SEQUENCE 461 AA; 50969 MM; 82F68B08 CRC32;

Query Match 34.68; Score 809; DB 1; Length 461;
Best Local Similarity 68.5%; Pred. No. 5.98e-164;
Matches 98; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Db 41 DNLCPGKTYAHKNNISICCTCKHKGTYLVSDCPSPGQDYVCECEKGTFTASQNYLRQCL 100
QY 23 DSVCPGKTYIHPONNSICCTCKHKGTYLVSDCPSPGQDYVCECEKGTFTASQNYLRQCL 82
Db 101 SCCTCKREKMFQVETISPCQADKDTVCCKENQFQRYLSETHFQCVDSPCFNGTYTPCKE 160
QY 83 SCCTCKREKMFQVETISPCQADKDTVCCKENQFQRYLSETHFQCVDSPCFNGTYTPCKE 160
QY 83 SCCTCKREKMFQVETISPCQADKDTVCCKENQFQRYLSETHFQCVDSPCFNGTYTPCKE 160
Db 161 TQNTVCHAGGFLRESECVCS 183
QY 143 KQNTVCHAGGFLRESECVCSA 165
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RESULT 7
ID LSHB_HUMAN STANDARD: PRT: 141 AA.
AC P01229.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).
GN LHB.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE; 84093590.
RA TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;
RL NATURE 307:37-40(1984).
RN [2]
RX SEQUENCE OF 21-141.
RX MEDLINE; 76062547.
RA SAIRAM M.R., LI C.H.;
RL BIOCHIM. BIOPHYS. ACTA 412:70-81(1975).
RN [3]
RX PRELIMINARY SEQUENCE OF 21-141.
RX MEDLINE; 73090987.
RA SHOME B., PARLOW A.F.;
RL J. CLIN. ENDOCRINOL. METAB. 36:618-621(1973).
RN [4]
RX PRELIMINARY PARTIAL SEQUENCE.
RX MEDLINE; 73221227.
RA CLOSET J., HENNEN G., LEQUIN R.M.;
RL FEBS LETT. 29:97-100(1973).
RN [5]
RX STRUCTURE OF CARBOHYDRATE.
RX MEDLINE; 91122088.
RA WEISSHAR G., HIYAMA J., RENWICK A.G.C., NIMTZ M.;
RL EUR. J. BIOCHEM. 195:257-268(1991).
RN [6]
RX STRUCTURE BY NMR OF 58-77.
RX MEDLINE; 92357029.
RA KEUTMANN H.T., HUA Q.-X., WEISS M.A.;
RL MOL. ENDOCRINOL. 6:904-913(1992).
RN [7]
RX VARIANT ARG-74.
RX MEDLINE; 92085985.
RA WEISS J., AXELROD L., WHITCOMB R.W., HARRIS P.E., CROWLEY W.F.,
RL JAMESON J.L.;
RN NEW ENGL. J. MED. 326:179-183(1992).
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- TISSUE SPECIFICITY: PITUITARY.
CC -1- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CHARACTERIZED BY INFERTILITY AND PSEUDOHENARPHRODITISM.
DR EMBL; X00264; E28368; -.
DR EMBL; S71273; E91454; -.
DR PIR; A01497; UTHUB.
DR HSSP; P01233; IHON.
DR MIM; 152780; -.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL; PSEUDOHENARPHRODITISM;
KW DISEASE MUTATION.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 50 50 BY SIMILARITY.

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FT VARIANT 74 74 Q -> R (IN HYPOGONADISM; LACK OF
FT CONFLICT 39 39 RECEPTOR-BINDING).
FT CONFLICT 76 76 E -> Q (IN REF. 2).
FT CONFLICT 132 135 MISSING (IN REF. 2).
FT SEQUENCE 141 AA; 15345 MW; A2457F6F CRC32;
SO
Query Match 31.6%; Score 740; DB 1; Length 141;
Best Local Similarity 84.4%; Pred. No. 5,556-147;
Matches 92; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
DB 27 PWCFPNAIILAVEKGCVCVTNTTICAGTCPTMRYLQAVLPPLPVQCYTRDVFES 86
QY 169 PRCRINNTLAVEKGCVCVTNTTICAGTCPTMRYLQAVLPPLPVQCYTRDVFES 228
DB 87 IRLPGCRGVDPVVSFPAVLSGRCGRCRRSTDCGGPRDHLTCDHPOL 135
QY 229 IRLPGCRGVDPVVSFPAVLSGRCGRCRRSTDCGGPRDHLTCDHPOL 277
RESULT 8
ID CGHB_CALTA STANDARD: PRT: 164 AA.
AC P51500.
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPIN BETA
SUBUNIT).
GN CGR.
OS CALLITHRIX JACCHUS (COMMON MARMOSETT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; PRIMATES.
RN [1]
RX SEQUENCE FROM N.A.
RX TISSUE-PLACENTA.
RX MEDLINE; 96115012.
RA SIMULA A.P., AMATO F., FAAST R., LOPATA A., BERKA J., NORMAN R.J.;
RL BIOL. REPROD. 53:380-389(1995).
CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- TISSUE SPECIFICITY: PLACENTA.
DR EMBL; U04447; G606607; -.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 164 CHORIOGONADOTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 50 50 BY SIMILARITY.
FT CARBOHYD 146 146 BY SIMILARITY.
FT CARBOHYD 151 151 BY SIMILARITY.
SO SEQUENCE 164 AA; 17712 MW; E36A4DB3 CRC32;
Query Match 30.3%; Score 709; DB 1; Length 164;
Best Local Similarity 64.7%; Pred. No. 2,186-139;
Matches 90; Conservative 25; Mismatches 23; Indels 1; Gaps 1;
DB 27 PLCRPVNAIILAVEKGCVCVTNTTICAGTCSSMYRVLQAVLPPLPVQCYTRDVFES 86
QY 169 PRCRINNTLAVEKGCVCVTNTTICAGTCPTMRYLQAVLPPLPVQCYTRDVFES 228
DB 87 VRLPGCRGVDPVVSFPAVLSGRCGRCRRSTDCGSLNRPGLCDYSTFOSSS-KDPPR 145
QY 229 IRLPGCRGVDPVVSFPAVLSGRCGRCRRSTDCGSLNRPGLCDYSTFOSSS-KDPPR 288

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Db 146 NLTSQSOLLEPADPLVPQ 164  
 QY 289 SLSPSRLPGSPDPLPQ 307

RESULT 9  
 ID LSHB\_EOVAS STANDARD: PRT: 169 AA.  
 AC P19794:  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-NOV-1993 (REL. 32, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).  
 GN LHB.  
 OS EQUUS ASINUS (DONKEY).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PERISSODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA CHORINEAU M., COMBARNOUS Y., ALLEN W.R., STEWART F.;  
 RL SUBMITTED (JUL-1994) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [2]  
 RP PRELIMINARY SEQUENCE OF 105-169 FROM N.A.  
 RC TISSUE-PLACENTA;  
 RX MEDLINE: 90262634.  
 RA LEIGH S.E.A., STEWART F.;  
 RL J. MOL. ENDOCRINO. 4:143-150(1990).  
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
 THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC EMBL: X80116; G510971; -;  
 DR EMBL: X53669; E27544; ALT-SEQ.  
 DR PIR: S15676; S15676.  
 DR HSSP: P01233; 1HCN.  
 DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 KW HORMONE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 20  
 FT CHAIN 1 169  
 FT DISULFID 29 77 LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.  
 FT DISULFID 43 92 BY SIMILARITY.  
 FT DISULFID 46 130 BY SIMILARITY.  
 FT DISULFID 54 108 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 113 120 BY SIMILARITY.  
 FT CARBOHYD 33 33 PROBABLE.  
 SQ SEQUENCE 169 AA; 17943 MW; 9DA85421 CRC32;

Query Match 26.98; Score 630; DB 1; Length 169;  
 Best Local Similarity 63.48; Pred. No. 3.88e-120;  
 Matches 85; Conservative 21; Mismatches 23; Indels 5; Gaps 4;

Db 27 PLCPRIATLAKEKPCITFTTSCAGYCSMRVMAALPPIQPCVCTYRELFGS 86  
 QY 169 PRCPRIATLAKEKPCITFTTSCAGYCSMRVMAALPPIQPCVCTYRELFGS 228  
 Db 87 IRLPGCPGVDPVMSFPVALSCGCGPCRLKTYCGGPRDPLACA-P--OTSSCKRPPS 143  
 QY 229 IRLPGCPGVDPVMSFPVALSCGCGPCRLKTYCGGPRDPLACA-P--OTSSCKRPPS 288

Db 144 QPLTSTSTPTPGAS 157  
 QY 289 -SLSPS-RLPGPS 300

RESULT 10  
 ID LSHB\_BOVIN STANDARD: PRT: 141 AA.  
 AC P04651:  
 DT 13-AUG-1987 (REL. 05, CREATED)  
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).  
 RN [1]

GN LHB.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA VIRGIN J.B., SILVER B.J., THOMASON A.R., NILSON J.H.;  
 RL J. BIOL. CHEM. 260:7072-7077(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 85207729.  
 RA MAURER R.A.;  
 RL J. BIOL. CHEM. 260:4684-4687(1985).  
 RN [3]  
 RP SEQUENCE OF 21-139.  
 RX MEDLINE: 74075724.  
 RA MAGUIN-ROGISTER G., HENNEN G.;  
 RL EUR. J. BIOCHEM. 39:235-253(1973).  
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
 THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC EMBL: M10077; G163301; -;  
 DR EMBL: M11506; G163299; -;  
 DR PIR: A01499; UTBOB.  
 DR HSSP: P01233; 1HCN.  
 DR PROSITE: PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE: PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 KW HORMONE; SIGNAL; GLYCOPROTEIN.  
 FT SIGNAL 1 20  
 FT CHAIN 1 141  
 FT DISULFID 29 77 LUTROPIN BETA CHAIN.  
 FT DISULFID 43 92 BY SIMILARITY.  
 FT DISULFID 46 130 BY SIMILARITY.  
 FT DISULFID 54 108 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 113 120 BY SIMILARITY.  
 FT CARBOHYD 33 33  
 FT CONFLICT 1 2 MISSING (IN REF. 2).  
 FT CONFLICT 74 74 O -> E (IN REF. 3).  
 FT CONFLICT 112 112 P -> S (IN REF. 2).  
 FT CONFLICT 122 123 GP -> PG (IN REF. 3).  
 FT CONFLICT 126 126 Q -> E (IN REF. 3).  
 SQ SEQUENCE 141 AA; 15202 MW; 82879D1F CRC32;

Query Match 26.28; Score 614; DB 1; Length 141;  
 Best Local Similarity 64.98; Pred. No. 2.94e-116;  
 Matches 72; Conservative 22; Mismatches 17; Indels 0; Gaps 0;

Db 27 PLCPRIATLAKEKPCITFTTSCAGYCSMRVLPVILPMPQRCVCTYHELRFAS 86  
 QY 169 PRCPRIATLAKEKPCITFTTSCAGYCSMRVLPVILPMPQRCVCTYHELRFAS 228  
 Db 87 VRLPGCPGVDPVMSFPVALSCGCGPCRLKTYCGGPRDPLACA-P--OTSSCKRPPS 137  
 QY 229 IRLPGCPGVDPVMSFPVALSCGCGPCRLKTYCGGPRDPLACA-P--OTSSCKRPPS 279

RESULT 11  
 ID LSHB\_HORSE STANDARD: PRT: 169 AA.  
 AC P08751; P01234;  
 DT 01-AUG-1988 (REL. 08, CREATED)  
 DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (LSH-B/CG-B).  
 GN LHB.  
 OS EQUUS CABALLUS (HORSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PERISSODACTYLA.  
 RN [1]





DE LUTROPIN BETA CHAIN (LUTEINIZING HORMONE) (LH-B) (LH-B).  
GN LH-B.  
OS BALAEOPTERA ACTUOSTRATA (MINKE WHALE) (LESSER RORQUAL).  
OC EOKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; CETACEA.  
RN [1]  
RP SEQUENCE.  
RA KARASEV V.S.; PANKOV Y.A.;  
RL BIOKHMIIA 50:1972-1986(1985).  
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
CC PIR; PNO139; PNO139.  
DR HSSP; P01233; 1HCN.  
DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
DR PROSITE; PS00689; GLYCO\_HORMONE\_BETA\_2; FALSE\_NEG.  
KM HORMONE; GLYCOPROTEIN.  
FT DISULFID 9 57 BY SIMILARITY.  
FT DISULFID 23 72 BY SIMILARITY.  
FT DISULFID 26 110 BY SIMILARITY.  
FT DISULFID 34 88 BY SIMILARITY.  
FT DISULFID 38 90 BY SIMILARITY.  
FT DISULFID 93 100 BY SIMILARITY.  
FT CARBOHYD 13 13 BY SIMILARITY.  
SQ SEQUENCE 118 AA; 12414 MW; DE251ECF CRC32;  
  
Query Match 25.4%; Score 595; DB 1; Length 118;  
Best Local Similarity 60.6%; Pred. No. 1,16e-111;  
Matches 66; Conservative 25; Mismatches 17; Indels 1; Gaps 1;  
  
Db 7 PLCRPINTLAZBACPVCITFTTISICAGYCPNMVRLPALPVP2PVCYTRZLRFAS 66  
QY 169 PCRPRINATLAVEKEGCPVCITVNTTICAGYCPMTWTRVLQGVLPALPQVVCNTRDVRRES 228  
  
Db 67 IRLGCCPGVPMWTFYALSCHCGPCRLSSBCCGPGRAZPLACBRSPR 115  
QY 229 IRLPGCPRGVNPVSYAVALSCOCALCRSTTDCGGPRDHPITCD-DPR 276

Search completed: Wed May 6 08:53:30 1998  
Job time : 19 secs.

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M P E R E F  
(TM)  
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MPsrch\_lp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed May 6 08:53:48 1998; Maspar time 15.81 Seconds  
817.861 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-804-166-4  
(1-307) from US08804166.pap  
Perfect Score: 2341

Sequence: 1 SRTSLAFLGILCLPWLQEG.....PSLPSRLPSPDTPILPQ 307

Scoring table:  
PAM 150  
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database:

sptrembl5  
1:sp-fungi 2:sp-human 3:sp-invertebrate 4:sp-mammal  
5:sp-mnc 6:sp-organelle 7:sp-phase 8:sp-plant  
9:sp-bacteria 10:sp-rodent 11:sp-virus 12:sp-vertebrate  
13:sp-unclassified

Statistics: Mean 42.863; Variance 77.650; scale 0.552

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1024	43.7	145	2	013991	BETA-GONADOTROPIN.	1.26e-200
2	1024	43.7	165	2	014000	CHORIONIC GONADOTROPIN	1.26e-200
3	945	40.4	180	4	095185	TUMOR NECROSIS FACTOR	1.78e-182
4	895	38.2	471	4	019131	TUMOR NECROSIS FACTOR-5	0.5e-171
5	596	25.5	135	4	019102	LUTEINIZING HORMONE BE	2.46e-103
6	595	25.4	139	10	062778	TESTICULAR LUTEINIZING	4.12e-103
7	582	24.9	141	10	060844	LUTEINIZING HORMONE BE	3.27e-100
8	430	18.4	140	12	098849	GONADOTROPIN II BETA S	9.70e-67
9	391	16.7	80	10	063013	TESTICULAR LUTEINIZING	2.54e-58
10	361	15.4	147	12	091121	GONADOTROPIN II BETA S	6.54e-52
11	353	15.1	137	12	090225	GONADOTROPIN BETA SUBU	3.27e-50
12	321	13.7	130	12	013050	GONADOTROPIN I BETA SU	1.80e-43
13	314	13.4	138	4	P79357	THYROTROPIN BETA CHAIN	5.23e-42
14	312	13.3	130	12	098848	GONADOTROPIN I BETA SU	1.37e-41
15	311	13.3	138	2	016153	THYROID-STIMULATING HO	2.21e-41
16	310	13.2	138	4	Q28376	THYROTROPIN BETA CHAIN	3.57e-41
17	301	12.9	150	12	013051	THYROTROPIN BETA SUBUN	2.64e-39
18	294	12.6	147	12	013052	THYROTROPIN BETA SUBUN	7.41e-38
19	289	12.3	150	12	013049	THYROTROPIN BETA SUBUN	7.96e-37
20	271	11.6	101	10	062550	BETA-THYROTROPIN (FRAG	3.87e-33

#### ALIGNMENTS

RESULT 1	ID	013991	PRELIMINARY;	PRT;	145 AA.
AC	013991;				
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DE	BETA-GONADOTROPIN.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 84093590.				
RA	TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;				
RL	NATURE 307:37-40(1984).				
DR	EMBL; X00266; E27486; -				
KW	SIGNAL.				
SO	SEQUENCE	145 AA;	15488 MW;	AC321C60 CRC32;	
Query Match		43.78;	Score 1024;	DB 2;	Length 145;
Best local Similarity		99.38;	Pred. No. 1.26e-200;		
Matches	138;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
DB	7	PROCPINATLAVEKCCPCITVNTTICAGYCPMTRVLGCVLPALPOVVCNTRDYREFS	66		
QY	169	PRCRPINATLAVEKCCPCITVNTTICAGYCPMTRVLGCVLPALPOVVCNTRDYREFS	228		
DB	67	IRLPGCPGPNVPSVAVALSCCALCRSTTDGCGPKDPLTCDDPFRFOASSSKRAPP	126		
QY	229	IRLPGCPGPNVPSVAVALSCCALCRSTTDGCGPKDPLTCDDPFRFOASSSKRAPP	208		
DB	127	SLPSRLPSPDTPILPQ 145			
QY	289	SLPSRLPSPDTPILPQ 307			
RESULT 2					
ID	014000	PRELIMINARY;	PRT;	165 AA.	
AC	014000;				
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)				
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)				

DE CHORIONIC GONADOTROPIN BETA SUBUNIT.  
GN CGB.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 8400814.  
RA POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,  
J. BIOL. CHEM. 258:11492-11499(1983).  
RL EMBL: K03183; G180444; JOINED.  
DR EMBL: K00092; G180444; JOINED.  
DR EMBL: K03182; G180444; JOINED.  
SQ SEQUENCE 165 AA; 17729 MW; B1CAAOB1 CRC32;  
  
Query Match 43.7%; Score 1024; DB 2; Length 165;  
Best Local Similarity 99.3%; Pred. No. 1,26e-200;  
Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Db 27 PCRPRINATLAENKESGCPCTIVNTTICAGCPTMTRVLOGVLPALPOVYCNRYDRFES 86  
Oy 169 PCRPRINATLAENKESGCPCTIVNTTICAGCPTMTRVLOGVLPALPOVYCNRYDRFES 228  
Oy 87 IRLPGCPGVNPNVSYAVALSCOCALCRSTTDCGGPKDHPPLTCDPRFOASSSSKAPP 146  
Oy 229 IRLPGCPGVNPNVSYAVALSCOCALCRSTTDCGGPKDHPPLTCDPRFOASSSSKAPP 288  
Db 147 SLSPSRLLPGSPDPTLPQ 165  
Oy 288 SLSPSRLLPGSPDPTLPQ 307  
  
RESULT 3  
ID 095185 PRELIMINARY; PRT; 180 AA.  
  
AC 095185.  
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).  
GN TNFR-1  
OS FELIS SILVESTRIS CATUS (CAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; CARNIVORA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA DUTHIE S., NASIR L., ECKERSALL P.D.,  
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U72344; G1613880; -.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
FT NON\_TER 1  
FT NON\_TER 180  
SQ SEQUENCE 180 AA; 20399 MW; 5452A6B2 CRC32;  
  
Query Match 40.4%; Score 945; DB 4; Length 180;  
Best Local Similarity 86.0%; Pred. No. 1.78e-182;  
Matches 117; Conservative 9; Mismatches 10; Indels 0; Gaps 0;  
  
Db 45 CPGGKTIHPDNDISCTCKTKTYLYNDCAAGGLDTCDECEGNGFTYASENTLRQCLSCS 104  
Oy 26 CPGGKTIHPDNDISCTCKTKTYLYNDCAAGGLDTCDECEGNGFTYASENTLRQCLSCS 85  
Db 105 KCRKEMGYEISPCYVYRDYVCGCRKNORYRYMSETHFOCLNGSICLNTVQISCKEON 164  
Oy 86 KCRKEMGYEISPCYVYRDYVCGCRKNORYRYMSETHFOCLNGSICLNTVQISCKEON 145  
Db 165 TVCTCHAGFFLGNBC 180  
Oy 146 TVCTCHAGFFLGNBC 161  
  
RESULT 4

ID 019131 PRELIMINARY; PRT; 471 AA.  
  
AC 019131.  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE TUMOUR NECROSIS FACTOR-RECEPTOR I.  
GN TNF-R1.  
OS BOS TAURUS (BOVINE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; ARTIODACTYLA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE-AORTA;  
RA LEE E.-K., TALYOR M.J., KEHLI M.E.;  
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U90937; G2290398; -.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
SQ SEQUENCE 471 AA; 51368 MW; 1D06FF4A CRC32;  
  
Query Match 38.2%; Score 895; DB 4; Length 471;  
Best Local Similarity 73.2%; Pred. No. 5.05e-171;  
Matches 104; Conservative 21; Mismatches 17; Indels 0; Gaps 0;  
  
Db 41 ESPCPQGYNHPDNSTICTCKTKTYLYNDCAAGGLDTCDECEGNGFTYASENTLRQCL 100  
Oy 23 DSVCPQGYNHPDNSTICTCKTKTYLYNDCAAGGLDTCDECEGNGFTYASENTLRQCL 82  
Oy 101 SCSRCRDEMFOVEISPCYVYRDYVCGCRKNORYRYMSETHFOCLNGSICLNTVQISCKEON 160  
Oy 83 SCSRCRDEMFOVEISPCYVYRDYVCGCRKNORYRYMSETHFOCLNGSICLNTVQISCKEON 142  
Db 161 RODTICHCMMGFELKARCISC 182  
Oy 143 KONTVCTCHAGFFLGNBCVSC 164  
  
RESULT 5  
ID 019102 PRELIMINARY; PRT; 135 AA.  
  
AC 019102.  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE LUTEINIZING HORMONE BETA SUBUNIT (FRAGMENT).  
GN CERATOTHERIUM SIMUM (WHITE RHINOCEROS).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
CC EUTHERIA; PERISSODACTYLA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE-PITUITARY GLAND;  
RC MEDLINE: 97449288.  
RA SHERMAN G.B., LUND L.A., BUNICK D., WINN R.J.;  
RL GENE 195:131-139(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-PITUITARY GLAND;  
RA SHERMAN G.B., LUND L.A.;  
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U72659; G2462779; -.  
FT NON\_TER 1  
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SQ SEQUENCE 135 AA; 14212 MW; F4F196D2 CRC32;  
  
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Db 21 PLCRPRINATLAENKESGCPCTIVNTTICAGCPTMTRVLOGVLPALPOVYCNRYDRFES 80  
Oy 169 PCRPRINATLAENKESGCPCTIVNTTICAGCPTMTRVLOGVLPALPOVYCNRYDRFES 228  
Db 81 IRLPGCPGVNPNVSYAVALSCOCALCRSTTDCGGPKDHPPLTCDPRFOASSSSKAPP 127  
Oy 146 TVCTCHAGFFLGNBC 161





ID	Sequence	Score	DB	Length	Indels	Gaps
DT	01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)					
DE	GONADOTROPIN II BETA SUBUNIT PRECURSOR.					
OS	MORONE SAKATilis (STRIPED BASS).					
CC	EUAROTIA, METAZOIA, CHORDATA, VERTEBRATA, PISCES; GNATHOSTOMATA;					
OC	OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.					
RN	SEQUENCE FROM N.A.					
RP	TISSUE-PITUITARY GLAND;					
RX	MEDLINE: 96020549.					
RA	HASSIN S., ELIZUR A., ZOHAR Y.;					
RL	J. MOL. ENDOCRINOL. 15:23-35(1995).					
DR	EMBL; L35096; G598255; -.					
KW	SIGNAL.					
FT	SIGNAL.					
FT	CHAIN					
SO	SEQUENCE					
Query Match	Best Local Similarity	44.5%	Pred. No. 6.54e-52;	Length 147;		
Matches	49; Conservative	24; Mismatches	36; Indels	1; Gaps	1;	
Db	36 PCOLINOTVSLKRGCKRPVETTTICSGCITKDPYIKIPFSNYYQHWCTYRDLHYKT					
Qy	169 PCRINATITLAVEKGCPCVCTITVNTTICAGCPTMTRYLQGVLPALPQVYCNRYDVAFES					
Db	96 FELPCPCGVDPPTYTPYPAOSCHGRCAMDSDCTFESLQNFQMDIPE					
Qy	229 IRLPCPCGVNPVSVAYALSCQCALCRSTTDCGGPRDHLTC-DDPRF					
RESULT	11	PRELIMINARY:	PRT;	137 AA.		
ID	Q90225					
AC	Q90225;					
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)					
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DE	GONADOTROPIN BETA-SUBUNIT.					
OS	ACANTHOPAGRUS LATUS.					
CC	EUAROTIA, ANIMALIA, METAZOIA, CHORDATA, VERTEBRATA; OSTEICHTHYES;					
OC	ACTINOPTERYGII; PERCIFORMES; PERCOIDEI; SPARIDAE.					
RN	SEQUENCE FROM N.A.					
RP	TSAI H.J., YANG L.T.;					
RL	SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.					
DR	EMBL; L11722; G437308; -.					
SO	SEQUENCE					
Query Match	Best Local Similarity	44.5%	Pred. No. 3.27e-50;	Length 137;		
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Db	28 PCOLINOTVSLKRGCKRPVETTTICSGCITKDPYIKIPFSNYYQHWCTYRDLHYKT					
Qy	169 PCRINATITLAVEKGCPCVCTITVNTTICAGCPTMTRYLQGVLPALPQVYCNRYDVAFES					
Db	86 FELPCPCGVDPPTYTPYPAVSCNGCLCAMDSDCTFESLQNFQMDIPE					
Qy	229 IRLPCPCGVNPVSVAYALSCQCALCRSTTDCGGPRDHLTC-DDPRF					
RESULT	12	PRELIMINARY:	PRT;	130 AA.		
ID	Q13050					
AC	Q13050;					
DT	01-JUL-1997 (TREMBLREL. 04, CREATED)					
DT	01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)					
DE	GONADOTROPIN I BETA SUBUNIT PRECURSOR.					
OS	CYPRINUS CARPIO (COMMON CARP).					
CC	EUAROTIA, METAZOIA, CHORDATA, VERTEBRATA, PISCES; GNATHOSTOMATA;					
OC	OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.					
RN	SEQUENCE FROM N.A.					
RP	TISSUE-PITUITARY GLAND;					
RX	MEDLINE: 96020549.					
RA	HASSIN S., ELIZUR A., ZOHAR Y.;					
RL	J. MOL. ENDOCRINOL. 15:23-35(1995).					
DR	EMBL; L35096; G598255; -.					
KW	SIGNAL.					
FT	SIGNAL.					
FT	CHAIN					
SO	SEQUENCE					
Query Match	Best Local Similarity	44.5%	Pred. No. 6.54e-52;	Length 147;		
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Qy	169 PCRINATITLAVEKGCPCVCTITVNTTICAGCPTMTRYLQGVLPALPQVYCNRYDVAFES					
Db	96 FELPCPCGVDPPTYTPYPAOSCHGRCAMDSDCTFESLQNFQMDIPE					
Qy	229 IRLPCPCGVNPVSVAYALSCQCALCRSTTDCGGPRDHLTC-DDPRF					

[illegible]

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SQ SEQUENCE 130 AA; 1442 MW; 3C222BFD CRC32;

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Best Local Similarity 40.48; Pred. No. 1.37e-41;

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Qy 230 RLPGCPRGVNPVSYAAVALSCQCALCRSTTDCGGPKDPLTCD 273

RESULT	15	
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PRELIMINARY; PRT; 138 AA.

AC Q16163;  
DE 01 NOV 1966

DT	01-NOV-1996	(TREMBLREL. 01, CREATED)
DT	01-NOV-1996	(TREMBLREL. 01, PAGE SEC)

DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE),
DT	01-NOV-1996	(TREMBLREL. 01, LAST ANNOTATION UPDAT

DE THYROID-STIMULATING HORMONE BETA SUBUNIT (ERAGMENT)  
DI 01-NOV-1996 (TREMBLER. 01, LAST ANNOTATION UPDATE)

DE IRIKOID-STIMULATING HORMONE BETA SUBUNIT (FRAGMENT)  
HOMO SAPIENS (HUMAN) .  
OS

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA

OC EUTHERIA; PRIMATES, ~~VERVETIDAE~~, ~~LEININGIDAE~~, ~~VERVETIDAE~~

$$\mathbf{R}^N \quad [1]$$

RP SEQUENCE FROM N.A.  
BY MED. TWR. 04054240

RX MEDLINE; 94254248.  
PA MYOSHT T KASAT N

RA MIYOSHI I., KASAI N  
RL NIPPON RINSHO 52.94

DR EMBL: S70587; G546849: -;  
RL NIPPON KINSHO 52:940-94/(1994).  
KL

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FT	NON_TER 138 138

NO.	SEQUENCE	AA	15627
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100

Query Match	13.38; Score 311; DB 2;
Post Translational	45.70; Score 303; DB 1;

Matches 48; Conservative 22; Mismatches 29; Indels

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13 LACGQAMSFCTEYTMHIERRECAVCLINTMCAGYC--MTRDINGKLFLPKYALSQD 70

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Db 71 VCTYBDETYRVTETPGCP LHVAPYESYPVALSCCKGKNTDYSNC 115

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218 YCNYBDVFEESTRLPGCPBGVPVSYAVAI$COCAI$CRSTDC 262
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Search completed: Wed May 6 08:55:06 1998  
Job time : 78 secs.

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 QY 704 AAACGAAACACCGGTGTGCAAGCCTGCTGCTCAATGGAGCCGTCACCTGCTCCGACGAG 763  
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 QY 824 AATGTTAAGGCACTGAGAGTGCAGAGCAGCAGCAGCAGT-GCTGTTGCCCTGGT 874

RESULT 2  
 LOCUS A29098 1368 bp DNA PAT 03-JUL-1995

DEFINITION Synthetic DNA for TNF-receptor from patent EP0393438.  
 ACCESSION A29098  
 MID g1248892  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 1368)  
 AUTHORS Hauptmann, R., Himmler, A., Maurer-Fogy, I. and Stratova, C.  
 TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
 JOURNAL Patent: EP 0393438-A 48 24-OCT-1990;  
 BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

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QY 584 CGGGACACCGGTGTGGGTGCGAGGAAGAACAGTACCGGCATTTATGAGTGAACCTT 643  
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 Db 481 AAACGAAACACCGGTGTGCAAGCCTGAGAGTGCAGAAAGTTGGCTTACCCAGATTGAG 540  
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 QY 764 TCCGTAGTAACTGTAAAGAAAAGCCTGAGAGTGCAGAAAGTTGGCTTACCCAGATTGAG 823  
 Db 601 AATGTTAAGGCACTGAGAGTGCAGAGCAGCAGCAGT-GCTGTTGCCCTGGT 650  
 QY 824 AATGTTAAGGCACTGAGAGTGCAGAGCAGCAGCAGCAGT-GCTGTTGCCCTGGT 874

RESULT 3  
 LOCUS HUWTFRP 2050 bp mRNA PRI 11-OCT-1991

DEFINITION Human tumor necrosis factor receptor (TNF) mRNA, complete cds.  
 ACCESSION M60275 M37764  
 MID g339759  
 KEYWORDS  
 SOURCE TNF receptor; transmembrane receptor; tumor necrosis factor receptor.  
 ORGANISM Human placenta, cDNA to mRNA.  
 REFERENCE 1 (bases 1 to 2050)  
 AUTHORS Gray, P.W., Barrett, K.J., Chantry, D., Turner, M. and Feldman, M.  
 TITLE Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)  
 MEDLINE 91017509  
 COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-Aug-1990.

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BASE COUNT 429 a 611 c 566 g 444 t

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Query Match 44.1%; Score 506; DB 27; Length 2050;  
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344 GATAGTGTGTGTCACCAAGGAAATATATATCCACCTCAAAATATTCGATTTGCTGAC 403  
DB 335 AAGTCCCAAGGAACTACTTGTACATGACTGTCCAGGCGCGGCGCAGATACGAC 394  
QY 404 AAGTCCCAAGGAACTACTTGTACATGACTGTCCAGGCGCGGCGCAGATACGAC 463  
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QY 464 TGCAGGAGTGTGAGAGGCGGCTCTTCCACCGCTTCCAGAAACACCTCAGACACTGCTC 523  
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QY 584 CGGACACCGGTGTGTGCTGCGAGAAACAGTACCGGCATTTATTGGAGTGAACCTT 643  
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QY 644 TTCCAGTCTCAATTTGAGAGCTGCGCTCAATGGAGCGCTCAGCTCTCCGCGAGAG 703  
DB 635 AAACAGAACACCGGTGTGAGAGCTGCGCTCAATGGAGCGCTCAGCTCTCCGCGAGAG 694  
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QY 764 TCCTGTACTACTGTAAAGAAAGCTGAGTGCAGAAAGTTGCTTACCCAGATTGAG 823  
DB 755 AATGTTAAGGCGACTGAGAGCTCAGGACACACAGT-GCTGTGCCCCCTGT 804  
QY 824 AATGTTAAGGCGACTGAGAGCTCAGGACACACAGT-GCTGTGCCCCCTGT 874

RESULT 4 A21522 2062 bp RNA PAT 26-JUL-1994  
LOCUS  
DEFINITION TNF alpha gene.  
ACCESSION A21522  
NID 9579599  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2062)  
JOURNAL Patent: GB 2246569-A 1 05-FEB-1992;  
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BASE COUNT 429 a 617 c 573 g 443 t  
ORIGIN  
Query Match 44.1%; Score 506; DB 25; Length 2062;

Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
DB 275 GATAGTGTGTGTCACCAAGGAAATATATATCCACCTCAAAATATTCGATTTGCTGAC 334  
QY 344 GATAGTGTGTGTCACCAAGGAAATATATATCCACCTCAAAATATTCGATTTGCTGAC 403  
DB 335 AAGTCCCAAGGAACTACTTGTACATGACTGTCCAGGCGCGGCGCAGATACGAC 394  
QY 404 AAGTCCCAAGGAACTACTTGTACATGACTGTCCAGGCGCGGCGCAGATACGAC 463  
DB 395 TGCAGGAGTGTGAGAGGCGGCTCTTCCACCGCTTCCAGAAACACCTCAGACACTGCTC 454  
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QY 584 CGGACACCGGTGTGTGCTGCGAGAAACAGTACCGGCATTTATTGGAGTGAACCTT 643  
DB 575 TTCCAGTCTCAATTTGAGAGCTGCGCTCAATGGAGCGCTCAGCTCTCCGCGAGAG 634  
QY 644 TTCCAGTCTCAATTTGAGAGCTGCGCTCAATGGAGCGCTCAGCTCTCCGCGAGAG 703  
DB 635 AAACAGAACACCGGTGTGAGAGCTGCGCTCAATGGAGCGCTCAGCTCTCCGCGAGAG 694  
QY 704 AAACAGAACACCGGTGTGAGAGCTGCGCTCAATGGAGCGCTCAGCTCTCCGCGAGAG 763  
DB 695 TCCTGTACTACTGTAAAGAAAGCTGAGTGCAGAAAGTTGCTTACCCAGATTGAG 754  
QY 764 TCCTGTACTACTGTAAAGAAAGCTGAGTGCAGAAAGTTGCTTACCCAGATTGAG 823  
DB 755 AATGTTAAGGCGACTGAGAGCTCAGGACACACAGT-GCTGTGCCCCCTGT 804  
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RESULT 5 I43805 2062 bp DNA PAT 10-JUL-1997  
LOCUS  
DEFINITION Sequence 24 from patent US 5633145.  
ACCESSION I43805  
NID 92468903  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2062)  
JOURNAL Feldmann, M., Gray, P.W., Turner, M.J.C. and Brennan, F.M.  
TITLE TNF alpha, receptor-derived binding protein  
JOURNAL Patent: US 5633145-A 24 27-MAY-1997;  
FEATURES  
SOURCE Location/Qualifiers  
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BASE COUNT 429 a 617 c 573 g 443 t  
ORIGIN  
Query Match 44.1%; Score 506; DB 25; Length 2062;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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DB 455 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTTCTTGACAGTGGAC 514
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DB 515 CGGACACACCGTGTGTGCTGAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 574
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DB 635 AACAGAAACACCGTGTGTGCTGAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 694
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OY 764 TCCTGTAGTAAGTGAAGAAAGCCGTGAGTGCAGAAATGTTGCTACCCAGATTGAG 823
DB 755 AATGTTAAGGCACTGAGGACTCAGGACCAAGT-GCTGTTGCCCTGCT 804
OY 824 AATGTTAAGGCACTGAGGACTCAGGACCAAGT-GCTGTTGCCCTGCT 874

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RESULT 6 HUMTNR 2087 bp mRNA PRI 10-NOV-1993

LOCUS

DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.

ACCESSION M33294

NID 9339744

KEYWORDS cell surface receptor; tumor necrosis factor receptor.

SOURCE Human placenta, cDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2087)

AUTHORS Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Wong, G.H., Catana, T., Granger, G.A., Lentz, R., Raab, H., Kohr, W.J., and Goeddel, D.V.

TITLE Molecular cloning and expression of a receptor for human tumor necrosis factor

JOURNAL Cell 61, 361-370 (1990)

MEDLINE 90235285

COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by T. Schall, 26-Mar-1990.

FEATURES

source

1. 2087

location/Qualifiers

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/note="tumor necrosis factor receptor"

/codon\_start=1

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BASE COUNT 433 a 624 c 581 g 449 t

ORIGIN

Query Match 44.1%; Score 506; DB 27; Length 2087;

Best Local Similarity 98.1%; Pred. No. 0.00e+00;

Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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DB 302 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATATGATTTGCTGACC 361
OY 344 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATATGATTTGCTGACC 403
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OY 404 AAGTGCCCAAGAAACCTTACTTGTACATGACTGTCCAGGCCCGGGGACGATACGAC 463
DB 422 TGCAGGAGTGTGAGACGGGCTCTTCACCGCTTCAGAAAACCACTCAGACATGCTC 481
OY 464 TGCAGGAGTGTGAGACGGGCTCTTCACCGCTTCAGAAAACCACTCAGACATGCTC 523
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OY 524 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTTCTTGACAGTGGAC 583
DB 542 CGGACACACCGTGTGTGCTGAGAGAAACAGTACCGGCAATTAATGAGTGAACCTT 601
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RESULT 7 HUMTNR 2111 bp mRNA PRI 14-NOV-1990

LOCUS

DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.

ACCESSION M58286

NID M33480

KEYWORDS tumor necrosis factor receptor.

SOURCE Human cell line HL60, cDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2111)

AUTHORS Loetscher, H., Pan, Y.-C.E., Lehm, H.-W., Gentz, R., Brockhaus, M.,

TITLE Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.

JOURNAL Cell 61, 351-359 (1990)

MEDLINE 90235284

FEATURES

source

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location/Qualifiers

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187. 1554  
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mat\_peptide 274. 1551  
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BASE COUNT 445 a 629 c 587 g 450 t  
ORIGIN

Query Match 44.1%; Score 506; DB 27; Length 2111;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Db 307 GATAGTGTGTGCCAGAGAAATATATCCACCTCAAAATATGATTTGCTGTACC 366  
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Oy 344 GATAGTGTGTGCCAGAGAAATATATCCACCTCAAAATATGATTTGCTGTACC 403  
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Db 367 AAGTGCACAAAGAACTTCTTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 426  
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Oy 404 AAGTGCACAAAGAACTTCTTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 463  
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Db 787 AATGTTAAGGGCACTGAGACTGAGCACCACAGT-GCTGTTGCCCTGCT 836  
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Oy 824 AATGTTAAGGGCACTGAGACTGAGCACCACAGTGGCTGCTGCCAGGT 874  
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RESULT 8 A26412 2111 bp DNA PAT 26-APR-1995  
LOCUS

DEFINITION CDNA for (55KD TNF-BF) tumor necrosis factor binding protein from  
patent EP0417563.  
ACCESSION A26412  
NID 9904968  
KEYWORDS  
ORGANISM unidentified.  
SOURCE unidentified  
REFERENCE 1 (bases 1 to 2111)  
AUTHORS Brockhaus M., Dembic Z., Gentz R., Leeslauner W., Loetscher H. and  
TITLE TNF-binding proteins  
JOURNAL Patent: EP 0417563-A 24 20-MAR-1991;  
F. HOFMANN-LA ROCHE AG  
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source 1. 2111  
Location/Qualifiers

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PSLNR"  
BASE COUNT 445 a 629 c 587 g 450 t  
ORIGIN

Query Match 44.1%; Score 506; DB 25; Length 2111;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Db 307 GATAGTGTGTGCCAGAGAAATATATCCACCTCAAAATATGATTTGCTGTACC 366  
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Oy 344 GATAGTGTGTGCCAGAGAAATATATCCACCTCAAAATATGATTTGCTGTACC 403  
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Db 367 AAGTGCACAAAGAACTTCTTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 426  
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Oy 404 AAGTGCACAAAGAACTTCTTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 463  
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Oy 764 TCCTGTAGTACTGTAAAGAAACCTGAGTGCAGCAAGTTGTCTTACCCAGATTGAG 823  
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Db 787 AATGTTAAGGGCACTGAGACTGAGCACCACAGT-GCTGTTGCCCTGCT 836  
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Oy 824 AATGTTAAGGGCACTGAGACTGAGCACCACAGTGGCTGCTGCCAGGT 874  
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RESULT 9 HUMTNFR 2112 bp mRNA PRI 30-SEP-1991  
LOCUS

DEFINITION Human tumor necrosis factor receptor (TNF receptor) mRNA, complete  
cds.  
ACCESSION M63121 M75861  
NID 9339755  
KEYWORDS tumor necrosis factor receptor.  
SOURCE Human cDNA to mRNA.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2112)  
AUTHORS Himmler A., Maurer-Fogy I., Krenke M., Scheurich P.,

Pfizenmayer, K., Lantz, M., Olsson, I., Hauptmann, R., Stratowa, C. and Adolt, G. R.  
Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein  
JOURNAL DNA Cell Biol. 9, 705-715 (1990)

## FEATURES

Location/Qualifiers  
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PSLLR"

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294. .1571  
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BASE COUNT 435 a 632 c 589 g 456 t  
ORIGIN

Query Match 44.1%; Score 506; DB 27; Length 2112;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

327 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATGATTTGCTGAC 386  
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387 AAGTGCACAAAGAACCTTACTTGTACATGCTGTCCAGGCCCGGGGACAGATACGAC 446  
404 AAGTGCACAAAGAACCTTACTTGTACATGCTGTCCAGGCCCGGGGACAGATACGAC 463  
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464 TGCAGGAGTGTGAGACGGCTCTTACACCGCTTACAGAAAACCACTTACACCTGCTC 523  
507 AAGTGCACAAAGAACCTTACTTGTACATGCTGTCCAGGCCCGGGGACAGATACGAC 566  
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764 TCCTGTAGTACTTAAGAAAAGCTGAGTGCAGAGTGTGCTTACCCCAATTGAG 823  
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QY 824 AATGTTAAGGCACTGAGAGCTACAGCACCAACCGGTGCTGCCCAAGT 874

RESULT 10 HSTNR1A 2161 bp RNA PRI 18-JAN-1993

LOCUS HSTNR1A 2161 bp RNA PRI 18-JAN-1993

DEFINITION H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.

ACCESSION X55313  
NID 937223  
KEYWORDS TNF-R gene; tumor necrosis factor receptor 1.

SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 2161)

AUTHORS Nophar, Y., Kemper, O., Brakebusch, C., Englemann, H., Zhang, R.,  
Adler, D., Holman, H., and Wallach, D.

TITLE Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA  
for the type I TNF-R, cloned using amino acid sequence data of its  
soluble form, encodes both the cell surface and a soluble form of  
the receptor

JOURNAL EMBO J. 9 (10), 3269-3278 (1990)  
MEDLINE 91060021  
FEATURES

Location/Qualifiers  
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BASE COUNT 459 a 642 c 604 g 456 t  
ORIGIN

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Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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344 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATGATTTGCTGAC 403

436 AAGTGCACAAAGAACCTTACTTGTACATGCTGTCCAGGCCCGGGGACAGATACGAC 495  
404 AAGTGCACAAAGAACCTTACTTGTACATGCTGTCCAGGCCCGGGGACAGATACGAC 463

496 TGCAGGAGTGTGAGACCGGTCTTACACCGCTTACAGAAAACCACTTACAGAACTGCTC 555

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QY 764 TCCTGTAGTACTGTAAAGAAAGCCGTGAGTGCAGAGTTGCTTACCCAGATTGAG 823  
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Db 856 AATGTTAAGGGCACTGAGACTGAGACCTGAGGACGACAGAGTTGCTTACCCAGATTGAG 905  
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QY 824 AATGTTAAGGGCACTGAGACTGAGACCTGAGGACGACGCGGTGCTGCCAGGT 874  
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RESULT 11 164751 2175 bp DNA PAT 26-SEP-1997  
LOCUS  
DEFINITION Sequence 1 from patent US 5665859.  
ACCESSION 164751  
NID 92481645  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2175)  
AUTHORS Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.  
TITLE Molecules influencing the shedding of the TNF receptor, their  
preparation and their use  
JOURNAL Patent: US 5665859-A 1 09-SEP-1997;  
FEATURES  
source Location/Qualifiers  
1..2175  
BASE COUNT 474 a 641 c 604 g 456 t  
ORIGIN  
Query Match 44.1%; Score 506; DB 25; Length 2175;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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QY 764 TCCTGTAGTACTGTAAAGAAAGCCGTGAGTGCAGAGTTGCTTACCCAGATTGAG 823  
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Db 856 AATGTTAAGGGCACTGAGACTGAGACCTGAGGACGACAGAGTTGCTTACCCAGATTGAG 905  
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QY 824 AATGTTAAGGGCACTGAGACTGAGACCTGAGGACGACGCGGTGCTGCCAGGT 874  
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RESULT 12 A43873 2175 bp DNA PAT 06-MAR-1997  
LOCUS  
DEFINITION Sequence 1 from Patent EP0657336.  
ACCESSION A43873  
NID 92299022  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2175)  
AUTHORS Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.  
TITLE Proteases capable of shedding the soluble TNF-receptor and TNF-R  
derived peptides and antibodies against the proteases inhibiting  
the shedding  
JOURNAL Patent: EP 0657336-A 1 14-JUN-1995;  
COMMENT YEDA RES & DEV (IL)  
Other publication ZA 9407962 951121  
Other publication JP 7194376 950801  
Other publication AU 7574294 950504  
Other publication CA 2133872 950413.  
FEATURES  
source Location/Qualifiers  
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PSLR"  
BASE COUNT 474 a 641 c 604 g 456 t  
ORIGIN  
Query Match 44.1%; Score 506; DB 25; Length 2175;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 464 TGCAGGAGTGTGAGAGCGGCTCCTTCAACCGCTTACAAAAACCACTCAGACATGCTCCTC 523

Db 556 AGCTGCTCCAAATGCGGAAAGAAATGGGTGTCAGTGAATCTCTTCTTGACAGTGCAC 615

QY 524 AGCTGCTCCAAATGCGGAAAGAAATGGGTGTCAGTGAATCTCTTCTTGACAGTGCAC 583

Db 616 CGGACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 675

QY 584 CGGACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 643

Db 676 TTCCAGTCTTCAATTTGACAGCGCTGCTCAATGGAGACCGTCCCTCCGCGAGAG 735

QY 644 TTCCAGTCTTCAATTTGACAGCGCTGCTCAATGGAGACCGTCCCTCCGCGAGAG 703

Db 736 AACAGAACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 795

QY 704 AACAGAACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 763

Db 796 TCCTGTAGTACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGTGCTTACCCAGATTGAG 855

QY 764 TCCTGTAGTACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGTGCTTACCCAGATTGAG 823

Db 856 AATGTTAAGGCGACTGAGAGACTCAGACACCAAGT-GCTGTGCCCCCTGCT 905

QY 824 AATGTTAAGGCGACTGAGAGACTCAGACACCAAGT-GCTGTGCCCCCTGCT 874

RESULT 13 A19907 2176 bp DNA PAT 04-OCT-1994

LOCUS A19907 2176 bp DNA PAT 04-OCT-1994

DEFINITION Synthetic nucleotide sequence Type I TNF receptor gene.

ACCESSION A19907

NID 9641222

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 2176)

AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakheusch,C. and Adorika,D.

TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-I)

JOURNAL Patent: EP 0439900-A 28 JUN-1991;

YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED

FEATURES

source 1..2176

location/Qualifiers

BASE COUNT 474 a 642 c 604 g 456 t

ORIGIN

Query Match 44.1%; Score 506; DB 25; Length 2176;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Db 376 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 435

QY 344 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 403

Db 436 AAGTCCCAAAAGAAAGAACTTGTGTAATGACTGTCCAGGCGCGGGGAGAGATACGGAC 495

QY 404 AAGTCCCAAAAGAAAGAACTTGTGTAATGACTGTCCAGGCGCGGGGAGAGATACGGAC 463

Db 496 TGCAGGAGTGTGAGAGCGGCTCCTTCAACCGCTCAGAAAACACCTCAGACATGCGTC 555

QY 464 TGCAGGAGTGTGAGAGCGGCTCCTTCAACCGCTCAGAAAACACCTCAGACATGCGTC 523

Db 556 AGCTGCTCCAAATGCGGAAAGAAATGGGTGTCAGTGAATCTCTTCTTGACAGTGCAC 615

QY 524 AGCTGCTCCAAATGCGGAAAGAAATGGGTGTCAGTGAATCTCTTCTTGACAGTGCAC 583

Db 616 CGGACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 675

QY 584 CGGACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 643

Db 676 TTCCAGTCTTCAATTTGACAGCGCTGCTCAATGGAGACCGTCCCTCCGCGAGAG 735

QY 644 TTCCAGTCTTCAATTTGACAGCGCTGCTCAATGGAGACCGTCCCTCCGCGAGAG 703

Db 736 AACAGAACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 795

QY 704 AACAGAACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 763

Db 796 TCCTGTAGTACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGTGCTTACCCAGATTGAG 855

QY 764 TCCTGTAGTACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGTGCTTACCCAGATTGAG 823

Db 856 AATGTTAAGGCGACTGAGAGACTCAGACACCAAGT-GCTGTGCCCCCTGCT 905

QY 824 AATGTTAAGGCGACTGAGAGACTCAGACACCAAGT-GCTGTGCCCCCTGCT 874

RESULT 14 126928 6889 bp DNA PAT 01-OCT-1996

LOCUS 126928 6889 bp DNA PAT 01-OCT-1996

DEFINITION Sequence 2 from patent US 5561053.

ACCESSION 126928

NID 91606798

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 6889)

AUTHORS Crowley,C.W.

TITLE Method for selecting high-expressing host cells

JOURNAL Patent: US 5561053-A 2 01-OCT-1996;

FEATURES

source 1..6889

location/Qualifiers

BASE COUNT 1729 a 1826 c 1681 g 1653 t

ORIGIN

Query Match 43.9%; Score 504; DB 25; Length 6889;  
Best Local Similarity 99.0%; Pred. No. 0.00e+00;  
Matches 509; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1725 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 1784

QY 344 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATTAATTCGATTGCTGTACC 403

Db 1785 AAGTCCCAAAAGAAAGAACTTGTGTAATGACTGTCCAGGCGCGGGGAGAGATACGGAC 1844

QY 404 AAGTCCCAAAAGAAAGAACTTGTGTAATGACTGTCCAGGCGCGGGGAGAGATACGGAC 463

Db 1845 TGCAGGAGTGTGAGAGCGGCTCCTTCAACCGCTTCAAGAAAACACCTCAGACATGCGTC 1904

QY 464 TGCAGGAGTGTGAGAGCGGCTCCTTCAACCGCTTCAAGAAAACACCTCAGACATGCGTC 523

Db 1905 AGCTGCTCCAAATGCGGAAAGAAATGGGTGTCAGTGAATCTCTTCTTGACAGTGCAC 1964

QY 524 AGCTGCTCCAAATGCGGAAAGAAATGGGTGTCAGTGAATCTCTTCTTGACAGTGCAC 583

Db 1965 CGGACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 2024

QY 584 CGGACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 643

Db 2025 TTCCAGTCTTCAATTTGACAGCGCTGCTCAATGGAGACCGTCCCTCCGCGAGAG 2084

QY 644 TTCCAGTCTTCAATTTGACAGCGCTGCTCAATGGAGACCGTCCCTCCGCGAGAG 703

Db 2085 AACAGAACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 2144

QY 704 AACAGAACACCGGTGTGCTGTCAGAGAAACAGTACCGGCATTATTGGAGTAAAACTT 763

Db 2145 TCCTGTAGTACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGTGCTTACCCAGATTGAG 2204

QY 764 TCCTGTAGTACTGTAAAGAAAAGCTGAGTGCACGAAAGTTGTGCTTACCCAGATTGAG 823



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Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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D 344 GATAGTGTGTGTCCCAAGGAATAATATATCCACCTCAAAATAATTCATTTGCTGTACC 403
D 393 aagtgccacaaaggaactactgttacaatgactgtccagccggggaagatcagac 452
D 404 AAGTCCACAAAGGAACCTACTGTATGATGATCTCCAGCCGGGCGAGATACCGAC 463
D 433 tgcagagagtgtagaagagcggtccttcacacgcttcaagaacacacctcagacatgcctc 512
D 464 TGCAGAGAGTGTGAAGAGCGGCTCTTCACCGCTTCAGAAAACACACTCAGACACTGCCGC 523
D 513 agctgtcccaaatgcccgaagaagaatggttcaggtgagagatctctcttcagcaatgac 572
D 524 AGCTCTCCAAATATGCCGAAAGAAATAGGTGAGGTGAGATCTCTTTCACACTGAGAC 583
D 573 cggagacacggtgtgtgtcgcagagaacacgataccggcatatttgagtgtaaaacctt 632
D 584 CGGACACCGGTGTGTGCGTCAGAGAAACAGTACCGCATATTGAGTAAAACTT 643
D 633 ttccagtgcttcaatcagacgctctgcctcaatggagacggtgcacctctcctcgcagagag 692
D 644 TTCCAGTGTCTCAATTTGCACTCCCTGCTCAATGGAGACCGTGCACCTCTCTGTGAGAG 703
D 693 aaacaggaacacggtgtgtgcacccgtcagaggttctcttcttaaggaagaagagtgatc 752
D 704 AAACGAAACACCGGTGTGCACTGCACTGCAAGGTCTTCTTAAAGAAACAGAGTGTGC 763
D 753 tccgttaactgtgaagaagaagcctgtgagtgacagaaatgtgtcctaccacagattgag 812
D 764 TCCTGTACTGTAAGTGAAGAAAGCCTGAGTGCAGAAATTTCCCTACCCCAAGATTGAG 823
D 813 aatgttaaggagcactgagagactcagagcaccaagat-gctgtttgcccctgt 862
D 824 AATGTTAAGGCGACTGAGAGACTCAGGACACACAGCCGGGTGCTGCCCAAGT 874
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RESULT 2  
ID Q49932 standard; cDNA to mRNA; 1368 BP.  
AC Q49932;  
DT 29-APR-1994 (first entry)  
DE Lambda-derived TNF-R cDNA.  
KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
pulmonary fibrosis; silicosis; allograft; xenograft; rejection;  
KW graft versus host disease; sepsis; inflammation; allergy;  
KW autoimmune dysfunction; ss.  
OS Homo sapiens.  
LN Lambda-gli0-7-ctnfbp.  
FH Key Location/Qualifiers  
FT CDS 1..1366  
FT /tag- a  
FT /product- hTNF-R  
FT /sig-peptide 1..120  
FT /tag- b  
FT mat\_peptide 121..1363  
FT /\*tag- c  
FT /\*tag- C  
FT MO319777-A.  
PD 14-OCT-1993.  
PE 26-MAR-1993; U02938.  
PR 30-MAR-1992; US-860710.  
PA (IMV ) IMMUNEX CORP.  
PI Smith CA;  
DR WPI; 93-336592/42.  
DR P-PSDB; RA2059.  
PT New fusion protein tumour necrosis factor and human interleukin-1  
receptor - useful in therapy, diagnosis and assays of e.g.  
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.  
PS Disclosure: Page 57-59; 85pp; English.

CC The sequences given in Q49931-32 encode human tumour necrosis factor  
CC receptor (TNF-R) and the sequences in Q49933-34 encode human  
CC interleukin-1 receptor (IL-1R). These sequences were used in the  
CC production of a fusion protein which conformed to one of the  
CC formulae:  
CC TNF-R-linker-TNF-R-linker-IL-1R  
CC IL-1R-linker-TNF-R-linker-TNF-R or  
CC TNF-R-linker-TNF-R  
CC The linker may comprise 5-100 amino acids selected from Gly, Asp,  
CC Ser, Thr and Ala. These linkers separate the individual moieties  
CC by such a distance that each component of the fusion protein is  
CC capable of folding into the secondary or tertiary structure required  
CC for its biological activity. These fusion proteins may be used in  
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
CC particularly in conditions in which both TNF and IL-1 play a causative  
CC role. They may be used to treat cachexia, rheumatoid arthritis,  
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
CC cerebral malaria, allograft and xenograft rejection in graft versus  
CC host disease, sepsis, septic shock, inflammation, allergies and  
CC autoimmune dysfunctions.  
SQ Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T;

Query Match 44.1%; Score 506; DB 8; Length 1368;  
Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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D 121 gataatggtgtgtccccaaggaataatataccacccctcaaaataatgttgcgtacc 180
D 344 GATAGTGTGTGTCCCAAGGAATAATATATCCACCTCAAAATAATTCATTTGCTGTACC 403
D 181 aagtgccacaaaggaactactgttacaatgactgtccagccggggaagatcagac 240
D 404 AAGTCCACAAAGGAACCTACTGTATGATGATCTCCAGCCGGGCGAGATACCGAC 463
D 464 TGCAGAGAGTGTGAAGAGCGGCTCCTTCAACCGCTTCAGAAAACACACTCAGACACTGCCGC 523
D 241 tgcagagagtgtagaagagcggtccttcacacgcttcagagaacacacctcagacatgcctc 300
D 464 TGCAGAGAGTGTGAAGAGCGGCTCCTTCAACCGCTTCAGAAAACACACTCAGACACTGCCGC 523
D 301 agctgtcccaaatgcgaagaagaatggtgtcaggtgtgagatcctcttcagacagtgac 360
D 524 AGCTCTCCAAATATGCCGAAAGAAATAGGTGAGGTGAGATCTCTTTCAGCACTGAGAC 583
D 361 cggagacacggtgtgtgtcgcagagaacacgataccggcatatttgagtgtaaaacctt 420
D 584 CGGACACCGGTGTGTGCTGCTGCAAGAAACAGTACCGCATATTGAGTGAATAAACTT 643
D 421 ttccagtgcttcaatcagacgctctgcctcaatggagacggtgcacctctcctcgcagagag 480
D 644 TTCCAGTGTCTCAATTTGCACTCCCTGCTCAATGGAGACCGTGCACCTCTCTGTGAGAG 703
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D 704 AAACGAAACACCGGTGTGCACTGCACTGCAATGATTTCTTAAAGAAACAGAGTGTGC 763
D 541 tccgttaactgtgaagaagaagcctgtgagtgagcagaagtggtgctaccacagattgag 600
D 764 TCCTGTACTGTAAGTGAAGAAAGCCTGAGAGTGCAGAAATTTCCCTACCCCAAGATTGAG 823
D 601 aatgttaaggagcactgagagactcagagcaccaagat-gctgtttgcccctgt 650
D 824 AATGTTAAGGCGACTGAGAGACTCAGGACACACAGCCGGGTGCTGCCCAAGT 874
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RESULT 3  
ID Q20973 standard; DNA; 2062 BP.  
AC Q20973;  
DT 11-MAY-1992 (first entry)  
DE TNF-alpha binding protein gene.  
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;  
KW extracellular domain.  
OS Homo sapiens.  
LN  
FH Key Location/Qualifiers  
FT CDS 155..1522



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FT      sig_peptide
FT      /*tag- b      275..1522
FT      mat_peptide
FT      /*tag- c      473..532
FT      misc_feature
FT      /*tag- d
FT      /*note- "homologous to probe Q20974"
FT      misc_feature      242..751
FT      /*tag- e
FT      /*note- "encodes the extracellular domain of human
FT      TNF alpha receptor."
FT      TNF_alpha_receptor
FT      GB2246569-A.
FT      05-FEB-1992.
FT      15-JUN-1990; 013410.
FT      15-JUN-1990; GB-013410.
FT      (CHAR-) CHARING CROSS SUNLE.
FT      Feldman M, Gray P, Turner M, Brennan F;
FT      WPI: 92-043613/06.
FT      P-PSDB: R20787.
FT      DR
PT      New tumour necrosis factor alpha binding protein and polypeptide
PT      - useful in treating cachexia, sepsis and auto immune diseases
PT      e.g. rheumatoid arthritis
PT      Disclosure; Fig 1; 25pp; English.
PS      The sequence is that of DNA encoding tumour necrosis factor alpha
CC      binding protein which was obt. from a human placental cDNA library
CC      in lambda gtl1 using a probe (Q20974). The DNA also encodes the
CC      extracellular domain of human TNF alpha receptor and as such it is
CC      useful for treating diseases where TNF alpha is involved as a
CC      causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC      specifically rheumatoid arthritis. See also Q20974.
SO      Sequence      2062 BP;      429 A;      616 C;      573 G;      444 T;

Query Match      44.1%; Score 506; DB 3; Length 2062;
Best Local Similarity 98.1%; Pred. NO. 0.00e+00;
Matches      521; Conservative      0; Mismatches      9; Indels      1; Gaps      1;

DB      275      gatagtgtgtgtcccaagaagaataatataccaccctcaaatattcgtatctgtacc      334
OY      344      GATAGTGTGTGTCCCAAGGAATAATATATCCACCCTCAATAATTCGATTCTGTACC      403
DB      335      aatgtccacaagaacctctgtacaatgactgtccagcgccggggagcagatacggac      394
OY      404      AAGTGCACAAAGAACTCTGTACAAATGATGTCTCAGGCCCGGGGCGATACCGAC      463
DB      395      tgcaggagatgtgagagcggtctcctcaccgcttcagaaaacacctcagacactgctc      454
OY      464      TGCAGGAGATGTGAGAGCGGCTCTTCACCGCTTCAGAAAACACACCTCAGACTGCTC      523
DB      455      agctgtcccaaatgcccgaagaatgggtcagggtggagatctctctctgcacagtggac      514
OY      524      AGCTGTCTCCAAATGCGGAAGAAATGGGTGAGGTGAGATCTCTTTCACAGAGTGAC      583
DB      515      cgggagacggtgtgtgtgtcgcaggaagaacacgtaccgagatattggagtgaaacct      574
OY      584      CGGGACACCGTGTGTGTGTGCTGCAGGAAGAACCACTACCGGATTAATGGAATGAAACCTT      643
DB      575      ttccagtgtctcaaatgtcagacctgtgcctcaatgagacgtgtcaccctctcctcagag      634
OY      644      TTCACATGTCTCAATGTACACCTCTGTGCTCAATGAGACCTGTGACCTCTCTGTACAGAG      703
DB      635      aaacagaacacggtgtgacacctgcattgacaggttctcttctaaagagaacagagtgctc      694
OY      704      AAACACAACACCTCTGTGACCTCTCCATGACAGGTCTTCTTCTTAAGAGAAAAGAGTGTGTC      763
DB      695      tctgtgaagtaactgttaagaaagcctggagtgaggaagtgatgtgtgcacccacagatgag      754
OY      764      TCTGTGTAAGTAAGTAAGAAAGCCTGGAGTGCACGAAGTGTGCCATCCCGAGATTGAG      823
DB      755      aatgttaaggagcactgagagcactcagagcaccagat-gctgttgcacctgtgt      804
OY      824      AATGTTAAGGCACTGAGGACTCAGGACACACACGCGGCTCTGCCACAGGT      874

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RESULT      4
ID      024440 standard; DNA; 2062 BP.
AC      024440;
DE      05-NOV-1992 (first entry)
DT      Encodes TNF-alpha 55kD receptor.
KW      tumour necrosis factor alpha; extracellular binding domain;
KW      treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW      malaria; viral meningitis; graft versus host disease;
KW      autoimmune disease; rheumatoid arthritis.
OS      Homo sapiens.
FH      Key
FT      CDS      Location/Qualifiers
FT      FT      156..1517
FT      /*tag- a
FT      /*product- human TNF-alpha
FT      mat_peptide      1265..1267
FT      /*tag- b
FT      /*note- "3"
FT      mat_peptide      1265..1267
FT      /*tag- c
FT      /*codon- seq: "TGC", aa: Thr
FT      mat_peptide      1258..1260
FT      /*tag- d
FT      /*codon- Seq "AAG", aa: Leu
FT      mat_peptide      1433..1435
FT      /*tag- e
FT      /*codon- Seq: "GAC", aa: Asn
FT      sig_peptide      156..274
FT      /*tag- f
FT      /*tag- f
FT      PN      MO9207076-A.
FT      30-APR-1992.
FT      18-OCT-1991; G01826.
FT      18-OCT-1990; GB-022648.
FT      (CHAR-) CHARING CROSS SUNLEY RES CENT.
FT      Brennan FM, Feldmann M, Gray PM, Turner MJC;
FT      WPI: 92-167156/20.
FT      P-PSDB: R24000
PT      New polypeptide capable of binding human TNF alpha - comprises
PT      first three cysteine-rich subdomains of TNF alpha receptor for
PT      treating autoimmune disease, septic shock, HIV etc.
PS      Claim 4; Fig 1; 43pp; English.
CC      This sequence encodes human TNF-alpha 55kD receptor. A placenta cDNA
CC      library in gtl1 was screened with probe Q29236. Ten hybridising clones
CC      were plaque purified and cDNA size determined by PAGE against an
CC      Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC      sequenced. The coding region of the majority of the human TNF-alpha
CC      55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC      acids, and cloned into a mammalian cell expression vector, resulting
CC      in pTRNF. A derivative of the TNF-alpha receptor was produced by
CC      engineering a termination codon just prior to the transmembrane
CC      domain. PCR with primers Q29237,8 generated a 300bp
CC      restriction fragment which was cloned into pTRNF, giving pTRNFrec.
CC      DNA sequencing confirmed this contained the designed DNA sequence.
CC      The TNF-alpha receptor expression plasmids were then transfected
CC      into monkey COS-7 cells.
CC      See also Q24440-51, R24000, R24080-84, R27585, Q29236-8
SO      Sequence      2062 BP;      429 A;      618 C;      572 G;      443 T;

Query Match      44.1%; Score 506; DB 4; Length 2062;
Best Local Similarity 98.1%; Pred. NO. 0.00e+00;
Matches      521; Conservative      0; Mismatches      9; Indels      1; Gaps      1;

DB      275      gatagtgtgtgtcccaagaagaataatataccaccctcaaatattcgtatctgtacc      334
OY      344      GATAGTGTGTGTCCCAAGGAATAATATATCCACCCTCAATAATTCGATTCTGTACC      403
DB      335      aatgtccacaagaacctctgtacaatgactgtccagcgccggggagcagatacggac      394
OY      404      AAGTGCACAAAGAACTCTGTACAAATGATGTCTCAGGCCCGGGGCGAGATACCGAC      463
DB      395      tgcaggagatgtgagagcggtctcctcaccgcttcagaaaacacctcagacactgctc      454
OY      464      TGCAGGAGATGTGAGAGCGGCTCTTCACCGCTTCAGAAAACACACCTCAGACACTGCTC      523

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Db	455	agcgcgtcccaatgcccgaagaagaatggtcaggtggaagatctctcttcacacagtgcac	51.4
Oy	524	AGCTGCTCCAAATCCCGAAAGAAATGGGTAGGTGGAGATCTCTTTTCCACAGTGGAC	58.3
Db	515	cggagacacgcgtgtgtgcgtgaggaagaacacagacacgcgaatctttgagttgaaaaactt	57.4
Oy	584	CGGAGCACCCGTGTGTGGCTGCAGAGACACAGTACCGGCATTATTTGGAGTGAATCCTT	64.3
Db	575	ttccagtgcttcaattgcagccctctgcctcaatgtgagacgctgcacctctcctgcagagag	63.4
Oy	644	TTCCAGTGCTTCAATTGGACCCCTTGCGCTCAATGGAGACCGGCACCTCTCTGTCAGAG	70.3
Db	635	aaacagaaacacgcgtgtgcacctgcacatgcaggttctcttctaagagaaaaagagtygtc	69.4
Oy	704	AAACAGAAACACCGTGTGCACCTGCCATGCCATGAGTTCTTTCAAGAAAAAGAGATGTGC	76.3
Db	695	tccctgtagttaactgtaaagaaaagcctgtagtgcacgaattgtgtccctaacccacagattgag	74.4
Oy	764	TCCCTGTATTAATCTGTAAGAAAAAGCTTGAGTGCACGAAGTTGTCCATACCCCAATTGAG	82.3
Db	755	aactgttaagggacatgagactcagacacacacagtt-actgtgtgccttggt	80.4
Oy	824	AATGTAAAGGCACATGAGAGATTCAGGCACACACCCGCTGTGCCCCAGGT	87.4

[illegible]

RESULT	5
ID	Q10883 standard; cDNA; 2088 BP.
AC	Q10883:
DT	13-MAY-1991 (first entry)
DE	30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfp.
KW	Tumour necrosis factor; Inhibitor; ss.
OS	Homo sapiens.
FH	Key
FT	CDS Location/Qualifiers
FT	CDS 171..1536
FT	/tag= 2
FN	AU038976-A.
PD	24-JAN-1991.
PE	16-JUL-1990; 058976.
PR	18-JUL-1989; US-381080.
PR	11-DEC-1989; US-450329.
PR	07-FEB-1990; US-479661.
PA	(STNF-) STNERGEN INC.
DR	WPI: 91-073847/11.
DR	P-PSDB: R10986.
PT	Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT	and -beta, useful as therapeutic agent.
PS	Disclosure: Fig 21; 142pp; English.
CC	The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC	which the sequence was obt'd. was isolated from a cDNA library
CC	prep'd. from RNA form U937 cells treated with PMA/PMA. The whole
CC	gene can be inserted into expression vectors for prep'n. of TNF
CC	inhibitor for use in the treatment of inflammatory and degenerative
CC	diseases.
CC	See also Q10878, Q10884 and Q10907.
SQ	Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T;
<hr/>	
Query Match	44.1%; Score 506; DB 2; Length 2088;
Best Local Similarity	98.1%; Pred. NO. 0.00e+00;
Matches 521; Conservative	0; Mismatches 9; Indels 1; Gaps
Db	289 gatagtggtgcccccaagaanaatatcacccctcaaaataatcgaattgtgtacc 348
OY	344 GATAGTGTGTCGCCCAAGAANAATAATATCACCCCTCAAATAATTGGATTGCTGACC 4033
Db	349 aaagtcacaaaagaacctactttgtacaatgaatgcgtgccaggccggggcagatacgac 4088
OY	404 AAGTCCCAACAAGGAACACTTGTAACATATCATCTGCAGGCCCGGGGCGAGATACCGAC 4633
Db	409 tgcacggaggtgttgagagcgctcctctaaccgcttcagaaaaaacaccccagaacctgctc 4688
OY	464 TGCAAGGAGGTGTGAAGACGCGCTCCTTACCCGCTTCAGAAACCACTCAGACACTGCTC 5233

ID	Q10955 standard; cDNA; 2111 BP.
AC	Q10955:
DT	24-MAY-1991 (first entry)
DE	Encodes human 55kD TNF-binding protein.
KW	Tumour Necrosis Factor; binding proteins; septic shock;
FM	autoimmune glomerulonephritis; lymphokine; cytokine.
FT	Key
FT	sig-peptide
FT	187..273
FT	Location/Qualifiers
FT	mat-peptide
FT	274..1551
FT	/*tag- b
FT	/product= 55kD TNF-BP
PN	EP-417563-A.
PD	20-MAR-1991.
PE	31-AUG-1990; 116707.
PR	12-SEP-1989; CH-003319.
PR	08-MAR-1990; CH-000746.
PR	20-APR-1990; CH-001347.
PA	(HOFF) HOFFMANN-LA ROCHE AG.
PI	Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
PI	Schlaeger EJ;
DR	WPI; 91-081851/12.
DR	P-PSDB; R11082.
PT	Insoluble tumour necrosis factor binding proteins - and DNA
PT	encoding them, useful in pharmaceutical prods. and for antibody
PT	prodn.
PS	Claim 4; Fig 1; 26pp; German.
CC	Partial amino acid sequences were determined for the 55 and 75kD
CC	TNF-Bps (see R11072-R11081) and oligonucleotide primers were
CC	synthesised based on these partial sequences. The primers were used
CC	to produce a cDNA fragment for use as a probe to screen a human
CC	placental cDNA bank constructed in lambda g11. Positive clones were
CC	identified and sequenced. DNA constructs comprising the TNF-BP coding
CC	sequence may also contain a fragment encoding a human Ig domain.
CC	Recombinant constructs are used to transform cells to confer
CC	improved TNF-binding properties.
CC	See also Q10956.
SC	Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;
Db	Query Match 44.1%; Score 506; DB 2; Length 2111;
	Best Local Similarity 98.1%; Pred. NO. 0.00e+00;
	Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1
307	gataatggtgtgtccccaaggaataatataccaccctcaaaataattgattgtctgtacc 366
344	gataatggtgtgtccccaaggaataatataccaccctcaaaataattgattgtctgtacc 403

Db 367 aagtgccacaaagaaacctactgttacaatgactgtccagggccgggagagatagac 426  
 |||||||  
 Qy 404 AAGTGCACAAAGAAAGAACTCTGTACATGACTGTCCAGGCCGGGAGATACCGAC 463  
 |||||||  
 Db 427 tgcaggagatgtgagagcggtctcttaccggttcagaaaaaacactcagactgtctc 486  
 |||||||  
 Qy 464 TGCAGGAGAGTGAAGCGGCTCTTCACCGCTTCAAGAAAACCACTCAGACACTGCCTC 523  
 |||||||  
 Db 487 agtgtctccaaatgcggaagaagaatggttcagatgtgagatctcttccacagtgtac 546  
 |||||||  
 Qy 524 AGGTGCTCCCAATGCGCAAGGAATGGGTGAGGTGAGATCTCTTCTTCCACAGTGGAC 583  
 |||||||  
 Db 547 cgggacacgctgtgtgctgcagaaagacagtaacggcattatgtgagtgaaacct 606  
 |||||||  
 Qy 584 CGGAGACACCTGTGTGCTCTCAGAGAAACAGTACCGGATTTTGGATGAAAACCTT 643  
 |||||||  
 Db 607 ttcagtgcttcaatgtcagcgtctctgcctcaatgagacgtgtgcacgtccagag 666  
 |||||||  
 Qy 644 TTCAGAGCTTCAATGTGACACCTGTGCTCAATGGAGACGCTGCTCTGTCAAGAG 703  
 |||||||  
 Db 667 aaacagaacacgctgtgcacgtccatgcaggttcttcttaagagaagaacagatgtctc 726  
 |||||||  
 Qy 704 AAACAGAACACCGCTGTGACCTGTGCAATGAGGTTCTTCTTAAGAGAAAAGAGTGTCTC 763  
 |||||||  
 Db 727 tctgtagtaactgttaagaaagcctgtgagtgacagagttgtgtccacccagattgag 786  
 |||||||  
 Qy 764 TCTGTAGTACTGTAAAGAAAGCCTTGAGTGCAGAAAGTTGTCCTTACCCCGATTGAG 823  
 |||||||  
 Db 787 aatgttaagggcactgagacatcagacacagat-gctgtgcccctgtgt 836  
 |||||||  
 Qy 824 AATGTTAAGGGCACTGAGACTCAGGCACCAAGCGGTGTGCTGCCCCAGGT 874  
 |||||||

RESULT 7  
 ID 090513 standard; DNA; 2175 BP.  
 AC 090513;  
 DT 19-JAN-1996 (first entry)  
 DE p55 TNF-R gene.  
 KM p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 256..1623  
 FT /\*tag= a  
 FT /product= p55 TNF-R  
 FT /misc\_signal 2143..2149  
 FT /\*tag= b  
 FT /note= "possible poly-A signal"  
 PN A09475742-A.  
 PD 04-MAY-1993.  
 PF 11-OCT-1994; 075742.  
 PR 12-OCT-1993; IL-107268.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;  
 DR MPI: 95-194342/26.  
 DR P-PSDB; R75084.  
 PT New protease capable of cleaving soluble tumour necrosis factor  
 PT (TNF) receptor - from cell-bound TNF- receptor, useful for  
 PT antaonising deleterious effects of TNF.  
 PS Disclosure: Fig 1: 40pp; English.  
 CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.  
 CC Expression of this receptor is regulated by shedding of the extracellular  
 CC receptor fragment. The p55 TNF-R can be shed in response to different  
 CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell  
 CC type. The only region of the receptor whose structure affects the  
 CC shedding response is the spacer region (see R75012) in the extracellular  
 CC domain. This region is located close to a site of cleavage of the  
 CC molecule, and links the Cys rich module to the transmembrane domain. The  
 CC spacer region of the encoded protein was used to create the chimera  
 CC between human p55 TNF-R and murine epidermal growth factor receptor  
 CC (EGF-R) that are represented by R75007-11. This spacer region was  
 CC subjected to deletion mutations (R75013-25) and substitutions

CC (R75026-47). Of the spacer region, the most important residues are  
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most  
 CC important of these. The shedding of the receptor is independent of the  
 CC side chain identity of these residues, with the exception of a limited  
 CC dependence on the identity of Val 173. Mutations which alter the  
 CC conformation of the protein adversely effect the shedding process. The  
 CC mutations shown in R75013-47 were introduced in order to create an  
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R  
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in  
 CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can  
 CC be used for enhancing TNF function.  
 SQ Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;

Query Match 44.1%; Score 506; DB 15; Length 2175;  
 Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
 Matches 521; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Db 376 gatagtgtgtccccaagaataatataccaccctcaataatcattgtgtgtacc 435  
 |||||||  
 Qy 344 GATAGTGTGTCTCCCAAGGAATATATATCCACCTTCAAAATTTGATTTGCTGTACC 403  
 |||||||  
 Db 436 aagtgccacaaagaaacctactgttacaatgactgtccagggccgggagagatagac 495  
 |||||||  
 Qy 404 AAGTGCACAAAGAAAGAACTCTGTACATGACTGTCCAGGCCGGGAGATACCGAC 463  
 |||||||  
 Db 496 tgcaggagatgtgagagcggtctcttaccggttcagaaaaaacactcagacactgtctc 555  
 |||||||  
 Qy 464 TGCAGGAGAGTGAAGCGGCTCTTCACCGCTTCAAGAAAACCACTCAGACACTGCCTC 523  
 |||||||  
 Db 556 agtgtctccaaatgcggaagaagaatggttcagatgtgagatctcttccacagtgtac 615  
 |||||||  
 Qy 524 AGGTGCTCCCAATGCGCAAGGAATGGGTGAGGTGAGATCTCTTCTTCCACAGTGGAC 583  
 |||||||  
 Db 616 cgggacacgctgtgtgctgcagaaagacagtaacggcattatgtgagtgaaacct 675  
 |||||||  
 Qy 584 CGGAGACACCGTGTGTGCTCTCAGAGAAACAGTACCGGATTTTGGATGAAAACCTT 643  
 |||||||  
 Db 676 ttcagtgcttcaatgtcagcgtctctgcctcaatgagacgtgtgcacgtccagag 735  
 |||||||  
 Qy 644 TTCAGAGCTTCAATGTGACACCTGTGCTCAATGGAGACCTGTGACCTCTGTCAAGAG 703  
 |||||||  
 Db 736 aaacagaacacgctgtgcacgtccatgcaggttcttcttaagagaagaacagatgtctc 795  
 |||||||  
 Qy 704 AAACAGAACACCGCTGTGACCTGTGCAATGAGGTTCTTCTTAAGAGAAAAGAGTGTCTC 763  
 |||||||  
 Db 796 tctgtagtaactgttaagaaagcctgtgagtgacagagttgtgtccacccagattgag 855  
 |||||||  
 Qy 764 TCTGTAGTACTGTAAAGAAAGCCTTGAGTGCAGAAAGTTGTCCTTACCCCGATTGAG 823  
 |||||||  
 Db 856 aatgttaagggcactgagacatcagacacagat-gctgtgcccctgtgt 905  
 |||||||  
 Qy 824 AATGTTAAGGGCACTGAGACTCAGGCACCAAGCGGTGTGCTGCCCCAGGT 874  
 |||||||

RESULT 8  
 ID 006285 standard; DNA; 2141 BP.  
 AC 006285;  
 DT 29-JAN-1991 (first entry)  
 DE Human Tumour Necrosis Factor-Receptor cDNA Insert.  
 KM Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
 KW lambdaTNF-R; ratNF-R; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 213..1577  
 FT /\*tag= a  
 FT /label=huTNF-R  
 FT BP-393438-A.  
 PN 24-OCT-1990.  
 PD 06-APR-1990; 106624.  
 PF 21-APR-1989; DE-913101.  
 PR 21-JUN-1989; DE-920282.  
 PA (BOER ) BOEHRINGER INGELHEIMINT.  
 PI Hauptmann R, Himmelier A, Maurer-Fogy I, Stratowa C;



|||||  
QY 584 CCGGACACCGTGTGTGCTGACGAGAAACCACTACCGCATATTATGGATGAAAACTTT 643  
DB 676 ttccagtgcttaaatgacgacctgctcctaataatggagccgtgacacctctctccagag 735  
QY 644 TTCCAGTGTCTTAATGACACCCCTCTCTCAATGGACCGTGACACTCTCTCTGACGAG 703  
DB 736 aaacagaaacccgtgtgacacctgacatgcaagtcttctctaagaaaaacaggtgtg 795  
QY 704 AAACAGAACACCGCTGTGACCTGACATGCAAGTTCTTTCTTAAGAGAAAAAGAGTGTTC 763  
DB 796 tccgtgagtaactgttaagaaaacccctggaggtgacgaagtgtgctacccccagattgag 855  
QY 764 TCTGTAGTACTGTAAGAAAAACCTGGAGTGCACGAAGTGTCTTACCCAGATTGAG 823  
DB 856 aatgttaaggacactgaggaactcaggacacacagt-gctgtgtccctgtg 905  
QY 824 AATGTTAAGGGCAGTGTGACGACTGACGACACACCGGCTGCTCCACAGT 874

RESULT 10  
ID T15931 standard; DNA: 6889 BP.

AC T15931;  
DE 20-JUN-1996 (first entry)  
KW DHFR/Inton (WTraSD)-Tnfr-IgG dicistronic vector.  
KW Recombinant host cell; dihydrofolate reductase; selectable marker;  
KW DHFR: ras splice donor; dicistronic vector; gene expression;  
KW Immunoadhesin; Tnfr-IgG; tumour necrosis factor; ds.  
OS Synthetic.  
PN WO9604391-A1.  
PF 15-FEB-1996.  
PR 28-JUL-1995: 009576.  
PA 05-AUG-1994: US-286740.  
(GETH ) GENENTECH INC.  
PI Crowley CW;  
DR WPI: 96-129407/13.  
PT Improved process for the selection of recombinant host cells  
PT expressing high level of a desired product - uses eukaryotic host  
PT cells contg. a DNA construct comprising a selectable gene  
PS Example 2; Page 36-42; 137pp; English.  
CC A dicistronic vector (T15930) comprises a regulatory region  
CC derived from the cytomegalovirus immediate-early gene, a  
CC selectable dihydrofolate reductase gene positioned within an  
CC Inton having a 5' wild-type ras splice donor site, a downstream  
CC sequence coding for an immunoadhesin, Tnfr-IgG, capable of binding  
CC tumour necrosis factor, and a poly-A sequence. Transfection of CHO  
CC DHFR- cells and subsequent methotrexate amplification and growth of  
CC the cells in nutrient-rich medium gave Tnfr-IgG in yields of 9.5  
CC ug/ml (15-fold higher compared to conventional vector amplified  
CC pools).  
SQ Sequence 6889 BP: 1729 A; 1826 C; 1681 G; 1653 T;

Query Match 43.9%; Score 504; DB 18; Length 6889;  
Best Local Similarity 99.0%; Pred. No. 0.00e+00;  
Matches 509; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 1725 gatagtgtgtgtccccaaggaataatataccacctcaataaattcattgtgtacc 1784  
QY 344 GATAGTGTGTGTCCTCCAGGAATAATATCCACCCCTCAATAATATTCGATTGCTGAC 403  
DB 1785 aagtgtcaaaaagaaacctctgtataatgactgttccagcccgaggagataagac 1844  
QY 404 AATGTCCACAAAGAACTTACTGTACAAATGATGTCAGGCCCGGGGCGAGTATCCGAC 463  
DB 1845 tgcaggaagtgtgaagcggtctctcaccgcttcagaaaacacactcaaacctgtc 1904  
QY 464 TGCAGGAGTGTGACAGCGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 523  
DB 1905 agctgtcccaaatgcccgaagaatggtgtcaggtgtgagatctctcttcacagtgac 1964  
QY 524 AGCTGCTCCAAATGCGAAAGAAATGGTGTGAGTGTCTTCTTCCACAGTGTGAC 583  
DB 1965 cggagacacggtgtgtgtgtgtcaggaagaacacagtaaccgcatattgtgagtaaacctt 2024

|||||  
QY 584 CCGGACACCGTGTGTGCTGACGAGAAACCACTACCGCATATTATGGATGAAAACTTT 643  
DB 2025 ttccagtgcttaaatgacgacctgctcctaataatggagccgtgacacctctctccagag 2084  
QY 644 TTCCAGTGTCTTAATGACACCCCTCTCTCAATGGACCGTGACACTCTCTCTGACGAG 703  
DB 2085 aaacagaaacccgtgtgacacctgacatgcaagtcttctctaagaaaaacaggtgtg 2144  
QY 704 AAACAGAACACCGCTGTGACCTGACATGCAAGTTCTTTCTTAAGAGAAAAAGAGTGTTC 763  
DB 2145 tccgtgagtaactgttaagaaaacccctggaggtgacgaagtgtgctacccccagattgag 2204  
QY 764 TCTGTAGTACTGTAAGAAAAACCTGGAGTGCACGAAGTGTCTTACCCAGATTGAG 823  
DB 2205 aatgttaaggacactgaggaactcaggacacacag 2238  
QY 824 AATGTTAAGGGCAGTGTGACGACTGACGACACACCGGCTGCTCCACAGT 857

RESULT 11  
ID Q50870 standard; DNA: 2170 BP.

AC Q50870;  
DE 13-MAY-1994 (first entry)  
KW p55 Tumour necrosis factor receptor coding sequence.  
KW TNF; tumour necrosis factor; receptor; disease; autoimmunity;  
KW Rheumatoid arthritis; graft rejection; graft vs. host; septic shock;  
KW effector protein; ss.  
OS Homo sapiens.  
FH Key  
FT CDS Location/Qualifiers  
FT 256..1623  
FT /\*tag= a  
FT /product= p55 Tumour necrosis factor receptor.  
FT EP-568925-A.  
PN 10-NOV-1993.  
PR 29-APR-1993: 106981.  
PA 03-MAY-1992: IL-101769.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PI Brakebusch C, Wallach D;  
DR WPI: 93-353057/45.  
PT P-PSDB: R42197.  
PT Modulating activity of tumour necrosis factor receptor - using  
PT peptides), antibodies, etc. which interact with critical regions  
PT of receptor or effector protein, for controlling auto-immune  
PT disease, septic shock, etc.  
PS Claim 2; Figure 1; 17pp; English.  
CC Modification of the tumour necrosis factor receptor by mutation or  
CC deletion modulates signal transduction and/or cleavage effected by  
CC the receptor. This modulation of activity can also be achieved  
CC using effector proteins which interact with the TNF receptor.  
CC Molecules which interact with the TNF receptor or the effector  
CC proteins can be used to treat or prevent diseases associated with  
CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft  
CC rejection; graft vs. host disease or septic shock. They can also  
CC be used to treat overdoses of exogenous TNF.  
SQ Sequence 2170 BP: 474 A; 657 C; 584 G; 455 T;

Query Match 43.8%; Score 502; DB 9; Length 2170;  
Best Local Similarity 97.7%; Pred. No. 0.00e+00;  
Matches 519; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

DB 376 gatagtgtgtgtccccaaggaataatataccacctcaataaattcattgtgtacc 435  
QY 344 GATAGTGTGTGTCCTCCAGGAATAATATCCACCCCTCAATAATATTCGATTGCTGAC 403  
DB 436 aagtgtcaaaaagaaacctctgtataatgactgttccagcccgaggagataagac 495  
QY 404 AATGTCCACAAAGAACTTACTGTACAAATGATGTCAGGCCCGGGGCGAGTATCCGAC 463  
DB 496 tgcaggaagtgtgaagcggtctctcaccgcttcagaaaacacactcaaacctgtc 555  
QY 464 TGCAGGAGTGTGACAGCGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 523

Dh 556 agctgctccaaatgcggaagaatggtcagtgtagatctctcttgcacagtgac 615  
|||  
Oy 524 AGCTGCTCCAAATGCGGAAGAAATGGTCAAGTGGAGATCTCTTGTGCACAGTGAC 583  
|||  
Dh 616 cggagacacggtgtgtgtcgcaggaagaacagtcacggcatttattgagtgaaaacctt 675  
|||  
Oy 584 CGGAGACACCGGTGTGTGTGCTGCAGGAAACCAATACCGCATTTATTGAGTGAAGAAACCTT 643  
|||  
Dh 676 ttccagtgcttcaattgtagcgtctgtcctcaatgtagcagcgacacctctcttgcagag 735  
|||  
Oy 644 TTCCAGTCTTCAATTCATTCACCTCTGCTCAATGGAGACCGTACACCTCTCTGTGAGAG 703  
|||  
Dh 736 aaacagaacacacggtgtgacacctgacatgacagttcttcttaagaagaacagagtgctc 795  
|||  
Oy 704 AAACAGAACACCGTCTGCACTGCACATGCAGATTCTTTCAAGAGAAAGAGTGTCTC 763  
|||  
Dh 796 tccgtgttaactgttaagaagaacgctcagtgacagagttgtgtcctaccagattag 855  
|||  
Oy 764 TCCGTGTAAGTAACTGTAAAGAAAGCTGGAGTGACAGAAATTGTCCCTACCCACAGATTGAG 823  
|||  
Dh 856 aatgttaaggcactgtagagactcagggacacacagat-gctgtgtccctcgt 905  
|||  
Oy 824 AATGTTAAGGCACCTGAGAGACTCAGACACACAGCCGCTGCTGCCAGGT 874  
|||

RESULT 12  
ID Q24441 standard; DNA: 608 BP.  
AC Q24441:  
DT 05-NOV-1992 (first entry)  
DE Encodes truncated TNF-alpha 55kd receptor (197 amino acids).  
KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
PN M09207076-A.  
PD 30-APR-1992.  
PE 18-OCT-1991; G01826.  
PR 18-OCT-1990; GB-022648.  
PI (CHAR-) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FM, Feldmann M, Gray PM, Turner MJC;  
PI WPI: 92-167156/20.  
DR P-PSDB; R24080.  
PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for  
PT treating autoimmune disease, septic shock, HIV etc.  
PS Example; Fig 7: 43pp; English.  
CC This sequence encodes the designed TNF-alpha 55kd receptor  
CC derivative, as present in pTNFRec. This was produced as described in  
CC Q24441. This derivative lacks the 81 carboxyl terminal residues of  
CC the cytoplasmic domain. The derivative could be used in the  
CC regulation of TNF-alpha mediated responses by binding and  
CC sequestering human TNF-alpha e.g. in the treatment of pulmonary  
CC diseases, septic shock, HIV infection, malaria, viral meningitis,  
CC graft versus host disease and autoimmune diseases, esp. Rheumatoid  
CC arthritis.  
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
CC Sequence 608 BP; 148 A; 159 C; 165 G; 136 T;  
SQ  
Query Match 40.8%; Score 468; DB 4; Length 608;  
Best Local Similarity 98.8%; Pred. No. 0.00e+00;  
Matches 474; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Dh 129 gatgtgtgttccccaaggaataatataccacctcaataatattgctgtacc 188  
|||  
Oy 344 GATGTGTGTTCCTCCCAAGAAATATATCCACCTCAAAATTAATTCATTGCTGTACC 403  
|||  
Dh 189 aagtgccacaagaagaaactactgtacatgactgtccaggccgggacagatacgac 248  
|||  
Oy 404 AAGTGCCACAAGAAAGAACTACTGTACAAATGACTGTCCAGGCCCGGGCAGATACCAAC 463  
|||  
Dh 249 tgcaggagagtgtagagcggtccttcacggttcagaaaaccacctcagacactgtcctc 308  
|||

Oy 464 TGCAAGGAGTGTGAGAGCGCTCCTTCACCGCTTCAGAAAACCACTCAGACAGTGCCTC 523  
|||  
Dh 309 agctgtccaaatgcccgaagaatggtcaggtgtgagatctcttgcacagtgtagc 368  
|||  
Oy 524 AGCTGCTCCAAATGCGGAAGAAATGGTCAAGTGGAGATCTCTTGTGCACAGTGAC 583  
|||  
Dh 369 cggagacacggtgtgtgtcgcaggaagaacagtcacggcatttattgagtgaaaacctt 428  
|||  
Oy 584 CGGAGACACCGGTGTGTGTGCTGCAGGAAACCAATACCGCATTTATTGAGTGAAGAAACCTT 643  
|||  
Dh 429 ttccagtgcttcaattgtagcgtctgtcctcaatgtagcagcgacacctctcttgcagag 488  
|||  
Oy 644 TTCCAGTCTTCAATTCATTCACCTCTGCTCAATGGAGACCGTACACCTCTCTGTGAGAG 703  
|||  
Dh 489 aaacagaacacacggtgtgacacctgacatgacagttcttcttaagaagaacagagtgctc 548  
|||  
Oy 704 AAACAGAACACCGTCTGCACTGCACATGCAGATTCTTTCAAGAGAAAGAGTGTCTC 763  
|||  
Dh 549 tccgtgttaactgttaagaagaacgctcagtgacagagttgtgtcctaccagattag 608  
|||  
Oy 764 TCCGTGTAAGTAACTGTAAAGAAAGCTGGAGTGACAGAAATTGTCCCTACCCACAGATTGAG 823  
|||

RESULT 13  
ID Q24445 standard; DNA: 504 BP.  
AC Q24445:  
DT 05-NOV-1992 (first entry)  
DE Encodes truncated TNF-alpha 55kd receptor (165 amino acids).  
KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
PN M09207076-A.  
PD 30-APR-1992.  
PE 18-OCT-1991; G01826.  
PR 18-OCT-1990; GB-022648.  
PI (CHAR-) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FM, Feldmann M, Gray PM, Turner MJC;  
PI WPI: 92-167156/20.  
DR P-PSDB; R24084.  
PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for  
PT treating autoimmune disease, septic shock, HIV etc.  
PS Example; Fig 11: 43pp; English.  
CC This sequence encodes the designed TNF-alpha 55kd receptor  
CC derivative, as present in pdeltaIV. This construct was generated by  
CC cloning of the BglII/HindIII digested product of a PCR using  
CC primers 5A and 4D into BglII/HindIII 5'-deltaIIA. This introduced  
CC a termination codon after amino acid 167, to yield pdeltaIV.  
CC This derivative lacks the membrane proximal 4th subdomain, yet  
CC retains the ability to bind TNF-alpha with high affinity  
CC (10power8 - 10power9 Mpower-1) The deriv. can be used in the  
CC regulation of TNF-alpha mediated responses by binding and  
CC sequestering human TNF-alpha e.g. in the treatment of pulmonary  
CC diseases, septic shock, HIV infection, malaria, viral meningitis,  
CC graft versus host disease and autoimmune diseases, esp. Rheumatoid  
CC arthritis. The deriv. is given at 10-100ug/dose.  
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
CC Sequence 504 BP; 122 A; 137 C; 138 G; 107 T;  
SQ  
Query Match 32.7%; Score 375; DB 4; Length 504;  
Best Local Similarity 99.0%; Pred. No. 1.89e-267;  
Matches 379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Dh 121 gatgtgtgttccccaaggaataatataccacctcaataatattgctgtacc 180  
|||  
Oy 344 GATGTGTGTTCCTCCCAAGAAATATATCCACCTCAAAATTAATTCATTGCTGTACC 403  
|||  
Dh 181 aagtgccacaagaagaaactactgtacatgactgtccaggccgggacagatacgac 240  
|||  
Oy 404 AAGTGCCACAAGAAAGAACTACTGTACAAATGACTGTCCAGGCCCGGGCAGATACCAAC 463  
|||

Db 241 tgcaggagtgtagagcggtctcttcaccgcttcagaaacaccaccctcagacatgctc 300  
|||  
Qy 464 TGCAGGAGGTGAGAGCGGCTCTTACCGCTTCAGAAAACACCACTCAGACTGCTC 523  
|||  
Db 301 agctgtcccaatgacgaaagaatggtcaggtggaatctctcttcacagtgagac 360  
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Qy 524 AGCTGCTCCCAAAATGCCGAAAGAAATGGTCAGGTGAGATCTCTTCTGCACAGTGCAC 583  
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Db 361 cggggaacccgtgtgtgcttcaggaagaacccagttaccggtattatggaatgaaacct 420  
|||  
Qy 584 CGGGACACCGCTGTGTGCTCAGAGAAACACGACCGGATTTAGAGTGAATGAAACCTT 643  
|||  
Db 421 ttccagtgctcaattcagcctctgctcattgagagcgtgcacctctctcagagag 480  
|||  
Qy 644 TTCCAGTGTCAATTGCACCTCTGCTCTCAATGGAGACCTGCACCTCTCTCTGACGAG 703  
|||  
Db 481 aaacagaacacgcgtgtgacctg 503  
|||  
Qy 704 AAACAGAACACGCTGACCTG 726  
|||  
RESULT 14  
ID 024442 standard: DNA; 474 BP.  
AC 024442;  
DT 05-NOV-1992 (first entry)  
DE Encodes truncated TNF-alpha 55KD receptor (155 amino acids).  
KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
PN MO9207076-A.  
PD 30-APR-1992.  
PR 18-OCT-1991: G01826.  
PR 18-OCT-1990: GB-022648.  
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;  
DR WPI: 92-167156/20.  
P-PSDB: R24081.  
PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for  
PT treating autoimmune disease, septic shock, HIV etc.  
PS Example: Fig 8: 43pp: English.  
CC This sequence encodes the designed TNF-alpha 55KD receptor  
CC derivative, as present in peltai. This construct was generated by  
CC joining PCR fragments by means of overlaps introduced into the  
CC primers used for PCR. Gel purified products of PCR's using  
CC 5'Cla, IA, IB, and 5D primers were mixed and subjected to further  
CC amplification using 5'Cla and 5D as primers. The resulting fragment  
CC was digested with ClaI and BglII and cloned into ClaI/BglII  
CC digested pINfRecd. to yield pdelat. containing the sequence given.  
CC This derivative could be used to regulate TNF-alpha mediated responses  
CC by binding and sequestering human TNF-alpha e.g. in the treatment of  
CC pulmonary diseases, septic shock, HIV infection, malaria, viral  
CC meningitis, graft versus host disease and autoimmune diseases, esp.  
CC rheumatoid arthritis.  
CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
CC Sequence 474 BP: 110 A; 126 C; 132 G; 106 T;  
SQ

Query Match 30.1%; Score 345; DR 4; Length 474;  
Best Local Similarity 98.3%; Pred. No. 1.15e-243;  
Matches 351; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 118 agagagtgtagagcggtctcttcaccgcttcagaaacaccaccctcagacatgctc 177  
|||  
Qy 467 AGGAGGTGAGAGCGGCTCTTACCGCTTCAGAAAACACCACTCAGACTGCTCAGC 526  
|||  
Db 178 tgcgtcccaatgacgaaagaatggtcaggtggaatctctcttcacagtgagacgg 237  
|||  
Qy 527 TGCCTCCAAATGCCGAAAGAAATGGTCAGGTGAGATCTCTTCTGCACAGTGCACGG 586  
|||  
Db 238 gacacccgtgtgtgctcaggaagaacccagttaccggtattatggaatgaaaccttc 297  
|||

Qy 587 GACACCGTGTGTGCTGCAGAGAACACGACGACGATATTGAGTGAACACTTTTC 646  
|||  
Db 298 cagtgcttaattgacagcctcttcctcaatggagacggtgacctcttcctgcaggagaa 357  
|||  
Qy 647 CAGTGTTCATTTGACACCCCTGCTCCTCAATGGAGCCGTGACCTCTCTCTCAGGAGAA 706  
|||  
Db 358 cagaacacccgtgtgacacctgcagtgaggtttctcttaagagaagaagtgctctcc 417  
|||  
Qy 707 CAGAACACCGCTTCGACACTGCTCCATGCAAGTCTTTCTTAAGAAAACAGTGTCTCC 766  
|||  
Db 418 tgaagtaactgtagaagaagcctgtagtcacgaagttgtcctaccagattag 474  
|||  
Qy 767 TGTAGTAAGTGTGAAGAAAGCCCTGAGTGACGAAGTGTGCTTACCCAGATTGAG 823  
|||  
RESULT 15  
ID T76770 standard: cDNA; 2771 BP.  
AC T76770;  
DT 15-SEP-1997 (first entry)  
DE Rat FabpI gut-specific promoter and human growth hormone exon 1.  
KW Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;  
KW GDP-L-fucose:beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase;  
KW alpha 1,2 FT; alpha 1,3/4 FT; tissue-specific promoter;  
KW rat liver fatty acid binding protein; transgene; transgenic mouse;  
KW animal model; intestinal adhesion; Helicobacter pylori infection;  
KW stomach; small intestine; gut; epithelial cell; surface receptor;  
KW carbohydrate antigen; gastritis; peptic ulcer; neoplasia;  
KW gastric adenocarcinoma; Lewis antigen; fucosylation; ds.  
OS Chimeric - Homo sapiens.  
PN OS Chimeric - Rattus sp.  
FH Key Location/Qualifiers  
FT promoter 1..617  
FT /\*tag= a  
FT /note= "Corresponds to nucleotides -596 to +21 of  
FT the rat liver fatty acid binding protein  
FT gene"  
FT exon 620..2771  
FT /\*tag= b  
FT /number= 1  
FT /note= "Corresponds to nucleotides +3 to +2150 of  
FT the human growth hormone (hGH) gene; it is  
FT desirable for cDNA coding for a human  
FT fucosyltransferase to be inserted into  
FT exon 1 of the hGH gene"  
PN US5625124-A.  
PD 29-APR-1997.  
PR 11-JUL-1994: 273411.  
PR 11-JUL-1994: US-273411.  
PA (UNITV ) UNITV WASHINGTON.  
PI Falk P, Gordon JT;  
DR WPI: 97-258275/23.  
PT Animal model for Helicobacter pylori infection - comprising  
PT transgenic mouse expressing human enzyme promoting intestinal  
PT adhesion  
PS Example 2; Columns 25-28: 24pp: English.  
CC A claimed transgenic mouse expresses, in its intestinal epithelial  
CC cells, the enzyme human GDP-L-fucose:beta-D-galactoside 2-alpha-L-  
CC fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose:  
CC beta-D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also  
CC called alpha 1,3/4 FT). The enzyme is expressed under the  
CC control of a gut epithelial cell-specific promoter and Helicobacter  
CC pylori adheres to the transgenic cells. The transgenic mouse and  
CC intestinal epithelial cells from it are useful as models for screening  
CC compounds for the ability to inhibit adhesion of H. pylori to gut  
CC epithelial cells. The first 617 nucleotides of the present chimeric  
CC sequence encode the promoter from rat liver fatty acid binding protein  
CC (FabpI) which can direct foreign gene expression to the pit cell  
CC lineage of the mouse gastric epithelium, to proliferating and non-  
CC proliferating cells in intestinal crypts, as well as to the four  
CC principal differentiated cell lineages along the crypt-to-villus axis  
CC of the small intestine. The remainder of the chimeric sequence  
CC corresponds to exon 1 of the human growth hormone (hGH) gene, into  
CC which a sequence coding for a human fucosyltransferase (hFT) can be

CC inserted. No hgh will be produced because the initiator Met codon  
CC and the first translation stop codon will be from the hft sequence  
CC and there is no ribosome re-entry sequence. The hgh exon 1 ensures  
CC efficient splicing of the transgene primary transcript, improves  
CC stability of the cytoplasmic hft mRNA and allows transgene  
CC expression to be monitored by in situ hybridisation using a  
CC digoxigenin-labelled hgh oligonucleotide.  
SQ Sequence 2771 BP; 666 A; 718 C; 704 G; 683 T;

Query Match 25.1%; Score 288; DB 31; Length 2771;

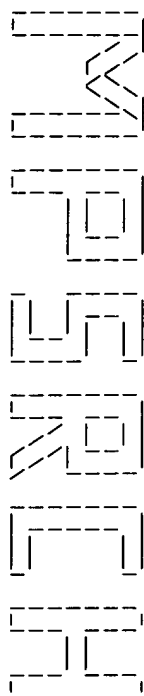
Best Local Similarity 95.6%; Pred. No. 1,27e-198;

Matches 323; Conservative 0; Mismatches 11; Indels 4; Gaps 3;

Db 680 atgctacaggtgaagcgccctaaatcccttgggcacatgtctctgagggagag 739  
Oy 6 ATGGCTACAGGTGAAGCGCCCTAAATCCCTTGGGCACATGTGCTGAGGGAGAG 65  
Db 740 cagcgaccctgtatggcgggcgacactaacctcaggttgggctctgaatg--ag 797  
Oy 66 CAGCGACCCTGTATGGCGGGCGACCTAACCTCAGGTTGGGCTTTGAATGTGAG 125  
Db 798 tatcgcatgtaagcccaatg-gcc-aatctcagaaagctcctggtccctgagggat 855  
Oy 126 TATGCGCATGAAGCCCAATTTGCCCAATCTCAGAAAGCTCTGTGCTCGAGGGAT 185  
Db 856 ggaagagagaaaaacaacacagctccttggagagagagtgctgaccttgcctccgc 915  
Oy 186 GGAGAGAGAAAAACAACAGCTCTGAGACAGGACACTCTGGCCTTGTGCTGCGGC 245  
Db 916 tccctctgtgcccctgtgttctcccccaggtcccgaggtccctgctcgtcttgg 975  
Oy 246 TCCGTGTGTGCCCTGTGTTCTCCCAAGCTCCCGAGCTCCGTGCTGCGCTTTG 305  
Db 976 gcctgctcgtcctgacctggtctcaagagagcgatgac 1013  
Oy 306 GCCTGCTCTGCTGCTGCTGCTCAAGAGGCGCATGCC 343

Search completed: Wed May 6 14:21:41 1998  
Job time : 155 secs.





(TM)

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Msprch.un n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Wed May 6 14:00:59 1998; Maspar time 1055.78 Seconds  
1320.756 Million cell updates/sec

Tabular output not generated.

Title: >US-08-804-166-5  
Description: (1-1147) from US08804166.seq  
Perfect Score: 1147  
N.A. Sequence: 1 TCGAGATGCGTACGCTAG.....AATCTAAGATCCCTCGAG 1147  
Comp: AGCTTACCGATGTCATTC.....TTAGATTCCTAGGAGCTC

Scoring table: TABLE default

Gap 6

Mismatch SMD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Database:

emb1-est  
1:em\_est1 2:em\_est2 3:em\_est3 4:em\_est4 5:em\_est5  
6:em\_est6 7:em\_est8 8:em\_gss 9:em\_est13  
genbank-est  
10:gb\_est1 11:gb\_est2 12:gb\_est3 13:gb\_est4 14:gb\_est5  
15:gb\_est6 16:gb\_est7 17:gb\_est8 18:gb\_est9 19:gb\_est10  
20:gb\_est11 21:gb\_est12 22:gb\_gss 23:gb\_est12 24:gb\_est13  
25:gb\_est14 26:gb\_est15 27:gb\_est16 28:gb\_est17  
29:gb\_est18 30:gb\_est19 31:gb\_est20

Statistics: Mean 11.165; Variance 1.901; scale 5.873

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	262	22.8	373	23	HUM505B08B	Human placenta cDNA 5', 0.00e+00
2	262	22.8	379	23	C18240	Human placenta cDNA 5', 0.00e+00
3	262	22.8	392	12	H00861	Human placenta cDNA 5', 0.00e+00
4	261	22.8	423	11	R006249	Human placenta cDNA 5', 0.00e+00
5	262	22.8	464	23	C17209	Human placenta cDNA 5', 0.00e+00
6	262	22.8	467	11	R71429	Human placenta cDNA 5', 0.00e+00
7	260	22.7	433	11	R23843	Human placenta cDNA 5', 0.00e+00
8	260	22.7	452	12	H00781	Human placenta cDNA 5', 0.00e+00
9	258	22.5	478	23	C17142	Human placenta cDNA 5', 0.00e+00
10	255	22.2	330	23	C18403	Human placenta cDNA 5', 0.00e+00
11	254	22.1	458	11	R77385	Human placenta cDNA 5', 0.00e+00
12	250	21.8	482	12	H03289	Human placenta cDNA 5', 0.00e+00
13	249	21.7	336	23	HUM530G10B	Human placenta cDNA 5', 0.00e+00

c	14	238	20.7	519	31	AA79136	z146h11.s1 Soares feta	0.00e+00
	15	236	20.6	423	23	C17966	Human placenta cDNA 5',	0.00e+00
	16	232	20.2	519	23	C18044	Human placenta cDNA 5',	0.00e+00
	17	230	20.1	386	17	W86367	zhs3h08.r1 Soares feta	0.00e+00
	18	231	20.1	403	11	R65664	y116a09.r1 Homo sapien	0.00e+00
	19	231	20.1	471	12	H47149	yp73d07.r1 Homo sapien	0.00e+00
	20	229	20.0	430	12	H00795	y130f02.r1 Homo sapien	0.00e+00
	21	228	19.9	439	12	H01069	y136c09.r1 Homo sapien	0.00e+00
	22	223	19.4	513	23	AA441787	z462b09.s1 Soares feta	0.00e+00
	23	221	19.3	336	11	R79875	y185a07.r1 Homo sapien	0.00e+00
	24	221	19.3	468	11	R23095	yh11g05.r1 Homo sapien	0.00e+00
	25	220	19.2	365	23	HUM505C02B	Human placenta cDNA 5',	0.00e+00
	26	220	19.2	526	16	H94810	yu11c05.r1 Soares feta	0.00e+00
	27	219	19.1	527	31	AA771267	y196b03.r1 Soares feta	0.00e+00
	28	218	19.0	294	10	T48916	yb07c06.r1 Homo sapien	0.00e+00
	29	218	19.0	360	14	HSC32B021	H. sapiens partial cDN	0.00e+00
	30	217	18.9	429	13	H77743	yu23f09.r1 Homo sapien	0.00e+00
	31	216	18.8	348	11	R33285	yh81d04.r1 Homo sapien	0.00e+00
	32	216	18.8	478	31	AA778170	z45c10.s1 Soares feta	0.00e+00
	33	212	18.5	420	10	T49525	ya76f03.r1 Homo sapien	0.00e+00
	34	207	18.0	291	23	HUM511F08B	Human placenta cDNA 5',	0.00e+00
	35	207	18.0	465	29	AA704477	zj19d06.s1 Soares feta	0.00e+00
	36	205	17.9	365	11	R23453	yh39b02.r1 Homo sapien	0.00e+00
	37	205	17.9	393	11	R33285	yh81d04.r1 Homo sapien	0.00e+00
	38	205	17.9	438	14	NS7230	ym65f07.r1 Homo sapien	0.00e+00
	39	204	17.8	261	23	HUM525D05B	Human placenta cDNA 5',	0.00e+00
	40	201	17.5	465	14	W01919	za35c04.r1 Soares feta	0.00e+00
	41	198	17.3	450	12	H04324	yj09g12.s1 Homo sapien	0.00e+00
	42	198	17.3	450	29	AA677403	zj32g07.s1 Soares feta	0.00e+00
	43	198	17.3	479	11	R68866	y137d07.r1 Homo sapien	0.00e+00
	44	197	17.2	347	11	R34458	yh85b04.r1 Homo sapien	0.00e+00
	45	193	16.8	344	11	R27121	yh52h07.r1 Homo sapien	0.00e+00

## ALIGNMENTS

RESULT	LOCUS	1	HUM505B08B	373 bp	MRNA	EST	21-MAY-1996
DEFINITION							
ACCESSION							
NID							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							
1							
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Fax : 0886-37-1035.

FEATURES  
Location/Qualifiers

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BASE COUNT 94 a 88 c 84 g 107 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 47 TTGCCCCAAGTGCAGCTACAGGAAAAACCATCTTCTCTCCAGCGGGTCCCAATACT 106  
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Oy 874 TTGCCAGATGACGACCTACAGGAAAAACCATCTTCTCTCCAGCGGGTCCCAATACT 933  
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Db 107 TCAGTCATGGGCTGCTGCTCTCTAGACATATCCCACTCCCAATAGGTCGAAGAAC 166  
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Oy 934 TCAGTCATGGGCTGCTGCTCTCTAGACATATCCCACTCCCAATAGGTCGAAGAAC 993  
|||||

Db 167 GATGTGTCACCAAGACCTACAGTCCACTTGTGTAGCTAAATCATATA 226  
|||||  
Oy 994 GATGTGTCACCAAGACCTACAGTCCACTTGTGTAGCTAAATCATATA 1053  
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Db 227 CAGGTCACAGTATGGGGGTTTCAAAGTGAAGAACACAGCGCGTCCACTGCAGTAC 286  
|||||  
Oy 1054 CAGGTCACAGTATGGGGGTTTCAAAGTGAAGAACACAGCGCGTCCACTGCAGTAC 1113  
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Db 287 TTGTTATATACAAATCTTAA 308  
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Oy 1114 TTGTTATATACAAATCTTAA 1135  
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RESULT 2  
LOCUS C18240 379 bp mRNA EST 09-SEP-1996

DEFINITION Human placenta cDNA 5'-end GEN:559D08.  
ACCESSION C18240  
NID 91579842  
KEYWORDS EST: EST (expressed sequence tag); Human placenta.  
SOURCE Homo sapiens placenta cDNA to mRNA. clone:559D08.  
ORGANISM Homo sapiens; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (sites)  
AUTHORS Fujiiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shimomura,H., Suzuki,M., Tairaichi,A., Takeda,S., Matsumoto,T., Maekawa,H., Nakamura,Y. and Takahashi,E.  
TITLE Otsuka cDNA project  
JOURNAL Unpublished (1996)  
REFERENCE 2 (bases 1 to 379)  
AUTHORS Fujiiwara,T.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd. 463-10 Kagasuno Kawanishi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)  
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Best Local Similarity 99.6%; Pred. No. 0.00e+00;  
Matches 261; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 67 TTGCCAGATGACGACCTACAGGAAAAACCATCTTCTCTCCAGCGGGTCCCAATACT 126  
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Oy 874 TTGCCAGATGACGACCTACAGGAAAAACCATCTTCTCTCCAGCGGGTCCCAATACT 933  
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Db 127 TCAGTCATGGGCTGCTGCTCTCTAGACATATCCCACTCCCAATAGGTCGAAGAAC 186  
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Oy 934 TCAGTCATGGGCTGCTGCTCTCTAGACATATCCCACTCCCAATAGGTCGAAGAAC 993  
|||||

Db 187 GATGTGTCACCAAGACCTACAGTCCACTTGTGTAGCTAAATCATATA 246  
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Oy 994 GATGTGTCACCAAGACCTACAGTCCACTTGTGTAGCTAAATCATATA 1053  
|||||

Db 247 CAGGTCACAGTATGGGGGTTTCAAAGTGAAGAACACAGCGCGTCCACTGCAGTAC 306  
|||||

Oy 1054 CAGGTCACAGTATGGGGGTTTCAAAGTGAAGAACACAGCGCGTCCACTGCAGTAC 1113  
|||||

Db 307 TTGTTATATACAAATCTTAA 328  
|||||

Oy 1114 TTGTTATATACAAATCTTAA 1135  
|||||

RESULT 3  
LOCUS R76249 392 bp mRNA EST 06-JUN-1995

DEFINITION y172b05.r1 Homo sapiens cDNA clone 144753 3' similar to gb:v00518  
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);  
ACCESSION R76249  
NID 9850931  
KEYWORDS EST:  
SOURCE human clone-144753 library-Soares placenta Mb2np vector-pt773D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-Promega -21m3 Rsite1-Not I Rsite2-Eco RI female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGATTCGCGCGCCAGAGATTTTCTTTTCTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Felima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Channata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 392)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Morris,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 328  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES  
source  
1. .392  
/organism="Homo sapiens"  
/clone="144753"

BASE COUNT 100 a 90 c 89 g 112 t 1 others  
ORIGIN

Query Match 22.8%: Score 262; DB 11; Length 392;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 35 TTGCCCCAGATGACGCTACAGAGAAACCATTTCTTCCAGCCGGGTGCCCCAATACT 94  
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 QY 874 TTGCCCCAGATGACGCTACAGAGAAACCATTTCTTCCAGCCGGGTGCCCCAATACT 933  
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Db 95 TCAGTCATGGGCTGCTCTCTAGAGCATATCCACATCCACTCACTAAGTCCAGAGAC 154  
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QY 934 TCAGTCATGGGCTGCTCTCTAGAGCATATCCACATCCACTCACTAAGTCCAGAGAC 993  
 |||||||

Db 155 GATGTTGGTCCAAAAGACGCTCAGAGTCACCTGCTGTGTACTAATCATATAA 214  
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QY 994 GATGTTGGTCCAAAAGACGCTCAGAGTCACCTGCTGTGTACTAATCATATAA 1053  
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Db 215 CAGGTCACAGTATGGGGGTTTCAAGTGGAGAACACACGCGGTGCCACTGCACTAC 274  
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QY 1054 CAGGTCACAGTATGGGGGTTTCAAGTGGAGAACACACGCGGTGCCACTGCACTAC 1113  
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Db 275 TTGTTATATACAAATCTTAA 296  
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QY 1114 TTGTTATATACAAATCTTAA 1135  
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RESULT 4 H00861 423 bp mRNA EST 19-JUN-1995

LOCUS  
 DEFINITION yj31h01.r1 Homo sapiens cDNA clone 150385 5' similar to gb:V00518  
 GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.

ACCESSION  
 H00861  
 NID 9863794

KEYWORDS  
 EST.  
 human clone-150385 library-Soares placenta NB2HP vector-pt773D  
 (Pharmacia) with a modified polylinker host-DH10B (ampicillin  
 resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta  
 obtained at birth (full term). 1st strand cDNA was primed with a  
 Not I - oligo(dT) primer [5']  
 AACTGAGAGATTCGGCGCGGAGAGATTTTTTTTTTTTTTTT 3', double-stranded  
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
 I and cloned into the Not I and Eco RI sites of the modified pT73  
 vector. Library went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo.

SOURCE  
 Homo sapiens  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 423)

REFERENCE  
 AUTHORS  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.  
 The Mashu-Merck EST Project  
 Unpublished (1995)

TITLE  
 JOURNAL  
 COMMENT

Contact: Wilson RK  
 Mashu-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 High quality sequence stops: 344  
 Source: IMAGE Consortium, LBNL  
 This clone is available royalty-free through LBNL; contact the  
 IMAGE Consortium (info@image.lbnl.gov) for further information.

FEATURES  
 source  
 1. 423  
 /organism="Homo sapiens"  
 /clone="150385"  
 BASE COUNT 109 a 95 c 95 g 119 t 5 others  
 ORIGIN

Query Match 22.8%; Score 261; DB 12; Length 423;  
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 Matches 261; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 18 TTGCCCCAGATGACGCTACAGAGAAACCATTTCTTCCAGCCGGGTGCCCCAATACT 77  
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 QY 874 TTGCCCCAGATGACGCTACAGAGAAACCATTTCTTCCAGCCGGGTGCCCCAATACT 933  
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Db 78 TCAGTCATGGGCTGCTCTCTAGAGCATATCCACATCCACTCACTAAGTCCAGAGAC 137  
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QY 934 TCAGTCATGGGCTGCTCTCTAGAGCATATCCACATCCACTCACTAAGTCCAGAGAC 993  
 |||||||

Db 138 GATGTTGGTCCAAAAGACGCTCAGAGTCACCTGCTGTGTACTAATCATATAA 197  
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QY 994 GATGTTGGTCCAAAAGACGCTCAGAGTCACCTGCTGTGTACTAATCATATAA 1053  
 |||||||

Db 198 CAGGTCACAGTATGGGGGTTTCAAGTGGAGAACACACGCGGTGCCACTGCACTAC 257  
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QY 1054 CAGGTCACAGTATGGGGGTTTCAAGTGGAGAACACACGCGGTGCCACTGCACTAC 1113  
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Db 258 TTGTTATATACAAATCTTAA 279  
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QY 1114 TTGTTATATACAAATCTTAA 1135  
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RESULT 5 C17209 464 bp mRNA EST 04-SEP-1996

LOCUS  
 DEFINITION Human placenta cDNA 5'-end GEN-541F08.  
 C17209

ACCESSION  
 C17209  
 NID 91571916

KEYWORDS  
 EST; EST (expressed sequence tag); Human placenta.  
 SOURCE  
 Homo sapiens placenta cDNA to mRNA, clone:541F08.

ORGANISM

Homo sapiens  
 Eukaryota; Eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
 Homo.

REFERENCE  
 1 (sites)  
 AUTHORS  
 Fujiwara, T., Hirano, H., Hishigaki, H., Horie, M., Kawai, A., Kuga, Y.,  
 Kyushiki, H., Nagata, M., Okuno, S., Ozaki, R., Shimizu, F., Shimada, Y.,  
 Shiomura, H., Suzuki, M., Takachi, A., Takeda, S., Watanabe, T.,  
 Maekawa, H., Nakamura, Y. and Takahashi, E.

TITLE  
 JOURNAL  
 REFERENCE  
 2 (bases 1 to 464)  
 AUTHORS  
 Fujiwara, T.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu  
 Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical  
 Co., Ltd, 463-10 Kagasuno Kawanuchi-cho, Tokushima, Tokushima 771-01,  
 Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)

FEATURES  
 source  
 1. 464  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="541F08"  
 /tissue="placenta"  
 BASE COUNT 114 a 117 c 95 g 138 t  
 ORIGIN

Query Match 22.8%; Score 262; DB 23; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 TTGCCCCAGATGACGCTACAGAGAAACCATTTCTTCCAGCCGGGTGCCCCAATACT 98  
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QY 874 TTGCCCCAGATGACGCTACAGAGAAACCATTTCTTCCAGCCGGGTGCCCCAATACT 933  
 |||||||

Db 99 TCAGTCATGGGCTGCTCTCTAGAGCATATCCACATCCACTCACTAAGTCCAGAGAC 158  
 |||||||

QY 934 TCAGTCATGGGCTGCTCTCTAGAGCATATCCACATCCACTCACTAAGTCCAGAGAC 993  
 |||||||

Db 159 GATGTTGGTCCAAAAGACGCTCAGAGTCACCTGCTGTGTACTAATCATATAA 218  
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QY	994	GATGTGGTGCCAAAAGAAAGCAGTCAACCTCCAGACAGTCCACTTCTGTGTAGTAATCAATATTA	1053
Db	219	CAGGGTCACAGTAATAGGGGGGTTTCAAAATGGAGAACACACAGGGGTGCACACTGCAGTAC	278
OY	1054	CAGGTCACAGTAATAGGGGGGTTTCAAAATGGAGAACACACAGGGGTGCACACTGCAGTAC	1113
Db	279	TTGTATATATATCAAAATCTTAA 300	
OY	1114	TTGTATATATATCAAAATCTTAA 1135	
RESULT	6		
LOCUS	R71429	467 bp	EST
DEFINITION	Y151d03.r1 Homo sapiens cDNA clone 142757 5' similar to gb:U00518		
ACCESSION	GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.		
NID	R71429		
KEYWORDS	9844946		
SOURCE	EST.		
REFERENCE	human clone-142757 library-Soares placenta Nb2HP vector-PT73D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13RPI RstIco-Not I RstIco-Eco RI female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5		
ORGANISM	A0C7GAGAGATTCGCGCCGACAGAGATTTTTTTTTTTTTTTTTT 3' ], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonadata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Carnivora; Homnidae; Homo. 1 (bases 1 to 467)		
TITLE	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Holtman,M., Kucba,T., Le,M., Lennon,G., Merre,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Tivewaslis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.		
JOURNAL	The Washu-Merck EST Project		
COMMENT	Unpublished (1995)		
CONTACT	Contact: Wilson RK		
WASHU-MERCK EST PROJECT	Washington University School of Medicine		
4444 FOREST PARK PARKWAY, BOX 8501, ST. LOUIS, MO 63108			
TEL: 314 286 1800			
FAX: 314 286 1810			
EMAIL: est@wustl.edu			
HIGH QUALITY SEQUENCE STOPS: 386			
SOURCE: IMAGE Consortium, LNL			
THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LNL; CONTACT THE IMAGE Consortium (info@image.lnl.gov) FOR FURTHER INFORMATION.			
FEATURES	Location/Qualifiers		
source	1..467		
BASE COUNT	/organism="Homo sapiens"		
ORIGIN	/clone="142757"		
Query Match	22.8%; Score 262; DB 11; Length 467;		
Best Local Similarity 100.0%; Pred. No. 0.00e+00;			
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	50	TTGCCAGATGCACGCTACAGAAAAACCATTTCTTCCACGCCGGGTGCCCAATACT 109	
OY	874	TTGCCAGATGCACGCTACAGAAAAACCATTTCTTCCACGCCGGGTGCCCAATACT 933	
Db	110	TTAGTGCATAGGGCTGTGCTTCTCTAGACATATCCCATCTCCACTTAAGTCCAAAGAAC 169	
OY	934	TTAGTGCATAGGGCTGTGCTTCTCTAGACATATCCCATCTCCACTTAAGTCCAAAGAAC 993	

DB	REFERENCE	AUTHORS	ORGANISM	TITLE	JOURNAL	COMMENT
Db	170	GATGTGGTCCAAAAGAACGTCACCTCAGAGCCACTTGCTGTGATAGCTAAATCATTTAA	170	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	230	CAGGCTCAGCTAAATGGGGGTTTCAAAAGTGAACAACACAGCGGCTCCACTGCAGTAC	230	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	1054	CAGGCTCAGCTAAATGGGGGTTTCAAAAGTGAACAACACAGCGGCTCCACTGCAGTAC	1054	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	290	TTGTTATATATCACAATCTTAA 311	290	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	1114	TTGTTATATATCACAATCTTAA 1135	1114	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	7	R23843 433 bp mRNA EST 20-APR-1995	7	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	870	CAGGCTCAGCTAAATGGGGGTTTCAAAAGTGAACAACACAGCGGCTCCACTGCAGTAC	870	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	62	TACTTCAGTGCATGGGCGCTGCTCTCTAGAGCATTCACCACTGCAGTCAAGTCCAGA	62	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo
Db	930	TACTTCAGTGCATGGGCGCTGCTCTCTAGAGCATTCACCACTGCAGTCAAGTCCAGA	930	human clone-132966 library=Soares placenta Nb2HP vector=PT773D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13R1 RsaI=Not I RsaI2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGAATTCGCGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonaldo.	Human sapiens	Eucaaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Carnivora; Canidae; Felidae; Felinae; Felis; Panthera; Panthera leo

Db 122 AGACATGTTGGTCCAAAGACGTCACCTGCTGCTGTAGCAATCAT 181  
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Qy 990 AACACATGTTGGTCCAAAGACGTCACCTGCTGCTGTAGCAATCAT 1049  
Db 182 ATACAGGTCACAGTAATGGGGGTTTCAAGTGAGAACACAGCGGCTGCCTGCA 241  
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Qy 1050 ATACAGGTCACAGTAATGGGGGTTTCAAGTGAGAACACAGCGGCTGCCTGCA 1109  
Db 242 GTACTGTATATATCAAAATCTTA 267  
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Qy 1110 GTACTGTATATATCAAAATCTTA 1135

RESULT 8  
LOCUS H00781 452 bp mRNA EST 19-JUN-1995

DEFINITION yj30d01.r1 Homo sapiens cDNA clone 150241 5' similar to gb:V00518  
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.

ACCESSION H00781  
NID 9863714  
KEYWORDS EST.  
SOURCE human clone-150241 library-Soares placenta Nb2HP vector-PT73D  
(Pharmacia) with a modified polylinker host-DH10B (ampicillin  
resistant) primer-M13RP1 Raitel-Not I Raitel-Eco RI Female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - oligo(dT) primer [5'  
ACTGGAAGATTCGGCGCCGACGAGAAATTTTTTTTTTTTTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified pT73  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 452)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Hollman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Merra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

CONTACT: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 322  
Source: IMAGE Consortium, LNL.  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Location/Qualifiers  
1. 452  
/organism="Homo sapiens"  
/clone="150241"

BASE COUNT 107 a 104 c 103 g 133 t 5 others

ORIGIN

Query Match 22.7%; Score 260; DB 12; Length 452;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 TTGCCAGATGAGCGCTACAGAAACCATCTCTCTCCACGGGCGGCCCACTACT 103  
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Qy 874 TTGCCAGATGAGCGCTACAGAAACCATCTCTCTCCACGGGCGGCCCACTACT 933  
Db 104 TCAGTCATGGGCTGCTCTCTAGACATATCCACTCCACTAAGTCCAAAGAGAC 163

Qy 934 TCAGTCATGGGCTGCTCTCTAGACATATCCACTCCACTAAGTCCAAAGAGAC 993  
|||||  
Db 164 GATGTTGGTCCAAAGACGTCACCTGCTGCTGTAGCAATCATATA 223  
|||||  
Qy 994 GATGTTGGTCCAAAGACGTCACCTGCTGCTGTAGCAATCATATA 1053  
Db 224 CAGGGTCACAGTAATGGGGGTTTCAAGTGAGAACACAGCGGCTGCCTGCA 283  
|||||  
Qy 1054 CAGGGTCACAGTAATGGGGGTTTCAAGTGAGAACACAGCGGCTGCCTGCA 1113  
Db 284 TTGTTATATATCAAAATCTT 303  
|||||  
Qy 1114 TTGTTATATATCAAAATCTT 1133

RESULT 9  
LOCUS C17142 478 bp mRNA EST 04-SEP-1996

DEFINITION Human Placenta cDNA 5'-end GEN-539G04.

ACCESSION C17142  
NID 91571849  
KEYWORDS EST; EST(expressed sequence tag); Human placenta.  
SOURCE Homo sapiens placenta cDNA to mRNA, clone:539G04.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;  
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
Homo.  
1 (sites)  
Fujiwara, T., Hirano, H., Hishigaki, H., Horie, M., Kawai, A., Kuga, Y.,  
Kushiki, H., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y.,  
Shinomura, H., Suzuki, M., Takai, A., Takeda, S., Watanabe, T.,  
Maekawa, H., Nakamura, Y. and Takahashi, E.  
Otsuka cDNA Project  
Unpublished (1996)  
2 (bases 1 to 478)  
Fujiwara, T.  
Direct Submission  
Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu  
Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical  
Co., Ltd. 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,  
Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
ORGANISM

TITLE  
JOURNAL  
COMMENT

CONTACT: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 322  
Source: IMAGE Consortium, LNL.  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Location/Qualifiers  
1. 478  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="539G04"  
/tissue="placenta"

BASE COUNT 125 a 113 c 96 g 144 t

ORIGIN

Query Match 22.5%; Score 258; DB 23; Length 478;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CCAGATGACGCTACAGAAACCATCTCTCTCCACGGGCGGCCCACTACTTACG 60  
|||||  
Qy 878 CCAGATGACGCTACAGAAACCATCTCTCTCCACGGGCGGCCCACTACTTACG 937  
Db 61 TCAGTCATGGGCTGCTCTCTAGACATATCCACTCCACTAAGTCCAAAGAGAG 120  
|||||  
Qy 938 TCAGTCATGGGCTGCTCTCTAGACATATCCACTCCACTAAGTCCAAAGAGAG 997  
Db 121 TTGTCACAAAGACGTCACCTGCTGCTGTAGCAATCATATAACAG 180  
|||||  
Qy 998 TTGTCACAAAGACGTCACCTGCTGCTGTAGCAATCATATAACAG 1057  
Db 181 GTACAGTAATGGGGGTTTCAAGTGAGAACACAGCGGCTGCCTGCACTACTT 240  
|||||  
Qy 1058 GTACAGTAATGGGGGTTTCAAGTGAGAACACAGCGGCTGCCTGCACTACTT 1117  
Db 241 TATATCAAAATCTTA 258  
|||||

OY 1118 TATTATCAAAATCTTAA 1135

RESULT 10  
LOCUS C18403 330 bp mRNA EST 09-SEP-1996

DEFINITION Human placenta cDNA 5'-end GSN-561H02.

ACCESSION C18403

NID g1580005

KEYWORDS EST; EST(expressed sequence tag); Human placenta.

SOURCE Homo sapiens placenta cDNA to mRNA, clone:561H02.

ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (sites)  
AUTHORS Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuge,Y., Kushiki,H., Nagata,M., Okuno,S., Osaki,K., Shimizu,F., Shimada,Y., Shionomiya,H., Suzuki,M., Takachi,A., Takeda,S., Watanabe,T., Mekawa,H., Nakamura,T. and Takahashi,E.  
TITLE Otsuka cDNA project  
JOURNAL Unpublished (1996)  
REFERENCE 2 (bases 1 to 330)  
AUTHORS Fujiwara,T.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUN-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GSN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawasuchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)

FEATURES  
source  
1..330  
location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="561H02"  
/issue\_type="placenta"

BASE COUNT 82 a 87 c 73 g 88 t

ORIGIN

Query Match 22.2%; Score 255; DB 23; Length 330;  
Best Local Similarity 99.6%; Pred. No. 0.00e+00;  
Matches 261; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 67 TTGCCGAATGACGCTACAGGAAACCCATTCTTCTCCAGCCGGGTGCCCAATCT 126  
|||||  
OY 874 TTGCCGAATGACGCTACAGGAAACCCATTCTTCTCCAGCCGGGTGCCCAATCT 933  
|||||

Db 127 TCACTGATGGGTGCTGCTCTAGAGCATATCCACTCCACTAAGTCCAAAGAGAC 186  
|||||  
OY 934 TCACTGATGGGTGCTGCTCTAGAGCATATCCACTCCACTAAGTCCAAAGAGAC 993  
|||||

Db 187 GATGTGTGTCACAAAGAACGTCACCTCAGATGCTGCTGTAGCTAATCATATAA 246  
|||||  
OY 994 GATGTGTGTCACAAAGAACGTCACCTCAGATGCTGCTGTAGCTAATCATATAA 1033  
|||||

Db 247 CAGGTCACAGTAATGGGGGTTTCAAAAGTGGAGA-CCACAGGCGGTGCCACTGCATAC 305  
|||||  
OY 1054 CAGGTCACAGTAATGGGGGTTTCAAAAGTGGAGAACCACACAGGCGGTGCCACTGCATAC 1113  
|||||

Db 306 TTGTTATTATCACAAAATCTTAA 327  
|||||  
OY 1114 TTGTTATTATCACAAAATCTTAA 1135  
|||||

RESULT 11  
LOCUS R77385 458 bp mRNA EST 06-JUN-1995

DEFINITION Y175111.r1 Homo sapiens cDNA clone 145077 5' similar to gb:V00518  
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.

ACCESSION R77385

NID 9852017

KEYWORDS EST.

SOURCE human clone=145077 library=Soares placenta NB2HP vector=pt773D  
(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer-M13RPI Rsite1-Not I Rsite2-Eco RI female placenta  
obtained at birth (full term). 1st strand cDNA was primed with a  
Not I - oligo(dT) primer [5',  
AATGAGAAATATCCCGCCGACGAGAAATTTTCTTTTCTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the modified p773  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM Homo sapiens  
Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostoma; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 458)  
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Matra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treviskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.  
TITLE The Washu-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT

CONTACT: Wilson RK  
Washu-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence stops: 393  
Source: IMAGE Consortium, LBNL  
This clone is available royalty-free through LBNL; contact the  
IMAGE Consortium (info@image.lbnl.gov) for further information.

FEATURES  
source  
1..458  
location/Qualifiers  
/organism="Homo sapiens"  
/clone="145077"

BASE COUNT 119 a 109 c 97 g 133 t

ORIGIN

Query Match 22.1%; Score 254; DB 11; Length 458;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 AATGACGCTACAGGAAACCCATTCTTCTCCAGCCGGGTGCCCAATCTCAGTCA 75  
|||||  
OY 882 AATGACGCTACAGGAAACCCATTCTTCTCCAGCCGGGTGCCCAATCTCAGTCA 941  
|||||

Db 76 TGGCTGCTGCTCTCTAGAGCATATCCACTCCACTAAGTCCAAAGAGATGTGG 135  
|||||  
OY 942 TGGCTGCTGCTCTCTAGAGCATATCCACTCCACTAAGTCCAAAGAGATGTGG 1001  
|||||

Db 136 TCCAAAGAACGTCACCTCAGATGCTGCTGTAGCTAATCATATAAGAGGTCA 195  
|||||  
OY 1002 TCCAAAGAACGTCACCTCAGATGCTGCTGTAGCTAATCATATAAGAGGTCA 1061  
|||||

Db 196 CAGTAATGGGGGTTTCAAAAGTGGAGAACCACAGGCGGTGCCACTGCAGTCTGTATT 255  
|||||  
OY 1062 CAGTAATGGGGGTTTCAAAAGTGGAGAACCACAGGCGGTGCCACTGCAGTCTGTATT 1121  
|||||

Db 256 ATCACAATCTTAA 269  
|||||  
OY 1122 ATCACAATCTTAA 1135  
|||||

RESULT 12  
LOCUS H03289 482 bp mRNA EST 20-JUN-1995

DEFINITION Y144110.r1 Homo sapiens cDNA clone 151651 5' similar to gb:V00518  
GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (HUMAN);.

ACCESSION H03289

NID 9866222

KEYWORDS EST.









QY 61 TDCREBSGFTASENHLRLCLSCSKCKREMGVEISSCTVDNRDTYVCGCKRKNORYHWS 120  
DB 121 nlfgcfnctclngtvlhscqekqntvctchagfflirencvscnckklectklspq 180  
QY 121 NLFQCFNCTCLNGTVALHSCQEKQNTVCTCHAGFFLRENCVSCSNCKKLECKTCLSPQ 180  
DB 181 lenvktedagtgtaagapcceptclqenpfisqgagapllqcmccsfarayptlrskktm 240  
QY 181 IENVKGTEDSGTTAGAAPGCEPCTLOENPFPSOPGAPILLQCMCCFSRAYPTLRSKKT 240  
DB 241 lvgknvtsestccvakeynrvtmvgfkenhbachstctyynhs 285  
QY 241 LVOKNVTSESTCCVAKSYNRYTMVGKFKENHACHSTCTYHNS 285

RESULT 2  
ID W33357 standard; Protein: 256 AA.  
AC W33357;  
DE 19-MAR-1998 (first entry)  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW alpha subunit; hCG-alpha.  
OS Homo sapiens.  
PN MO9730161-A1.  
PD 21-AUG-1997.  
PF 20-FEB-1997; U02315.  
PR 20-FEB-1996; U5-011936.  
PA (ISTR ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chapel SC, Jameson BA;  
DR MPI: 97-425036/39.  
DR N-PSDB; T94007.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PS hormone, especially FSH, for inducing follicular maturation  
PS Example; Pages 32-33; 60pp; English.  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotropin-alpha subunit  
CC (hCG-alpha) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.  
SQ Sequence 256 AA;

Query Match 76.4%: Score 1667; DB 26; Length 256;  
Best Local Similarity 89.1%: Pred. No. 1,50e-169;  
Matches 254; Conservative 2; Mismatches 0; Indels 29; Gaps 1;

DB 1 srtslllafgljllcpwlgsgsadvcpqgkyihpqnmslctckhkytylndcpqpgd 60  
QY 1 SRTSLLAFFLLCPWLGSGSADVCPQGKYIHPQNNISICCTCKHGTLYXNDCPGPGOD 60  
DB 61 tdcrcesgsftasenhrlhclscskckrmgveissctvdtdvcgckngryhws 120  
QY 61 TDCRECSGFTASENHLRLCLSCSKCKRMGVEISSCTVDNDRDTYVCGCKRKNORYHWS 120  
DB 121 nlfgcfnctclngtvlhscqekqntvctchagfflirencvsc----- 164  
QY 121 NLFQCFNCTCLNGTVALHSCQEKQNTVCTCHAGFFLRENCVSCSNCKKLECKTCLSPQ 180  
DB 165 -----agaaagpceptclqenpfisqgagapllqcmccsfarayptlrskktm 211  
QY 181 IENVKGTEDSGTTAGAAPGCEPCTLOENPFPSOPGAPILLQCMCCFSRAYPTLRSKKT 240  
DB 212 lvgknvtsestccvakeynrvtmvgfkenhbachstctyynhs 256  
QY 241 LVOKNVTSESTCCVAKSYNRYTMVGKFKENHACHSTCTYHNS 285

RESULT 3  
ID W33360 standard; Protein: 336 AA.  
AC W33360;  
DE 19-MAR-1998 (first entry)  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;  
KW beta subunit; hCG-beta.  
OS Homo sapiens.  
PN MO9730161-A1.  
PD 21-AUG-1997.  
PF 20-FEB-1997; U02315.  
PR 20-FEB-1996; U5-011936.  
PA (ISTR ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chapel SC, Jameson BA;  
DR MPI: 97-425036/39.  
DR N-PSDB; T94022.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PS hormone, especially FSH, for inducing follicular maturation  
PS Example; Pages 39-40; 60pp; English.  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotropin-beta subunit  
CC (hCG-beta) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.  
SQ Sequence 336 AA;

Query Match 68.9%: Score 1505; DB 26; Length 336;  
Best Local Similarity 98.0%: Pred. No. 1.76e-151;  
Matches 196; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 1 srtslllafgljllcpwlgsgsadvcpqgkyihpqnmslctckhkytylndcpqpgd 60  
QY 1 SRTSLLAFFLLCPWLGSGSADVCPQGKYIHPQNNISICCTCKHGTLYXNDCPGPGOD 60  
DB 61 tdcrcesgsftasenhrlhclscskckrmgveissctvdtdvcgckngryhws 120  
QY 61 TDCRECSGFTASENHLRLCLSCSKCKRMGVEISSCTVDNDRDTYVCGCKRKNORYHWS 120  
DB 121 nlfgcfnctclngtvlhscqekqntvctchagfflirencvscnckklectklspq 180  
QY 121 NLFQCFNCTCLNGTVALHSCQEKQNTVCTCHAGFFLRENCVSCSNCKKLECKTCLSPQ 180  
DB 181 lenvktedagtgtaagapcceptclqenpfisqgagapllqcmccsfarayptlrskktm 240  
QY 181 IENVKGTEDSGTTAGAAPGCEPCTLOENPFPSOPGAPILLQCMCCFSRAYPTLRSKKT 240

RESULT 4  
ID R07449 standard; Protein: 371 AA.  
AC R07449;  
DE 29-JAN-1991 (first entry)  
KW Tumour Necrosis Factor-Binding Protein from pTNF-BP15 CDNA.  
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KW pTNF-BP15; infectious disease; parastitic disease; cachexia;  
KW autoimmune disease; shock.  
OS Homo sapiens.  
PN EP-393438-A.  
PD 24-OCT-1990.  
PF 06-APR-1990; 106624.  
PR 21-APR-1989; DE-913101.  
PR 21-JUN-1989; DE-920282.  
PA (BOEH ) BOEHRINGER INGELHEIMINT.  
PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;  
DR MPI: 90-321987/43.  
DR N-PSDB; Q06282.  
PT DNA encoding TNF binding protein and TNF- receptor - used in

Query Match 59.8%; Score 1305; DB 13; Length 451;

Query Match	59.8%;	Score 1306;	DB 4;	Length 455;
Best Local Similarity	98.8%;	Pred. No. 2.45e-129;		
Matches	169;	Conservative	1;	Mismatches 0;
				Gaps 0



QY 23 DSVCPQCKYIHPPQNNISICTCKHKGTYLYNDPCPGPDOTDCECESGSFTASENHLRCL 82  
DB 101 scskcrkemgveissctvdtdtvcgcrknqyrhwsenlfcfcncslcngtyhlsce 160  
QY 83 SCSKCRKEMGVEISSCTVDHDTVCGCRKNQYRHWSENLFQCFNCTCLNGTYHLSCE 142  
DB 161 kmntvctchagffirenevcscnckkslectkiclpgienvktdesgtt 211  
QY 143 KQNTVCTCHAGFFIRENEVCSCNCKKSLBECTKLSPQIENVKGTEDSGTT 193

RESULT 9  
ID R42059 standard; Protein; 455 AA.  
AC R42059;  
DE 29-APR-1994 (first entry)  
DE Lambda derived TNF-R.  
KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
pulmonary fibrosis; silicosis; allograft; xenograft; rejection;  
graft versus host disease; sepsis; inflammation; allergy;  
OS Homo sapiens.  
KM Lambda-gt10-7ctnfbp.  
FH Key location/Qualifiers  
FT peptide 1..40  
FT /note- "Signal peptide"  
FT protein 41..455  
FT /note- "Mature hTNF-R"

MO9319777-A.  
PD 14-OCT-1993.  
PE 26-MAR-1993: U02938.  
PR 30-MAR-1992: US-860710.  
PA (TMV) IMMUNEX CORP.  
PI Smith CA.  
DR WPI: 93-336592/42.  
DR N-PSDB: 049932.  
PT New fusion protein tumour necrosis factor and human interleukin-1  
receptor - useful in therapy, diagnosis and assays of e.g.  
rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.  
PS Disclosure: Page 57-59; 85pp; English.  
CC The sequences given in R42058-59 represent human tumour necrosis  
factor receptor (TNF-R) and the sequences in R42060-61 represent  
human interleukin-1 receptor (IL-1R). These sequences were used in  
the production of a fusion protein which conformed to one of the  
formulae:  
CC TNF-R-linker-TNF-R-linker-IL-1R  
CC IL-1R-linker-TNF-R-linker-TNF-R or  
CC TNF-R-linker-TNF-R  
CC The linker may comprise 5-100 amino acids selected from Gly, Asp,  
Ser, Thr and Ala. These linkers separate the individual moieties  
by such a distance that each component of the fusion protein is  
capable of folding into the secondary or tertiary structure required  
for its biological activity. These fusion proteins may be used in  
therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
particularly in conditions in which both TNF and IL-1 play a causative  
role. They may be used to treat cachexia, rheumatoid arthritis,  
diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
cerebral malaria, allograft and xenograft rejection in graft versus  
host disease, sepsis, septic shock, inflammation, allergies and  
autoimmune dysfunctions.  
CC Sequence 455 AA;

Query Match 59.8%; Score 1306; DB 8; Length 455;  
Best Local Similarity 98.8%; Pred. No. 2,456-129;  
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 41 dsvcpqckylhpgmnsicctckhkgtylyndcpqpgdtdcecegsftasehnlrcl 100  
QY 23 DSVCPQCKYIHPPQNNISICTCKHKGTYLYNDPCPGPDOTDCECESGSFTASENHLRCL 82  
DB 101 scskcrkemgveissctvdtdtvcgcrknqyrhwsenlfcfcncslcngtyhlsce 160

QY 83 SCSKCRKEMGVEISSCTVDHDTVCGCRKNQYRHWSENLFQCFNCTCLNGTYHLSCE 142  
DB 161 kmntvctchagffirenevcscnckkslectkiclpgienvktdesgtt 211  
QY 143 KQNTVCTCHAGFFIRENEVCSCNCKKSLBECTKLSPQIENVKGTEDSGTT 193

RESULT 10  
ID R10986 standard; Protein; 455 AA.  
AC R10986;  
DE 13-MAY-1991 (first entry)  
DE 30KD TNF inhibitor precursor.  
KW Tumour necrosis factor; inhibitor.  
OS Homo sapiens.  
FH Key location/Qualifiers  
FT cleavage\_site 40..41  
FT /note- "cleavage gives active protein"

PN A09058976-A.  
PD 24-JAN-1991.  
PE 16-JUL-1990; 058976.  
PR 18-JUL-1989; US-381080.  
PR 11-DEC-1989; US-450329.  
PR 07-FEB-1990; US-479661.  
PA (SYNE-) SYNERGEN INC.  
DR WPI: 91-073847/11.  
DR N-PSDB: 010883.  
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha  
and -beta, useful as therapeutic agent.  
PS Disclosure: Fig 21; 142pp; English.  
CC The sequence comprises the entire 30 kD TNF inhibitor. The clone  
from which the sequence was deduced was isolated from a cDNA  
library prep. from RNA form U937 cells treated with PMA/PMA.  
CC The whole gene can be inserted into expression vectors for prepn.  
CC of TNF inhibitor for use in the treatment of inflammatory and  
degenerative diseases. The active protein is claimed (Claim 8).  
CC See also R10984 and R11001.  
CC Sequence 455 AA;

Query Match 59.8%; Score 1306; DB 2; Length 455;  
Best Local Similarity 98.8%; Pred. No. 2,456-129;  
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 41 dsvcpqckylhpgmnsicctckhkgtylyndcpqpgdtdcecegsftasehnlrcl 100  
QY 23 DSVCPQCKYIHPPQNNISICTCKHKGTYLYNDPCPGPDOTDCECESGSFTASENHLRCL 82  
DB 101 scskcrkemgveissctvdtdtvcgcrknqyrhwsenlfcfcncslcngtyhlsce 160  
QY 83 SCSKCRKEMGVEISSCTVDHDTVCGCRKNQYRHWSENLFQCFNCTCLNGTYHLSCE 142  
DB 161 kmntvctchagffirenevcscnckkslectkiclpgienvktdesgtt 211  
QY 143 KQNTVCTCHAGFFIRENEVCSCNCKKSLBECTKLSPQIENVKGTEDSGTT 193

RESULT 11  
ID R11082 standard; Protein; 455 AA.  
AC R11082;  
DE 24-MAY-1991 (first entry)  
DE Human 55KD TNF-binding protein.  
KW Tumour Necrosis Factor; binding proteins; septic shock;  
autoimmune glomerulonephritis; lymphokine; cytokine.  
FH Key location/Qualifiers  
FT modified\_site 54  
FT /label- putative N-glycosylation site  
FT modified\_site 145  
FT /label- putative N-glycosylation site  
FT modified\_site 151  
FT /label- putative N-glycosylation site  
FT modified\_site 270  
FT /label- putative N-glycosylation site  
FT region 212..230  
FT /label- transmembrane region



CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to CC pref. glycoprotein A, B and C. sialo glycoproteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free CC cytokines in the circulation to reduce pathological damage.

Sequence 309 AA;

Query Match 59.7%; Score 1303; DB 13; Length 309;

Best Local Similarity 98.2%; Pred. No. 5.28e-129;

Matches 168; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 20 dsvcpqgkylhpnqnsicctckhkytlyndcpqpgdtdceesgfsfasesnhlrlcl 79  
 |||||||  
 QY 23 DSVCPQGRYIHPQNNISICTCKCHKGTLYNDCCPGPDTCRECSGSFTASENHLRCL 82  
 |||||||  
 Db 80 scskcrkemqveissctvdtdtvcgcrknqyryhwsenlfqcfncslclngtvlhscqe 139  
 |||||||  
 QY 83 SCSCSKREMGVEISSCTVDTDVTCGCRKNQYRYHWSENLFCQCNCTCLNGTVAHLSQOE 142  
 |||||||  
 Db 140 kqntvctchagffirenevcscnckkslecktclclpqlenvkgtedsqts 190  
 |||||||  
 QY 143 KQNTVCTCHAGFFIRENEVCSCNCKKSLECKTCLSLPQIENVKGTEDSGTT 193  
 |||||||

RESULT 14

ID R07451 standard; protein; 455 AA.

AC R07451;

DT 29-JUN-1991 (first entry)

DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.

KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

CC Infectious disease; parasitic disease; cachexia;

KM autoimmune disease; shock; lambdaTNF-R2; ratTNF-R8.

OS Homo sapiens.

PN EP-393438-A.

PD 24-OCT-1990.

PF 06-APR-1990; 106624.

PR 21-APR-1989; DE-913101.

PT 21-JUN-1989; DE-920282.

PA (BOEH) BOEHRINGER INGELHEIMINT.

PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;

DR WFI; 90-321987/43.

DR N-PSB; 006285.

PT DNA encoding TNF binding protein and TNF-receptor - used in

tumour treatment and to understand mechanism to TNF action

PS Disclosure: Fig 91(1-2); 51pp; German.

CC rTNF-R8 (Q06284) was used to screen the HS913T cDNA library.

CC LambdaTNF-R2 encodes the complete human TNF-R2 and was used to

construct a plasmid (PADTNF-R) expressing the product the same way

CC as PADTNF-BP (see Q06282). The expressed proteins are useful

CC prophylactically and therapeutically to control disorders which

CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or

CC parasitic diseases, shock, cachexia, autoimmune diseases, adult

CC respiratory distress syndrome etc., or side effects of treatment with

CC TNF-alpha). They can also be used as diagnostic reagents for

CC assaying TNF and in study of TNF-receptor interactions.

CC See also Q06282-Q06285.

SO Sequence 455 AA;

Query Match 59.7%; Score 1303; DB 2; Length 455;

Best Local Similarity 98.2%; Pred. No. 5.28e-129;

Matches 168; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 41 dsvcpqgkylhpnqnsicctckhkytlyndcpqpgdtdceesgfsfasesnhlrlcl 100  
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 QY 23 DSVCPQGRYIHPQNNISICTCKCHKGTLYNDCCPGPDTCRECSGSFTASENHLRCL 82  
 |||||||  
 Db 101 scskcrkemqveissctvdtdtvcgcrknqyryhwsenlfqcfncslclngtvlhscqe 160  
 |||||||  
 QY 83 SCSCSKREMGVEISSCTVDTDVTCGCRKNQYRYHWSENLFCQCNCTCLNGTVAHLSQOE 142  
 |||||||  
 Db 161 kqntvctchagffirenevcscnckkslecktclclpqlenvkgtedsqts 211  
 |||||||  
 QY 143 KQNTVCTCHAGFFIRENEVCSCNCKKSLECKTCLSLPQIENVKGTEDSGTT 193  
 |||||||

RESULT 15

ID R70104 standard; Protein; 547 AA.

AC R70104;

DT 02-NOV-1995 (first entry)

DE TNF-R-GBPH fusion protein.

KW Hybrid peptide: malaria parasite; Plasmodium falciparum; fusion protein;

KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;

KW GBP 130; GBPH; glycoprotein binding peptide homologue; glycoprotein A;

KM tumour necrosis factor receptor; TNF-R.

OS Chimeric Plasmodium falciparum.

PN W09506737-A.

PD 09-MAR-1995.

PF 01-SEP-1994; G01900.

PR 03-SEP-1993; GB-018350.

PT 23-AUG-1994; GB-017021.

PA (PREN/) PRENDERGAST K F.

PI Prendergast KF.

DR WFI; 95.115452/15.

PT New hybrid peptide(s) for binding cytokine(s) - comprising a

PT malaria parasite peptide capable of binding a red blood cell and

PT a receptor peptide.

PS Example A: Page 47-48; 93pp; English.

CC Hybrid peptides for binding cytokines, comprising a malaria parasite

CC (Plasmodium falciparum) peptide (capable of binding to a red blood

CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples

CC of these hybrid peptides. R70104 is a fusion of tumour necrosis factor

CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)

CC and glycoprotein binding protein (GBP) homologue (GBPH). The use of

CC cytokine receptors not normally found on RBCs means that the

CC cytokine can bind harmlessly to the RBC without deleterious effect.

CC The RBC protects the hybrid peptides from excretion from the kidney, and

CC due to steric hindrance prevents the cytokines binding to a receptor in

CC another cell. GBP 130 or GBPH are the pref. malaria parasite peptides

CC used, others include EBA 175 (175 kDa erythrocyte binding antigen), PMMSA

CC (pre major merozoite surface antigen) and the Duffy binding receptor

CC molecule (eg. exhibited by Plasmodium vivax). These peptides bind to

CC pref. glycoprotein A, B and C. sialo glycoproteins, found on the surface

CC of RBCs. The hybrid peptides are thus used to lower the levels of free

CC cytokines in the circulation to reduce pathological damage.

SO Sequence 547 AA;

Query Match 59.7%; Score 1303; DB 13; Length 547;

Best Local Similarity 98.2%; Pred. No. 5.28e-129;

Matches 168; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 20 dsvcpqgkylhpnqnsicctckhkytlyndcpqpgdtdceesgfsfasesnhlrlcl 79  
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 QY 23 DSVCPQGRYIHPQNNISICTCKCHKGTLYNDCCPGPDTCRECSGSFTASENHLRCL 82  
 |||||||  
 Db 80 scskcrkemqveissctvdtdtvcgcrknqyryhwsenlfqcfncslclngtvlhscqe 139  
 |||||||  
 QY 83 SCSCSKREMGVEISSCTVDTDVTCGCRKNQYRYHWSENLFCQCNCTCLNGTVAHLSQOE 142  
 |||||||  
 Db 140 kqntvctchagffirenevcscnckkslecktclclpqlenvkgtedsqts 190  
 |||||||  
 QY 143 KQNTVCTCHAGFFIRENEVCSCNCKKSLECKTCLSLPQIENVKGTEDSGTT 193  
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Search completed: Wed May 6 09:03:11 1998

Job time : 97 secs.

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REFERENCE A36555  
#authors Himmelr, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.; Stratowa, C.; Adolf, G.R.  
#journal DNA Cell Biol. (1990) 9:705-715  
#title Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.  
#cross-references MUID:91090841  
#accession A36555  
##molecule\_type mRNA  
##residues 1-455 ##label HITM  
#cross-references GB:M63121; NID:9339755; PID:9339756  
#accession C36535  
##molecule\_type protein  
#residues 30-38:41-53,'X',55-79,'XX',82-94,'NK','XX',100-104; 107-128:162-167,'X',169-201 ##label HIT2  
#note the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the receptor

REFERENCE A38281  
#authors Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384  
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein.  
#cross-references MUID:91017509  
#accession A38281  
##molecule\_type mRNA  
##residues 1-455 ##label GRA  
#cross-references GB:M37764  
#note The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Leu, and GAC for residue 427 as Asn

REFERENCE S12057  
#authors Nopnar, Y.; Kemper, O.; Brakusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, H.; Wallach, D.  
#journal EMBO J. (1990) 9:3269-3278  
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.  
#cross-references MUID:91006021  
#accession S12057  
##molecule\_type mRNA  
##residues 1-455 ##label NOP  
#cross-references EMBL:X5513; NID:937223; PID:937224  
#note parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were confirmed by protein sequencing

REFERENCE JT0758  
#authors Kemper, O.; Wallach, D.  
#journal Gene (1993) 134:209-216  
#title Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor (TNF) receptor.  
#accession JT0758  
##molecule\_type DNA  
##residues 1-13 ##label KEM

REFERENCE A60231  
#authors Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
#journal Eur. J. Immunol. (1990) 20:1167-1174  
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.  
#cross-references MUID:90292116  
#accession A60231  
##molecule\_type protein  
#residues 41-43,'X',45-53,'X',55-57 ##label SEC

REFERENCE A38258  
#authors Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffers, E.W.B.; Lantz, R.; Tomich, J.; Yamamoto, R.S.; Granger, G.A.

#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784  
#title Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.  
#cross-references MUID:91062364  
#accession A38258  
##molecule\_type protein  
#residues 41-60 ##label GAT  
#experimental\_source cancer patient serum

REFERENCE A60594  
#authors Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
#journal Eur. J. Haematol. (1989) 42:270-275  
#title Isolation and characterization of a tumor necrosis factor binding protein from urine.  
#accession A60594  
##molecule\_type protein  
#residues 41-53,'X',45-53,'V',55-57,'XX',60 ##label OLS  
#experimental\_source renal failure patient urine

REFERENCE A35010  
#authors Engelmann, H.; Novick, D.; Wallach, D.  
#journal J. Biol. Chem. (1990) 265:1531-1536  
#title Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.  
#cross-references MUID:90110215  
#accession A35010  
##molecule\_type protein  
#residues 41-45 ##label ENG  
#experimental\_source normal urine

REFERENCE JC2404  
#authors Kailhara, J.; Asada, A.; Kirihara, S.; Kato, K.; Biosci. Biotechnol. Biochem. (1994) 58:2266-2268  
#title Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.  
#accession JC2404  
##molecule\_type protein  
#residues 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 ##label KAI

#experimental\_source urine  
#comment This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

GENETICS  
#gene GDB:TNFR1  
##cross-references GDB:125913; OMIM:191190  
#map\_position 12p13.2-12p13.2  
#introns 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
CLASSIFICATION  
#superfamily tumor necrosis factor receptor type 1, NGF receptor repeat homology  
KEYWORDS  
duplication; glycoprotein; receptor; transmembrane protein  
FEATURE  
1-21  
22-455  
30-211  
41-201  
44-82  
84-116  
127-167  
168-196  
212-234  
235-455  
54,145,151  
#domain signal sequence #status predicted #label SIG  
#product tumor necrosis factor receptor type 1 #status predicted #label MAT  
#domain extracellular #status predicted #label ECT  
#product TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status experimental #label TBP1  
#domain NGF receptor repeat homology #label NG1  
#domain NGF receptor repeat homology #label NG2  
#domain NGF receptor repeat homology #label NG3  
#domain NGF receptor repeat homology #label NG4  
#domain transmembrane #status predicted #label TM  
#domain intracellular #status predicted #label INT  
#binding\_site carboxylate (asn) (covalent) #status predicted

SUMMARY  
#length 455 #molecular\_weight 50494 #checksum 153

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Best Local Similarity 98.8%; Pred. No. 1,606-278;  
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 41 DSVCPGKVIHPNNSICTRCHKRTVLYNDGPGQDTDCRECSGSFTASENHLRCL 100

|||||  
QY 23 DSVCPGKXIIHQNNNSICCTKCHKGYLYLNDGPGPODPDCECEGSGSTASENHLRCL 82  
DB 101 SSCSKRKEKGVEISSCTVDRTVCGCRKNQYRHVSENLFOCFNCSLCLNGTVHLSCE 160  
QY 83 SSCSKRKEKGVEISSCTVDRTVCGCRKNQYRHVSENLFOCFNCCLNGTVHLSCE 142  
DB 161 KONTVCTCHAGFFLRENECVSCSNCKSLCETKRLCPQIENKGTEDSGT 211  
QY 143 KONTVCTCHAGFFLRENECVSCSNCKSLCETKRLCPQIENKGTEDSGT 193  
RESULT 2  
ENTRY 2  
TEXT #type complete  
TITLE tumor necrosis factor receptor extracellular domain, chain A  
PDB TITLE extracellular domain of the 55kda tumor necrosis factor  
ORGANISM #formal\_name Homo sapiens #common\_name man  
#note residues 12 to 172 of the mature sequence of the entire  
receptor. residue 11 is mutated to met as a result of the  
expression system  
REFERENCE A65560  
#authors Naismith, J.H.; Sprang, S.R.  
#submission submitted to the Brookhaven Protein Data Bank, July 1996  
REFERENCE TNO26248  
#authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.  
#journal J. Biol. Chem. (1995) 270:13303  
#title Crystallographic evidence for dimerization of unliganded  
tumor necrosis factor receptor.  
TN026249  
Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,  
K.; Naismith, J.H.; Sprang, S.R.  
J. Mol. Biol. (1994) 239:332  
Two crystal forms of the extracellular domain of type 1 tumor  
necrosis factor receptor.  
REFERENCE A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
Cell (1993) 73:431-445  
Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
COMMENT Resolution: 1.85 angstroms  
DETERMINATION: X-ray diffraction  
KEYWORDS R-value: no refinement  
binding protein; cytokine; signalling protein  
FEATURE  
66-68  
11-143  
131-154  
7-9,17-19  
131-134,137-140  
25-29,39-42  
71-74,83-85  
90-96,99-104  
111-115,124-127  
3-17  
18-31  
21-40  
43-58  
61-76  
64-84  
86-102  
105-117  
108-125  
127-138  
141-154  
144-150  
SUMMARY #length 160 #molecular-weight 18065 #checksum 2297

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Best Local Similarity 98.8%; Pred. No. 8,41e-263;  
Matches 156; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
DB 1 SVCPGKXIIHQNNNSICCTKCHKGYLYLNDGPGPODPDCECEGSGSTASENHLRCL 60  
QY 24 SVCPGKXIIHQNNNSICCTKCHKGYLYLNDGPGPODPDCECEGSGSTASENHLRCL 83  
DB 61 SSCSKRKEKGVEISSCTVDRTVCGCRKNQYRHVSENLFOCFNCSLCLNGTVHLSCE 120  
QY 84 SSCSKRKEKGVEISSCTVDRTVCGCRKNQYRHVSENLFOCFNCCLNGTVHLSCE 143  
DB 121 KONTVCTCHAGFFLRENECVSCSNCKSLCETKRLCPQIEN 160  
QY 144 KONTVCTCHAGFFLRENECVSCSNCKSLCETKRLCPQIEN 183  
RESULT 3  
ENTRY 3  
TEXT #type complete  
TITLE tumor necrosis factor receptor extracellular domain, chain B  
PDB TITLE extracellular domain of the 55kda tumor necrosis factor  
ORGANISM #formal\_name Homo sapiens #common\_name man  
#note residues 12 to 172 of the mature sequence of the entire  
receptor. residue 11 is mutated to met as a result of the  
expression system  
REFERENCE A65560  
#authors Naismith, J.H.; Sprang, S.R.  
#submission submitted to the Brookhaven Protein Data Bank, July 1996  
REFERENCE TNO26251  
#authors Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.  
#journal J. Biol. Chem. (1995) 270:13303  
#title Crystallographic evidence for dimerization of unliganded  
tumor necrosis factor receptor.  
TN026252  
Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,  
K.; Naismith, J.H.; Sprang, S.R.  
J. Mol. Biol. (1994) 239:332  
Two crystal forms of the extracellular domain of type 1 tumor  
necrosis factor receptor.  
REFERENCE A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
Cell (1993) 73:431-445  
Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
COMMENT Resolution: 1.85 angstroms  
DETERMINATION: X-ray diffraction  
KEYWORDS R-value: no refinement  
binding protein; cytokine; signalling protein  
FEATURE  
68-70  
143-145  
9-11,19-21  
133-136,139-142  
27-31,41-44  
73-76,85-87  
92-98,101-106  
113-117,126-129  
5-19  
20-33  
23-42  
43-60  
63-78  
66-86  
88-104  
107-119  
110-127  
129-140

143-156 #disulfide\_bonds\  
146-152 #disulfide\_bonds  
SUMMARY #length 158 #molecular-weight 17827 #checksum 5022

Query Match 56.0%: Score 1222; DB 5; Length 158;  
Best Local Similarity 98.7%; Pred. No. 3.27e-258;  
Matches 155; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 2 DSVCPGKRIHPONNSICCTCKHKGTYLYNDGPGGDDTCRCEGSGFTASENHLRHCL 61  
QY 23 DSVCPGKRIHPONNSICCTCKHKGTYLYNDGPGGDDTCRCEGSGFTASENHLRHCL 82

Db 62 SCSCREKMGVEISSCTVDYDTCGCRKNQRYHWSNLFQCFNCSLCINGTVHLSQEQ 121  
QY 83 SCSCREKMGVEISSCTVDYDTCGCRKNQRYHWSNLFQCFNCSLCINGTVHLSQEQ 142

Db 122 KONTVCTCHAGFFLRENECVSCSNCKRSLECKTCLSP 158  
QY 143 KONTVCTCHAGFFLRENECVSCSNCKRSLECKTCLSP 179

RESULT 4  
ENTRY INCFB #type complete

TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
chain B - hu

ALTERNATE\_NAMES stnfr1; type 1 receptor  
ORGANISM #formal\_name Homo sapiens #common\_name man  
#note expressed in Escherichia coli; residue 11 is mutated to met  
as a result of the expression system

REFERENCE A66195  
#authors Naismith, J.H.; Sprang, S.R.  
#submission submitted to the Brookhaven Protein Data Bank, October 1994  
#cross-references PDB:1NCF

REFERENCE TN029041  
#authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,  
J. Mol. Biol. (1994) 239:332  
#journal Two crystal forms of the extracellular domain of type 1 tumor  
#title necrosis factor receptor.  
A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
Cell (1993) 73:431-445  
#journal Crystal structure of the soluble human 55 kd TNF  
#title receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
Blinding protein; cytokine; signalling protein

COMMENT Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
Blinding protein; cytokine; signalling protein

KEYWORDS

FEATURES

2-16 #disulfide\_bonds\  
17-30 #disulfide\_bonds\  
20-39 #disulfide\_bonds\  
42-57 #disulfide\_bonds\  
60-75 #disulfide\_bonds\  
63-83 #disulfide\_bonds\  
85-101 #disulfide\_bonds\  
104-116 #disulfide\_bonds\  
107-124 #disulfide\_bonds\  
126-137 #disulfide\_bonds\  
SUMMARY #length 142 #molecular-weight 16046 #checksum 1225

Query Match 51.3%: Score 1119; DB 5; Length 142;  
Best Local Similarity 99.3%; Pred. No. 2.28e-233;  
Matches 141; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 VCPGKRIHPONNSICCTCKHKGTYLYNDGPGGDDTCRCEGSGFTASENHLRHCLSC 60  
QY 25 VCPGKRIHPONNSICCTCKHKGTYLYNDGPGGDDTCRCEGSGFTASENHLRHCLSC 84

Db 61 SKCRKMGVEISSCTVDYDTCGCRKNQRYHWSNLFQCFNCSLCINGTVHLSQEQ 120  
QY 85 SKCRKMGVEISSCTVDYDTCGCRKNQRYHWSNLFQCFNCSLCINGTVHLSQEQ 144

Db 121 NTVCTCHAGFFLRENECVSCSN 142  
QY 145 NTVCTCHAGFFLRENECVSCSN 166

RESULT 5  
ENTRY ITNRR #type complete

TITLE tumor necrosis factor receptor type 1 (p55 extracellular  
#formal\_name Homo sapiens #common\_name man  
#note recombinant form expressed in Baculovirus Sf9

REFERENCE A52442  
#authors Banner, D.W.  
#submission submitted to the Brookhaven Protein Data Bank, May 1994  
#cross-references PDB:1TNR

REFERENCE A40737  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
Cell (1993) 73:431-445  
#journal Crystal structure of the soluble human 55 kd TNF  
#title receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
TN034093

REFERENCE TN034093  
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Winkler, F.K.;  
Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;  
Lesslauer, W.  
J. Mol. Biol. (1993) 229:555  
#journal Crystalization and preliminary analysis of tnf-beta and a  
#title tnf-beta-55 kd tnf receptor complex.  
Resolution: 2.85 angstroms  
Determination: X-ray diffraction  
Complex(LymphokineRECEPTOR)

COMMENT Resolution: 2.85 angstroms  
Determination: X-ray diffraction  
Complex(LymphokineRECEPTOR)

KEYWORDS

FEATURES

1-15 #disulfide\_bonds\  
16-29 #disulfide\_bonds\  
19-38 #disulfide\_bonds\  
41-56 #disulfide\_bonds\  
59-74 #disulfide\_bonds\  
62-82 #disulfide\_bonds\  
84-100 #disulfide\_bonds\  
103-115 #disulfide\_bonds\  
106-123 #disulfide\_bonds\  
125-136 #disulfide\_bonds\  
SUMMARY #length 139 #molecular-weight 15746 #checksum 5235

Query Match 50.5%: Score 1103; DB 5; Length 139;  
Best Local Similarity 99.3%; Pred. No. 1.62e-229;  
Matches 138; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 CPQKRIHPONNSICCTCKHKGTYLYNDGPGGDDTCRCEGSGFTASENHLRHCLSCS 60  
QY 26 CPQKRIHPONNSICCTCKHKGTYLYNDGPGGDDTCRCEGSGFTASENHLRHCLSCS 85

Db 61 KCRKMGVEISSCTVDYDTCGCRKNQRYHWSNLFQCFNCSLCINGTVHLSQEQ 120  
QY 86 KCRKMGVEISSCTVDYDTCGCRKNQRYHWSNLFQCFNCSLCINGTVHLSQEQ 145

Db 121 TVCTCHAGFFLRENECVSC 139  
QY 146 TVCTCHAGFFLRENECVSC 164

RESULT 6  
ENTRY INCFB #type complete

TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
chain A - hu

ALTERNATE\_NAMES stnfr1; type 1 receptor

ORGANISM #formal\_name Homo sapiens #common\_name man  
#note expressed in Escherichia coli, residue 11 is mutated to met  
as a result of the expression system

REFERENCE #authors Natsmith, J.H.; Sprang, S.R.  
#submission submitted to the Brookhaven Protein Data Bank, October 1994  
#cross-references PDB:INCF  
#reference TNO29039

REFERENCE #authors Rodseth, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale, K.; Natsmith, J.H.; Sprang, S.R.  
#journal J. Mol. Biol. (1994) 239:332  
#title Two crystal forms of the extracellular domain of type 1 tumor necrosis factor receptor.  
#authors Banner, D.W.; D'Arcy, A.; Jones, W.; Gentz, R.; Schoenfeld, H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
#journal Cell (1993) 73:431-445  
#title Crystal structure of the soluble human 55 kd TNF receptor-human TNFbeta complex: implications for TNF receptor activation.

COMMENT Resolution: 2.25 angstroms  
#comment Determination: X-ray diffraction  
#comment R-value: no refinement  
#comment binding protein; cytokine; signalling protein

FEATURES  
5-19 #disulfide\_bonds\  
20-33 #disulfide\_bonds\  
23-42 #disulfide\_bonds\  
43-60 #disulfide\_bonds\  
63-78 #disulfide\_bonds\  
66-86 #disulfide\_bonds\  
88-104 #disulfide\_bonds\  
107-119 #disulfide\_bonds\  
110-127 #disulfide\_bonds\  
129-140 #disulfide\_bonds\  
SUMMARY #length 140 #molecular-weight 15889 #checksum 6622

Query Match 50.2%; Score 1096; DB 5; Length 140;  
Best Local Similarity 99.3%; Pred. No. 7.85e-228;  
Matches 138; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 2 DSVCPGKTYHPNNISICTCKHKGTYLVNDGPGQDPCRCESGSPFASENHLRHCL 61  
|||  
QY 23 DSVCPGKTYHPNNISICTCKHKGTYLVNDGPGQDPCRCESGSPFASENHLRHCL 82  
|||  
Db 62 SCCKCKEMQVVISCTVDRTVCGCRKQYRHYWSENLFQCFNCTLCINGTVHLSGCE 121  
|||  
QY 83 SCCKCKEMQVVISCTVDRTVCGCRKQYRHYWSENLFQCFNCTLCINGTVHLSGCE 142  
|||  
Db 122 KONTVCTCHAGFFLRENEC 140  
|||  
QY 143 KONTVCTCHAGFFLRENEC 161  
|||

RESULT 7 Jc4302 #type complete

ENTRY

TITLE tumor necrosis factor receptor p55 - pigORGANISM #formal\_name S  
DATE 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change  
12-Dec-1997  
Jc4302; PC4093

ACCESSIONS Jc4302  
#accession Jc4302  
#molecule\_type mRNA  
#residues 1-461 #label SURT  
#cross-references GB:019944; NID:g1141752; PID:g1141753  
#accession PC4093  
#journal  
#molecule\_type protein  
#residues 1-7 #label SUR2

GENETICS #experimental\_source kidney cell line 15

CLASSIFICATION #gene tnfr  
#superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology  
#product repeat homology  
#glycoprotein; kidney; receptor; transmembrane protein; tumor

FEATURES  
1-29 #domain signal sequence #status predicted #label SIG\  
30-461 #product tumor necrosis factor receptor p55 #status  
44-194 #domain extracellular cysteine rich #status predicted  
#label EXT\  
44-82 #domain NGF receptor repeat homology #label NG1\  
211-231 #domain transmembrane #status predicted #label TM1\  
361-447 #domain signal transduction #status predicted #label  
SIG\  
54,145,151 #binding\_site carbohydrate (Asn) (covalent) #status  
predicted

SUMMARY #length 461 #molecular-weight 50696 #checksum 8079

Query Match 46.4%; Score 1012; DB 2; Length 461;  
Best Local Similarity 71.9%; Pred. No. 1.20e-207;  
Matches 123; Conservative 25; Mismatches 22; Indels 1; Gaps 1;

Db 41 ESICPGKYSHPNNISICTCKHKGTYLVNDGPGQDPCRCESGSPFASENHLRHCL 100  
|||  
QY 23 DSVCPGKTYHPNNISICTCKHKGTYLVNDGPGQDPCRCESGSPFASENHLRHCL 82  
|||  
Db 101 SCCKCKEMQVVISCTVDRTVCGCRKQYRHYWSENLFQCFNCTLCINGTVHLSGCE 160  
|||  
QY 83 SCCKCKEMQVVISCTVDRTVCGCRKQYRHYWSENLFQCFNCTLCINGTVHLSGCE 142  
|||  
Db 161 KODTICNCHSGFFLRDKCEVCSCVKNKA-DCKNLCPATSETRNDPDTGTT 210  
|||  
QY 143 KONTVCTCHAGFFLRENECVSCNCKKSECTKSLPQLENVGTRDSDGTT 193  
|||

RESULT 8 I57826 #type complete

ENTRY

TITLE tumor necrosis factor receptor - mouseORGANISM #formal\_name  
DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change  
23-May-1997  
I57826

ACCESSIONS I57826  
#accession I57826  
#authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;  
Steinmetz, M.  
#journal Mol. Immunol. (1993) 30:165-176  
#title Genomic organization and promoter function of the murine  
tumor necrosis factor receptor beta gene.  
#cross-references M0ID:93156721  
#accession I57826  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 1-454 #label RES  
#cross-references GB:M/6556; NID:g202100; PID:g202102

GENETICS

CLASSIFICATION #gene TNFR-2  
#superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology  
#product repeat homology  
#cytokine receptor  
#length 454 #molecular-weight 50030 #checksum 4267

KEYWORDS

SUMMARY

Query Match 43.2%; Score 944; DB 2; Length 454;  
Best Local Similarity 67.4%; Pred. No. 2.33e-191;  
Matches 116; Conservative 28; Mismatches 27; Indels 1; Gaps 1;

Db 41 DSVCPGKTYHPNNISICTCKHKGTYLVNDGPGQDPCRCESGSPFASENHLRHCL 100  
|||  
QY 23 DSVCPGKTYHPNNISICTCKHKGTYLVNDGPGQDPCRCESGSPFASENHLRHCL 82  
|||  
Db 101 SCCKCKEMQVVISCTVDRTVCGCRKQYRHYWSENLFQCFNCTLCINGTVHLSGCE 160  
|||

```

Oy 83 SCSCRKEMGVEISSCTVDRDTVCGRKNQNRHWSLENLFCFCTCLNCTVHLSQOE 142
Db 161 TONTVCNCHAGFFLRESECPVCSHCKRNEBCKMLCLPPPLAVNTNPDSGTA 212
Oy 143 KONTVCTCHAGFFLRENECVCSNCKSLKCTKLSLPQ-IEINVKGTEDSGTT 193

RESULT 9 GQMST1 #type complete

TITLE tumor necrosis factor receptor type 1 precursor - mouseALTERNATE_NAMES
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
05-Sep-1997

ACCESSIONS A38634; B40254; S16677; S19021; I54532
A38634
#authors Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
#title Cloning and expression of cDNAs for two distinct murine tumor
necrosis factor receptors demonstrate one receptor is
species specific.
#cross-references MUID:91187885
#accession A38634
#molecule_type mRNA
#residues 1-454 #label LEW
#cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE A40254
#authors Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
#journal Mol. Cell. Biol. (1991) 11:3020-3026
#title Molecular cloning and expression of the type 1 and type 2
murine receptors for tumor necrosis factor.
#cross-references MUID:91246168
#accession B40254
#molecule_type mRNA
#residues 1-454 #label GO2
#cross-references GB:M60468; NID:g199825; PID:g199826
REFERENCE S16677
#authors Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kisonergis,
A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
#journal Eur. J. Immunol. (1991) 21:1649-1656
#title Cloning, expression and cross-linking analysis of the murine
p55 tumor necrosis factor receptor.
#cross-references MUID:91285014
#accession S16677
#molecule_type mRNA
#residues 1-454 #label BAR
#cross-references EMBL:X59238; NID:g53578; PID:g53579
REFERENCE S19021
#authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
#journal Immunogenetics (1991) 34:338-340
#title Molecular cloning and expression of the mouse Tnf receptor
Type B.
#cross-references MUID:92039815
#accession S19021
#molecule_type mRNA
#residues 1-454 #label ROT
#cross-references EMBL:X57796; NID:g54848; PID:g54849
REFERENCE I54532
#authors Bebo, B.F.
#journal Immunogenetics (1994) 39:450-451
#title Nucleotide sequence of the TNF type I receptor from a mouse
endothelioma cell line.
#cross-references MUID:94245292
#accession I54532
#status translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-454 #label RES
#cross-references GB:I26349; NID:g430732; PID:g430733
COMMENT This protein is one of two distantly related receptors for both
TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

```

```

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
FEATURE #product repeat homology; receptor; transmembrane protein
1-29
30-454
30-212
44-82
84-126
127-167
168-204
213-235
236-254
54,151,202
SUMMARY #length 454 #molecular_weight 50129 #checksum 4839
Query Match 43.2%; Score 944; DB 1; Length 454;
Best Local Similarity 67.4%; Pred. No. 2,336-191;
Matches 116; Conservative 28; Mismatches 27; Indels 1; Gaps 1;

Db 41 DSICPGKTVHSKNSICTCHKGTLYVSDCPSPGRTVCRCEKGFETASONTLRQCL 100
Oy 23 DVCPOGKTHPNNISICTCHKGTLYVNDPCPGGDTDCRCEGSGFTSENHRLCL 82
Db 101 SCTCRKEMSGVEISPCOADRDTVCGCKENOFRTLSRHCYDCSPCFNGTYTPCKE 160
Oy 83 SCSCRKEMGVEISSCTVDRDTVCGRKNQNRHWSLENLFCFCTCLNCTVHLSQOE 142
Db 161 TONTVCNCHAGFFLRESECPVCSHCKRNEBCKMLCLPPPLAVNTNPDSGTA 212
Oy 143 KONTVCTCHAGFFLRENECVCSNCKSLKCTKLSLPQ-IEINVKGTEDSGTT 193

RESULT 10 GQMST1 #type complete

ENTRY #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
05-Sep-1997

ACCESSIONS B36555
#authors Himmler, A.; Maurer-Poggy, I.; Kronke, M.; Scheurich, P.;
Pfeizmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
Stratowa, C.; Adolf, G.R.
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
#accession B36555
#molecule_type mRNA
#residues 1-461 #label HIM
#cross-references GB:M63122; NID:g207361; PID:g207362
COMMENT This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
FEATURE #product repeat homology; receptor; transmembrane protein
1-29
30-461
30-211
30-201
44-82
84-126
127-167
168-204
212-234
#domain signal sequence #status predicted #label SIG\
#product tumor necrosis factor receptor type 1 #status
predicted #label MAT\
#domain extracellular #status predicted #label EXT\
#product tumor necrosis factor binding protein #status
predicted #label TBP\
#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
predicted

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235-461      #domain intracellular #status predicted #label INT\
54,151,201   #binding_site carbohydrate (asn) (covalent) #status
                                     predicted
SUMMARY      #length 461 #molecular-weight 50969 #checksum 1617

Query Match          42.5% Score 928; DB 1; Length 461;
Best Local Similarity 66.1%; Pred. No. 1,566-157;
Matches 113; Conservative 26; Mismatches 32; Indels 0; Gaps 0;

Db 41 DNLCPQGRVAPRPNKNSICTCTCHKRTYLVSPDPSPGDETVCEVDKGFYASQNHVRCL 100
|:::||||||| | ||||| ||||| ||||| ::| :|::|::|::|::|::|::|::|::|::|
Oy 23 DSYCPGKGVIHPQNNSICTCTCHKRTYLXNDGPQGDDTDRRECSGSFYSENHRLCL 82
|:::||||||| | ||||| ||||| ||||| ::| :|::|::|::|::|::|::|::|::|::|
Db 101 SCTCKRKEMFOVEISPCADMDTVCGCKRNQFORYLSTFHQCVCDSFCFGVTYTIIPKE 160
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 83 SCSKRKEMGVIEISSCTYVDRTVCGCRKNQRYRWYSENLPQCFNCFTLCGLNGTVHLSCQE 142
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 161 KONTVCNHAPEFLSGNCTPCSCHKRNQECMKILCPYAVANTVPDSDGTA 211
||||| ||||| ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 143 KONTVCCHAGFELENECVSCSNCKSLSECTKLTLPLDIENVKGTEDSGTT 193
||||| ||||| ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11 TTHUAP #type complete

TITLE glycoprotein hormones alpha chain precursor - humanALTERNATE_NAMES chd
alpha chain; follitropin alpha chain; interstitial
cell-stimulating hormone alpha chain; lutinizizing hormone
alpha chain; lurotrophin alpha chain; thyroid-stimulating
hormone alpha chain; thyrotropin alpha chain
formal_name Homo sapiens #common_name man
13-Jul-1981 #sequence_revision 23-Oct-1981 #text_change
05-Sep-1997
ACCESSIONS A93213; A92832; B92303; A90751; A90179; A91461; A92184;
A94557; B92181; A92141; I58200; A01481
REFERENCE
#authors Fiddes, J.C.; Goodman, H.M.
#journal Nature (1979) 281:351-356
#title Isolation, cloning and sequence analysis of the cDNA for the
alpha-subunit of human chorionic gonadotropin.
#accession A93213
#molecule_type mRNA
#residues 1-116 #label FITD
#cross-references GB:V00518; NID:g31868; PID:g31869
REFERENCE
#authors Fiddes, J.C.; Goodman, H.M.
#journal J. Mol. Appl. Genet. (1981) 1:3-18
#title The gene encoding the common alpha subunit of the four human
glycoprotein hormones.
#cross-references MUID:82267643
#accession A92832
#molecule_type DNA
#residues 1-98 #label FIT2
#cross-references GB:V00484
REFERENCE
#authors Birken, S.; Featherston, J.; Canfield, R.; Bolme, I.
#journal J. Biol. Chem. (1981) 256:1816-1823
#title The amino acid sequences of the prepeptides contained in the
alpha and beta subunits of human choriongonadotropin.
#cross-references MUID:81117268
#accession B92303
#molecule_type protein
#residues 1-24 #label BIR
#note restriction endonuclease evidence indicates that a
single gene codes for the alpha chain common to the
four dimeric hormones: thyrotropin, lutrophi,
follitropin, and choriongonadotropin
previouslly the mature alpha chain (residues 25-116) was
isolated from each of the hormones and its sequence
was determined, as documented below
REFERENCE A90751
#authors Saltram, M.R.; Li, C.H.
```

```

#journal Can. J. Biochem. (1977) 55:755-760
#title Human pituitary thyrotropin. The primary structure of the
#       alpha and beta subunits.
#cross-references MUID:77243687
#accession A90751
#molecule_type protein
#residues 28-107,'SC',110-116 #label SAT
REFERENCE
#authors Saltram, M.R.; Papkoff, H.; Li, C.H.
#journal Biochem. Biophys. Res. Commun. (1972) 48:530-537
#title Human pituitary interstitial cell stimulating hormone:
#       primary structure of the alpha subunit.
#cross-references MUID:72242988
#accession A90179
#molecule_type protein
#residues 28-107,'SC',110-116 #label SA2
REFERENCE
#authors Keutmann, H.T.; Williams, R.M.; Bishop, W.H.; Ryan, R.J.
#journal Fed. Proc. (1978) 37:1828
#title Structure of human luteinizing hormone.
#accession A91461
#molecule_type protein
#residues 28-116 #label KEU
REFERENCE
#authors Rathnam, P.; Saxena, B.B.
#journal J. Biol. Chem. (1975) 250:6735-6746
#title Primary amino acid sequence of follicle-stimulating hormone
#       from human pituitary glands.
#cross-references MUID:76005558
#accession A92184
#molecule_type protein
#residues 25-28,'E',30-116 #label RAT
REFERENCE
#authors Shome, B.; Parlow, A.F.
#submission submitted to the Atlas, April 1975
#accession A94352
#molecule_type protein
#residues 28-116 #label SHO
REFERENCE
#authors Morgan, F.J.; Birken, S.; Canfield, R.E.
#journal J. Biol. Chem. (1975) 250:5247-5258
#title The amino acid sequence of human chorionic gonadotropin. The
#       alpha subunit and beta subunit.
#cross-references MUID:75211304
#accession B92181
#molecule_type protein
#residues 25-116 #label MOR
#note heterogeneity is found at the amino end. Approximately
#       10 and 30% of the chains lack residues 1-2 and 1-3,
#       respectively
REFERENCE
#authors Bellisario, R.; Carlsen, R.B.; Bahl, O.P.
#journal J. Biol. Chem. (1973) 248:6796-6809
#title Human chorionic gonadotropin. Linear amino acid sequence of
#       the alpha subunit.
#cross-references MUID:74011266
#accession A92141
#molecule_type protein
#residues 25-116 #label BEL
REFERENCE
#authors Shome, B.; Parlow, A.F.
#journal J. Clin. Endocrinol. Metab. (1974) 39:199-202
#title Human follicle stimulating hormone (hFSH): first proposal for
#       the amino acid sequence of the alpha-subunit (hFSHalpha)
#       and first demonstration of its identity with the
#       alpha-subunit of human luteinizing hormone (hLHalpha).
#cross-references MUID:74262937
#contents annotation
REFERENCE
#authors Fujiki, Y.; Rathnam, P.; Saxena, B.B.
#journal Biochim. Biophys. Acta (1980) 624:428-435
#title Studies on the disulfide bonds in human pituitary
#       follicle-stimulating hormone.

```

#cross-references MUID:81021713  
#contents annotation: preliminary disulfide bonds  
REFERENCE A44674  
#authors Laphorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs, N.W.  
#journal Nature (1994) 369:455-461  
#title Crystal structure of human chorionic gonadotropin. annotation: X-ray crystallography, 3.0 angstroms; correction of disulfide bonds  
#contents M158200  
#authors Miyoshi, I.; Kasai, N.; Hayashizaki, Y.  
#journal Nippon Rinsho (1994) 52:940-947  
#title [Structure and regulation of human thyroid-stimulating hormone (TSH) gene].  
#cross-references MUID:94254248  
#accession I58200  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 1-116 #label RES  
#cross-references GB:S70585; MID:9546844; PID:9546845  
GENETICS  
#gene GDB:CGA  
#cross-references GDB:119774; OMIM:118850  
#map\_position 6q14-q21  
#introns 30/1, 91/3  
CLASSIFICATION #superfamily glycoprotein hormones alpha chain  
KEYWORDS glycoprotein; heterodimer; hormone; pituitary  
FEATURE  
1-24 #domain signal sequence #status experimental #label SIG\  
25-116 #product glycoprotein hormones alpha chain #status experimental #label MAT\  
31-55, 34-84, 52-106, #disulfide\_bonds #status experimental\  
55-108, 83-111 #binding site carbohydrate (Asn) (covalent) #status experimental  
76,102 #length 116 #molecular\_weight 13075 #checksum 1664  
SUMMARY  
Query Match 30.8%; Score 672; DB 1; Length 116;  
Best Local Similarity 93.5%; Pred. No. 8,42e-127;  
Matches 87; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
DB 24 SAPDVQDCECTLOENPFPSQGPAPILQCGCCFSRAVPTPRSKTKMLVQKNVTSSTC 83  
OY 193 TAGAAPGCECTLOENPFPSQGPAPILQCGCCFSRAVPTPRSKTKMLVQKNVTSSTC 252  
DB 84 CVAKSYNRYTVMGFKEVNHRTACHCSTCYHKS 116  
OY 253 CVAKSYNRYTVMGFKEVNHRTACHCSTCYHKS 285  
RESULT 12  
ENTRY 1HRA #type complete  
TITLE chorionic gonadotropin, chain A - humanORGANISM #formal\_name HC  
#note Placental origin, urinary extracted  
REFERENCE A52806  
#authors Laphorn, A.J.; Harris, D.C.; Isaacs, N.W.  
#submission submitted to the Brookhaven Protein Data Bank, August 1994  
#cross-references PDB:1HRP  
REFERENCE TN02062  
#authors Laphorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Machin, K.J.; Morgan, F.J.; Isaacs, N.W.  
#journal Nature (1994) 369:455  
#title Crystal structure of human chorionic gonadotropin. TN022063  
#authors Harris, D.C.; Machin, K.J.; Evin, G.M.; Morgan, F.J.; Isaacs, N.W.  
#journal J. Biol. Chem. (1989) 264:6705  
#title Preliminary x-ray diffraction analysis of human chorionic gonadotropin.  
COMMENT Resolution: 3.0 angstroms

COMMENT Determination: X-ray diffraction  
KEYWORDS hormone  
FEATURE  
4-28 #disulfide\_bonds\  
7-57 #disulfide\_bonds\  
25-79 #disulfide\_bonds\  
29-81 #disulfide\_bonds\  
55-84 #disulfide\_bonds  
SUMMARY #length 86 #molecular\_weight 9572 #checksum 1371  
Query Match 29.8%; Score 650; DB 5; Length 86;  
Best Local Similarity 96.5%; Pred. No. 1,23e-121;  
Matches 83; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
DB 1 TODCECTLOENPFPSQGPAPILQCGCCFSRAVPTPRSKTKMLVQKNVTSSTCYAK 60  
OY 197 ABGCECTLOENPFPSQGPAPILQCGCCFSRAVPTPRSKTKMLVQKNVTSSTCYAK 256  
DB 61 SYNRYTVMGFKEVNHRTACHCSTCY 86  
OY 257 SYNRYTVMGFKEVNHRTACHCSTCY 282  
RESULT 13  
ENTRY 1XUUA #type complete  
TITLE chorionic gonadotropin, chain A - humanPDB\_TITLE theoretical  
ORGANISM #formal\_name Homo sapiens #common\_name man  
REFERENCE A66957  
#authors Jiang, X.; Dreano, M.; Buckler, D.R.; Chang, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N.  
#submission submitted to the Brookhaven Protein Data Bank, December 1996  
#cross-references PDB:1XUUA  
REFERENCE TN032623  
#authors Jiang, X.; Dreano, M.; Buckler, D.R.; Chang, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Tayar, N.  
#journal Structure (London) (1996) 3:1341  
#title Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions structure.  
REFERENCE TN032624  
#authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.; Hendrickson, W.A.  
#journal Structure (London) (1994) 2:545  
#title Structure of human chorionic gonadotropin at 2.6 a resolution from mad analysis of the selenomethionyl protein.  
COMMENT Resolution: not applicable  
COMMENT Determination: theoretical model  
KEYWORDS complex; glycoprotein hormone receptor glycoprotein; hormone; phosphorylation; receptor  
FEATURE  
37-41 #region helix (right hand alpha)\  
7-10, 22-25 #region beta sheet\  
49-53, 26-34 #region beta sheet\  
61-65, 71-75 #region beta sheet\  
55-60, 77-81 #region beta sheet\  
3-27 #disulfide\_bonds\  
6-56 #disulfide\_bonds\  
24-78 #disulfide\_bonds\  
28-80 #disulfide\_bonds\  
55-83 #disulfide\_bonds  
SUMMARY #length 85 #molecular\_weight 9471 #checksum 9656  
Query Match 29.7%; Score 648; DB 5; Length 85;  
Best Local Similarity 100.0%; Pred. No. 3,63e-121;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 3 CPECTLOENPFPSQGPAPILQCGCCFSRAVPTPRSKTKMLVQKNVTSSTCYAKSYN 62  
OY 200 CPECTLOENPFPSQGPAPILQCGCCFSRAVPTPRSKTKMLVQKNVTSSTCYAKSYN 259  
DB 63 RYTVMGFKEVNHRTACHCSTCY 85



OY 260 RVTVMGKFVENHTACHCSTCY 282

RESULT 14 IHCNA #type complete

TITLE Human chorionic gonadotropin, chain A - humanORGANISM #format\_r

REFERENCE A52587 Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;

#authors Hendrickson, W.A. #submission submitted to the Brookhaven Protein Data Bank, July 1994

#cross-references PDB:IHCN TNO20262

REFERENCE #journal Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.;

#title Hendrickson, W.A. Structure (1994) 2:545

COMMENT Resolution: 2.6 angstroms

KEYWORDS Determination: X-ray diffraction

FEATURE #region helix (right hand alpha)\

36-43 #region beta sheet\

4-11,21-28 #region beta sheet\

29-35,48-54 #disulfide\_bonds\

3-27 #disulfide\_bonds\

6-56 #disulfide\_bonds\

24-78 #disulfide\_bonds\

28-80 #disulfide\_bonds\

55-83 #disulfide\_bonds

SUMMARY #length 85 #molecular-weight 9471 #checksum 9656

Query Match 29.7%; Score 648; DB 5; Length 85;

Best Local Similarity 100.0%; Pred. No. 3.63e-121;

Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 CPCTIQENPFESQPGAPILIQMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 62

OY 200 CPCTIQENPFESQPGAPILIQMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db 63 RVTVMGKFVENHTACHCSTCY 85

OY 260 RVTVMGKFVENHTACHCSTCY 282

RESULT 15 A39555 #type complete

ENTRY A39555 #type complete

TITLE glycoprotein hormones alpha chain precursor - rhesus macaqueORGANISM

DATE 08-Nov-1991 #sequence-revision 08-Nov-1991 #text\_change

ACCESSION A39555

REFERENCE A39555

#authors Goto, T.G.; Durning, M.; Fisher, J.M.

#journal DNA Cell Biol. (1991) 10:367-380

#title Molecular cloning of the rhesus glycoprotein hormone

#cross-references MIM:91321740

#accession A39555

#status preliminary; not compared with conceptual translation

#molecule\_type DNA

#residues 1-120 #label GOL

CLASSIFICATION #superfamily glycoprotein hormones alpha chain

KEYWORDS glycoprotein

SUMMARY #length 120 #molecular-weight 13785 #checksum 5074

Query Match 25.3%; Score 552; DB 2; Length 120;

Best Local Similarity 83.5%; Pred. No. 8.95e-99;

Matches 71; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Db 35 CPBCKPRENFKFGAPITQMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSLT 94

OY 200 CPCTIQENPFESQPGAPILIQMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYN 259

Db 95 RVTVMGKFVENHTACHCSTCY 119

OY 260 RVTVMGKFVENHTACHCSTCY 284

Search completed: Wed May 6 09:01:17 1998

Job time : 34 secs.

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 W P E R E H (TM)  
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MPearch\_p protein - protein database search, using Smith-Waterman algorithm  
 Run on: Wed May 6 08:58:14 1998; Maspar time 8.40 Seconds  
 Tabular output not generated. 851.426 Million cell updates/sec

Title: >US-08-804-166-6  
 Description: (1-285) from US08804166.pep  
 Perfect Score: 2183  
 Sequence: 1 SRTSLLAFLGLCLCPMLQEG.....GFKVENHTRACHCTCYTHKS 285

Scoring table:  
 PAM 150  
 Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 08  
 Listing first 45 summaries

Database: swiss-prot35  
 1:swiss1

Statistics: Mean 42.622; Variance 62.749; scale 0.679

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description	Pred. No.
1	1306	59.8	455	1. TNRI_HUMAN TUMOR NECROSIS FACTOR	0.00e+00
2	1012	46.4	461	1. TNRI_PIG TUMOR NECROSIS FACTOR	1.63e-244
3	944	43.2	454	1. TNRI_MOUSE TUMOR NECROSIS FACTOR	2.69e-225
4	928	42.5	461	1. TNRI_RAT TUMOR NECROSIS FACTOR	8.75e-221
5	672	30.8	116	1. GLHA_HUMAN GLYCOPROTEIN HORMONES	3.55e-149
6	552	25.3	120	1. GLHA_MACM GLYCOPROTEIN HORMONES	3.70e-116
7	547	25.1	96	1. GLHA_RABIT GLYCOPROTEIN HORMONES	8.57e-115
8	549	25.1	120	1. GLHA_BOVIN GLYCOPROTEIN HORMONES	2.44e-115
9	549	25.1	120	1. GLHA_SHEEP GLYCOPROTEIN HORMONES	5.64e-114
10	544	24.9	120	1. GLHA_RAT GLYCOPROTEIN HORMONES	1.98e-113
11	542	24.8	96	1. GLHA_BALC GLYCOPROTEIN HORMONES	1.98e-113
12	542	24.8	120	1. GLH2_RAT GLYCOPROTEIN HORMONES	1.98e-113
13	542	24.8	120	1. GLHA_MOUSE GLYCOPROTEIN HORMONES	1.98e-113
14	542	24.8	120	1. GLHA_PIG GLYCOPROTEIN HORMONES	1.98e-113
15	539	24.7	96	1. GLHA_STRCA GLYCOPROTEIN HORMONES	1.30e-112
16	540	24.7	120	1. GLHA_CALJA GLYCOPROTEIN HORMONES	6.95e-113
17	536	24.6	96	1. GLHA_PHYCA GLYCOPROTEIN HORMONES	8.55e-112
18	537	24.6	120	1. GLHA_MERGA GLYCOPROTEIN HORMONES	4.57e-112
19	507	23.2	118	1. GLH2_CYPCA GLYCOPROTEIN HORMONES	6.51e-104
20	503	23.1	120	1. GLHA_EQUAS GLYCOPROTEIN HORMONES	2.27e-103
21	503	23.0	96	1. GLHA_HORSE GLYCOPROTEIN HORMONES	7.90e-103
22	499	22.9	116	1. GLHA_CLAGA GLYCOPROTEIN HORMONES	9.58e-102
23	500	22.9	118	1. GLHA_HYPMO GLYCOPROTEIN HORMONES	5.13e-102

RESULT	1	STANDARD;	PRT;	455 AA.
ID	TNRI_HUMAN			
AC	P19438;			
DT	01-FEB-1991 (REL. 17, CREATED)			
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 1) (TNFRI) (P60) (TNF-R1) (P55) (CD120A).			
GN	TNFR1 OR TNFR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PLACENTA;			
RX	MEDLINE: 90235285.			
RA	SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W., GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDEL D.V., CELL 61:361-370(1990).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE: 90235284.			
RA	LOESCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M., TABUCHI H., LESSLAUER W., CELL 61:351-359(1990).			
RL	[3]			
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RP	MEDLINE: 91006021.			
RX	MEDLINE: 91006021.			
RA	NOPAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R., ADERKA D., HOLTSMANN H., WALDACH D., EMBO J. 9:3269-3278(1990).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE: 91090841.			
RA	HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PILZENMAIER K., LANTZ M., OLSSON I., HADTMANN R., STRATOWA C., ADOLF G.R., DNA CELL BIOL. 9:705-715(1990).			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE-PLACENTA;			
RX	MEDLINE: 91017509.			
RA	GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M., PROC. NATL. ACAD. SCI. U.S.A. 87:7380-7384(1990).			
RL	[6]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE: 92250049.			
RA	FUCHS P., STREHL S., DMORZAK M., HIMMLER A., AMBROS P.F.,			

24	500	22.9	118	1	GLH1_CYPCA	GLYCOPROTEIN HORMONES	5.13e-102
25	500	22.9	118	1	GLHA_CTEID	GLYCOPROTEIN HORMONES <td>5.13e-102</td>	5.13e-102
26	478	21.9	93	1	GLHA_MRCI	GLYCOPROTEIN HORMONES <td>4.53e-96</td>	4.53e-96
27	478	21.9	97	1	GLHA_RANCA	GLYCOPROTEIN HORMONES <td>2.43e-96</td>	2.43e-96
28	474	21.7	117	1	GLHA_ANGAN	GLYCOPROTEIN HORMONES <td>5.42e-95</td>	5.42e-95
29	450	20.6	114	1	GLH2_ONCKE	GLYCOPROTEIN HORMONES <td>1.53e-88</td>	1.53e-88
30	448	20.5	108	1	GLH1_ONCKE	GLYCOPROTEIN HORMONES <td>5.27e-88</td>	5.27e-88
31	427	19.6	94	1	GLHA_THUOB	GLYCOPROTEIN HORMONES <td>2.17e-82</td>	2.17e-82
32	424	19.4	117	1	GLHA_ACALA	GLYCOPROTEIN HORMONES <td>1.37e-81</td>	1.37e-81
33	376	17.2	125	1	GLHA_FUNHE	GLYCOPROTEIN HORMONES <td>6.97e-69</td>	6.97e-69
34	247	11.3	417	1	WSL1_HUMAN	WSL-1 PROTEIN PRECURSOR	6.68e-36
35	245	11.2	435	1	TNRC_HUMAN	LYMPHOTOXIN-BETA RECEPTOR	2.07e-35
36	225	10.3	325	1	VT2_SFVKA	TUMOR NECROSIS FACTOR	1.55e-30
37	221	10.1	326	1	VT2_MYXYL	TUMOR NECROSIS FACTOR	1.43e-29
38	216	9.9	415	1	TNRC_MOUSE	LYMPHOTOXIN-BETA RECEPTOR	2.26e-28
39	214	9.8	349	1	VC22_VARY	PROTEIN C22/B28 HOMOLOG	6.80e-28
40	211	9.7	425	1	NGFR_RAT	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR	3.53e-27
41	212	9.7	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR	2.04e-27
42	212	9.7	474	1	TNFR2_MOUSE	TUMOR NECROSIS FACTOR	2.04e-27
43	204	9.3	260	1	CD27_HUMAN	CD27L RECEPTOR PRECURSOR	1.61e-25
44	191	8.7	323	1	FASL_BOVIN	FASL RECEPTOR PRECURSOR	1.77e-22
45	183	8.4	595	1	CD30_HUMAN	CD30L RECEPTOR PRECURSOR	1.24e-20

RL GENOMICS 13:219-224(1992).  
 RN [7]  
 RP SEQUENCE OF 41-45.  
 RX MEDLINE: 90110215.  
 RA ENGELMANN H., NOVICK D., WALLACH D.;  
 RL J. BIOL. CHEM. 265:1531-1536(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
 RX MEDLINE: 93258809.  
 RA BANNER D.W., D'ARCY A., JAMES W., GENTZ R., SCHOENFELD H.-J.,  
 RA BROGER C., LOETSCHER H., LESSLAUER W.,  
 RL CELL 73:431-445(1993).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE: 97094982.  
 RA NAIMSMITH J.H., DEVINE T.O., KHONO H., SPRANG S.R.;  
 RL STRUCTURE 4:1251-1262(1996).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS.  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: X55313; G37224; -;  
 DR EMBL: M33294; G339745; -;  
 DR EMBL: M58286; G339754; -;  
 DR EMBL: M63121; G339756; -;  
 DR EMBL: M75866; G339750; -;  
 DR EMBL: M75864; G339750; JOINED.  
 DR EMBL: M75865; G339750; JOINED.  
 DR EMBL: M60275; G339760; -;  
 DR EMBL: A21522; G579600; -;  
 DR PIR: A34899; G0HUT1.  
 DR PIR: A35010; A35010.  
 DR PIR: S12057; S12057.  
 DR PIR: A38208; A38208.  
 DR PDB: 1TNR; 31-JUL-94.  
 DR PDB: 1NCF; 07-DEC-95.  
 DR PDB: 1EXT; 11-JAN-97.  
 DR MIM: 191190; -;  
 DR PROSITE: PS00652; TNFR\_NGFR.1; 3.  
 DR PROSITE: PS00500; TNFR\_NGFR.2; 3.  
 DR PROSITE: PS50017; DEATH\_DOMAIN.1.  
 KW RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, REPEAT, SIGNAL, APOPTOSIS;  
 KW 3D-STRUCTURE.  
 FT SIGNAL 1 21  
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.  
 FT CHAIN 41 291 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 212 234 POTENTIAL.  
 FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 43 196 4 X TNFR-CYS.  
 FT REPEAT 43 82 TNFR-CYS 1.  
 FT REPEAT 83 125 TNFR-CYS 2.  
 FT REPEAT 126 166 TNFR-CYS 3.  
 FT REPEAT 167 196 TNFR-CYS 4.  
 FT DOMAIN 356 441 DEATH DOMAIN.  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125

FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 191  
 FT DISULFID 185 195  
 FT CARBOHYD 54 54  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 FT CARBOHYD 412 412  
 FT CONFLICT 443 446  
 FT CONFLICT 443 446  
 SQ SEQUENCE 455 AA; 50494 MW; CE0EA06F CRC32;  
 Query Match 59.8%; Score 1306; DB 1; Length 455;  
 Best Local Similarity 98.8%; Pred. No. 0.00e+00;  
 Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Db 41 DSVCPGQYIHPNNSICTCTCHKGTIYNDCPGGQDTCRECEGSGFTASENHLRCL 100  
 Qy 23 DSVCPGQYIHPNNSICTCTCHKGTIYNDCPGGQDTCRECEGSGFTASENHLRCL 82  
 Db 101 SCSKCRKMGVEYISSCTVDYDVGCGKRNQRYHWSNLPFCFNCSTLNGTVHLSQCE 160  
 Qy 83 SCSKCRKMGVEYISSCTVDYDVGCGKRNQRYHWSNLPFCFNCSTLNGTVHLSQCE 142  
 Db 161 KONTVCTCHAGFFLENECVCSNCKSLCTKTLCPQIENVKGTEDSGT 211  
 Qy 143 KONTVCTCHAGFFLENECVCSNCKSLCTKTLCPQIENVKGTEDSGT 193  
 RESULT 2  
 ID TNFR1\_PIG STANDARD; PRT; 461 AA.  
 AC P50555;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFR1.  
 OS SUS SCROFA (PIG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; ARTIODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-KIDNEY;  
 RX MEDLINE: 96011645.  
 RA SUMER B., PAULI U.H.;  
 RL GENE 163:263-266(1995).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: U19994; G1141753; -;  
 DR PROSITE: PS00652; TNFR\_NGFR.1; 3.  
 DR PROSITE: PS00500; TNFR\_NGFR.2; 2.  
 DR PROSITE: PS50017; DEATH\_DOMAIN.1.  
 KW RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, REPEAT, SIGNAL, APOPTOSIS;  
 KW SIGNAL 1 21  
 FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR 1.  
 FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 211 233 POTENTIAL.  
 FT DOMAIN 234 461 CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	43	195	4 X TNFR-CYS.
FT	REPEAT	43	82	TNFR-CYS 1.
FT	REPEAT	83	125	TNFR-CYS 2.
FT	REPEAT	126	166	TNFR-CYS 3.
FT	REPEAT	167	195	TNFR-CYS 4.
FT	DOMAIN	362	447	DEATH DOMAIN.
FT	DISULFID	44	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	81	BY SIMILARITY.
FT	DISULFID	84	99	BY SIMILARITY.
FT	DISULFID	102	117	BY SIMILARITY.
FT	DISULFID	105	125	BY SIMILARITY.
FT	DISULFID	127	143	BY SIMILARITY.
FT	DISULFID	146	158	BY SIMILARITY.
FT	DISULFID	149	166	BY SIMILARITY.
FT	DISULFID	168	179	BY SIMILARITY.
FT	DISULFID	182	190	BY SIMILARITY.
FT	DISULFID	185	194	BY SIMILARITY.
FT	CARBOHYD	54	54	POTENTIAL.
FT	CARBOHYD	86	86	POTENTIAL.
FT	CARBOHYD	145	145	POTENTIAL.
FT	CARBOHYD	151	151	POTENTIAL.
QY	SEQUENCE	461 AA;	50696 MW;	8E2C350A CRC32;
QY	Query Match	46.4%;	Score 1012;	DB 1;
QY	Best Local Similarity	71.9%;	Pred. No. 1.63e-244;	Length 461;
QY	Matches 123;	Conservative 25;	Mismatches 22;	Indels 1;
QY				Gaps 1.
Db	41	ESLCPQKGYHSPQRNSICCTCKHKGTYLHNDCLPGLDTCRECDNGTFYASNNHLC	100	
QY	23	DVCPQKGYHSPQRNSICCTCKHKGTYLHNDCLPGLDTCRECDNGTFYASNNHLC	82	
Db	101	SCSKRSEMSQVEISLPTVDKRDYVCGCRKNQYRKYRSEITLFCQCLNCSLCPNGVQDPCLE	160	
QY	83	SCSKRSEMSQVEISLPTVDKRDYVCGCRKNQYRKYRSEITLFCQCLNCSLCPNGVQDPCLE	142	
Db	161	KQDITCNCHSGFFLDRKCEVSCVNCCKNA-DCKNLCPLATSEKNDPOTDGT	210	
QY	143	KQDITCNCHSGFFLDRKCEVSCVNCCKNA-DCKNLCPLATSEKNDPOTDGT	193	
RESULT	3	TNFR_MOUSE	STANDARD;	PRT; 454 AA.
AC	P25118;			
DT	01-MAY-1992	(REL. 22, CREATED)		
DT	01-MAY-1992	(REL. 22, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)		
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).			
GN	TNFR1 OR TNFR-1.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 9118785.			
RX	LEWIS M., TATAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,			
RX	WONG G.H., CHEN E.Y., GOEDEL D.V.;			
RL	PROC. NATL. ACAD. SCI. U.S.A. 86:2830-2834(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 91246168.			
RX	GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANDAN C.I.,			
RA	COPELAND N.G., JENKINS N.A., SMITH C.A.;			
RL	MOL. CELL. BIOL. 11:3020-3026(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 91285014.			
RX	BARRETT R., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,			
RA	GRAY P.W., FELDMANN M., FOXWELL B.M.J.;			
RL	EUR. J. IMMUNOL. 21:1649-1656(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
OC	TISSUE-SPLEEN;			

RX	MEDLINE; 92039815.	
RX	ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;	
RL	IMMUNOGENETICS 34:338-340(1991).	
RN	[5]	
RN	SEQUENCE FROM N.A.	
RP	MEDLINE; 94245292.	
RX	BREO B.F., LINTHICUM D.S.;	
RL	IMMUNOGENETICS 39:450-451(1994).	
RN	[6]	
RP	SEQUENCE FROM N.A.	
RA	MEDLINE; 93156721.	
RX	ROTHE J., BUEHLMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;	
RL	MOL. IMMUNOL. 30:165-175(1993).	
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).	
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.	
DR	EMBL; M60466; G199826; -.	
DR	EMBL; M59377; G202097; -.	
DR	EMBL; X59238; G33579; -.	
DR	EMBL; X57796; G54849; -.	
DR	EMBL; L26349; G430733; -.	
DR	EMBL; M76656; G202102; -.	
DR	EMBL; M88067; G202102; JOINED.	
DR	EMBL; M76655; G202102; JOINED.	
DR	PIR; A38634; GQMST1.	
DR	PIR; S16677; S16677.	
DR	PIR; S19021; S19021.	
DR	HSSP; P19438; 11TR.	
DR	MGI:98781; TNFR1.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	
DR	PROSITE; PS00050; TNFR_NGFR_2; 3.	
DR	PROSITE; PS00117; DEATH_DOMAIN_1.	
KM	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.	
FT	SIGNAL	1 21
FT	CHAIN	22 454
FT	DOMAIN	22 212
FT	TRANSSEM	213 235
FT	DOMAIN	236 454
FT	DOMAIN	43 196
FT	REPEAT	43 82
FT	REPEAT	83 125
FT	REPEAT	126 166
FT	REPEAT	167 196
FT	DOMAIN	356 441
FT	DISULFID	44 58
FT	DISULFID	59 72
FT	DISULFID	62 81
FT	DISULFID	84 99
FT	DISULFID	102 117
FT	DISULFID	105 125
FT	DISULFID	127 143
FT	DISULFID	146 158
FT	DISULFID	149 166
FT	DISULFID	168 179
FT	DISULFID	182 191
FT	DISULFID	185 195
FT	CARBOHYD	54 55
FT	CARBOHYD	151 151
FT	CARBOHYD	202 202
FT	CONFLICT	394 394
FT	R -> G (IN REF. 6).	



RP	SEQUENCE, AND REVISIONS.
RA	KEUTMANN H.T., WILLIAMS R.M., BISHOP W.H., RYAN R.J.;
RL	FED. PROC. 37:1828-1828(1978).
RL	[8]
RP	SEQUENCE OF 25-116.
RX	MEDLINE; 76005558.
RA	-RATHNAM P., SAXENA B.B.;
RL	J. BIOL. CHEM. 250:6735-6746(1975).
RN	[9]
RP	SEQUENCE OF 28-116.
RX	MEDLINE; 74262937.
RA	SHOME B., PARLOW A.F.;
RL	J. CLIN. ENDOCRINOL. METAB. 39:199-202(1974).
RL	[10]
RP	SEQUENCE OF 25-116.
RX	MEDLINE; 75211304.
RA	MORGAN F.J., BIRKEN S., CANFIELD R.E.;
RL	J. BIOL. CHEM. 250:5247-5258(1975).
RN	[11]
RP	SEQUENCE OF 25-116.
RX	MEDLINE; 74011266.
RA	BELLISARIO R., CARLSEN R.B., BAHL O.P.;
RL	J. BIOL. CHEM. 248:6796-6809(1973).
RN	[12]
RP	PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX	MEDLINE; 81021713.
RA	FUJIKI Y., RATHNAM P., SAXENA B.B.;
RL	BIOCHIM. BIOPHYS. ACTA 624:428-435(1980).
RN	[13]
RP	PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX	MEDLINE; 81006887.
RA	MISE T., BAHL O.P.;
RL	J. BIOL. CHEM. 255:8516-8522(1980).
RN	[14]
RP	STRUCTURE OF CARBOHYDRATES.
RX	MEDLINE; 91122088.
RA	WEISSHAR G., HIYAMA J., REMWICK A.G.C., NIMTZ M.;
RL	EUR. J. BIOCHEM. 195:257-268(1991).
RN	[15]
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX	MEDLINE; 94261179.
RA	LAPTHORN A.J., HARRIS D.C., LITTLEJOHN A., LUSTBADER J.W.,
RL	CANFIELD R.E., MACHIN K.J., MORGAN F.J., ISAACS N.W.;
RN	NATURE 369:455-461(1994).
RN	[16]
RP	STRUCTURE BY NMR.
RX	MEDLINE; 97054614.
RA	DE BEER T., VAN ZUYLEN C.W.E.M., LEEFLANG B.R., HARD K., BOELENS R.
RL	KAPTEIN R., KAMERLING J.P., VLEGENTHART J.F.G.;
RN	EUR. J. BIOCHEM. 241:229-242(1996).
CC	- SUBUNIT: HETERO DIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC	CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROXIN,
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
DR	EMBL; J00152; G183319; JOINED.
DR	EMBL; J00150; G183319; JOINED.
DR	EMBL; J00151; G183319; JOINED.
DR	EMBL; S70585; G546845; JOINED.
DR	EMBL; S70583; G546845; JOINED.
DR	EMBL; S70584; G546845; JOINED.
DR	EMBL; V00518; G31869; JOINED.
DR	EMBL; V00485; G669156; JOINED.
DR	EMBL; V00486; G669156; JOINED.
DR	EMBL; V00487; G669156; JOINED.
DR	PIR; A01481; TRHUAP.
DR	PDB; 1HCR: 30-SEP-94.
DR	PDB; 1HRP: 01-NOV-94.
DR	MM: 118850; -.
DR	MM: 118850; -.
DR	PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR	PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW	HORMONE; GLYCOPROTEIN; SIGNAL; 3D-STRUCTURE.
FT	SIGNAL 1 24
CT	CHAIN 25 116 GLYCOPROTEIN HORMONES ALPHA CHAIN.

FT	DISULFID	31	55
FT	DISULFID	34	84
FT	DISULFID	52	106
FT	DISULFID	56	108
FT	DISULFID	83	111
FT	CARBOHYD	63	63
FT	CARBOHYD	76	76
FT	CARBOHYD	102	102
FT	CONFLICT	29	29
FT	CONFLICT	108	109
QY	SEQUENCE	116 AA;	13075 MW; 3BAI9E2P CRC32;

Q -> E (IN REF. 8).  
CS -> SC (IN REF. 5 AND 6).

Query Match		30.88;	Score 672;	DB 1;	Length 116;
Best Local Similarity		93.58;	Pred. No. 3.35e-149;		
Matches	87;	Conservative	1;	Mismatches	5;
				Indels	0;
				Gaps	0;

Dd	24	SAPVDQCPECTLOENFFSOGAPILQCMGCCFSRAYPTPLRSKTMVLQKNVTSSTC	83
OY	193	TAGAAQCCPECTLOENFFSOGAPILQCMGCCFSRAYPTPLRSKTMVLQKNVTSSTC	252
Dd	84	CVAKSYNRVTVMGGFKVENNTACHSCSTCYHKS	116
OY	253	CVAKSYNRVTVMGGFKVENNTACHSCSTCYHKS	285

RESULT	6	STANDARD:	PRT:	120 AA.
ID	GLHA_MACMU			
AC	P22762;			
DT	01-AUG-1991 (REL. 19, CREATED)			
DT	01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR CGA.			
OS	MACACA MULATTA (RHESUS MACAQUE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUHAEIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 91321740.			
RA	GOLOS T.G., DURING M., FISHER J.M.;			
RL	DNA CELL. BIOL. 10:367-380(1991).			
CC	-1 SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA			
CC	CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,			
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.			
CC	PIR; A39555; A39555.			
DR	HSSP; P01215; 1HCN.			
DR	PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.			
DR	PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.			
KW	HORMONE; GLYCOPROTEIN; SIGNAL.			
FT	SIGNAL	1	24	BY SIMILARITY.
FT	CHAIN	25	120	GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT	DISULEID	35	59	BY SIMILARITY.
FT	DISULEID	38	88	BY SIMILARITY.
FT	DISULEID	56	110	BY SIMILARITY.
FT	DISULEID	60	112	BY SIMILARITY.
FT	DISULEID	87	115	BY SIMILARITY.
FT	CARBOHYD	67	67	BY SIMILARITY.
FT	CARBOHYD	80	80	BY SIMILARITY.
FT	CARBOHYD	106	106	BY SIMILARITY.
FT	SEQUENCE	120 AA;	13785 MW;	85ELF9F4 CRC32;
Query Match		25.3%;	Score 552;	DB 1; Length 120;
Best Local	Similarity 83.5%;	Pred. No. 3,70e-116;		
Matches	71; Conservative	4; Mismatches	10; Indels	0; Gaps
Db	35 CPECKPKNKFKSGAPITQCMGCCFSRAYPPVRSKRTMLVQKNVTSSTCCVAKSLT 94			
QY	200 CPECTLOENFFSOPGAPILQCMGCCFSRAYPPVPLRSKRTMLVQKNVTSSTCCVAKSYN 259			
Db	95 RVMVMSVRENVHTEHCSTCYHK 119			
QY	260 RVTVMGKFKVENHTEHCSTCYHK 284			

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RESULT 7
ID GLHA_RABIT STANDARD: PRT: 96 AA.
AC P07474;
DT 01-APR-1988 (REL. 07, CREATED)
DT 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN.
GN CGA.
OS ORCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; LAGOMORPHA.
RN [1]
RP SEQUENCE.
RA GLENN S.D., NAHM H.S., WARD D.N.;
RL J. BIOL. CHEM. 249:143-156(1984).
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC PIR: A05096; A05096.
DR HSSP; P01233; 1HRP.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN.
FT DISULFID 11 35 BY SIMILARITY.
FT DISULFID 14 64 BY SIMILARITY.
FT DISULFID 32 86 BY SIMILARITY.
FT DISULFID 36 88 BY SIMILARITY.
FT DISULFID 63 91 BY SIMILARITY.
FT CARBOHYD 56 56
FT CARBOHYD 82 82
SQ SEQUENCE 96 AA; 10663 MW; CD56D255 CRC32;

Query Match 25.1%; Score 547; DB 1; Length 96;
Best Local Similarity 76.7%; Pred. No. 8.57e-115;
Matches 65; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Db 7 AMOGCEPEKLEENKFKSLGAPFYOCMCCFSRAVPTPARSKKTMVPRNITSEATCCVA 66
QY 196 AAPGCEPCTLDENPFSGAPFILOCMGCCFSRAVPTPLRSKKTMLVQKNVTSSTCCVA 255
DB 67 KAFITATVMGNKAKVNHTECHSCSTCYHKS 96
QY 256 KSYNRYVMGFKVENHTACHSCSTCYHKS 285

RESULT 8
ID GLHA_BOVIN STANDARD: PRT: 120 AA.
AC P01217;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 23-OCT-1986 (REL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN CGA.
OS BOS TAURUS (BOVINE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84041490.
RA GOODMAN R.G., MONCMAN C.L., ROTHMAN F.M., NILSON J.H.;
RL NUCLEIC ACIDS RES. 11:6873-6882(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84024633.
RA ERWIN C., CROYLE M.L., DONELSON J., MAURER R.;
RL BIOCHEMISTRY 22:4856-4860(1983).
RN [3]
RP SEQUENCE OF 8-133 FROM N.A.
RX MEDLINE; 83161058.
RA NILSON J.H., THOMASON A.R., CSERBAK M.T., MONCMAN C.L., WOYCHIK R.P.;
RL J. BIOL. CHEM. 258:4679-4682(1983).
RN [4]

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RP SEQUENCE OF 25-120.
RX MEDLINE; 7111428.
RA LIAO T.-H., PIERCE J.G.;
RL J. BIOL. CHEM. 246:850-865(1971).
RN [5]
RP PRELIMINARY PARTIAL SEQUENCE.
RX MEDLINE; 7111429.
RA PIERCE J.G., LIAO T.-H., CARLSEN R.B., REIMO T.;
RL J. BIOL. CHEM. 246:866-872(1971).
RN [6]
RP SEQUENCE OF 80-91 AND 100-120.
RX MEDLINE; 72012932.
RA MAGHUIR-ROGISTER G., HENNEN G.P.;
RL EUR. J. BIOCHEM. 21:489-497(1971).
RN [7]
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX MEDLINE; 74307752.
RA CORNELL J.S., PIERCE J.G.;
RL J. BIOL. CHEM. 249:4166-4174(1974).
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC EMBL; X00003; E274391; -.
DR EMBL; X00004; E274391; JOINED.
DR EMBL; X00050; G607; -.
DR PIR; A01483; TTRBOA.
DR PIR; A05132; A05132.
DR HSSP; P01215; 1HCN.
DR PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
DR PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
KW HORMONE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 120
FT DISULFID 35 59 GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 56 110 BY SIMILARITY.
FT DISULFID 60 112 BY SIMILARITY.
FT DISULFID 87 115 BY SIMILARITY.
FT CARBOHYD 80 80
FT CARBOHYD 106 106
FT CONFLICT 13 13 A -> T (IN REF. 2).
FT CONFLICT 37 37 E -> Q (IN REF. 4).
FT CONFLICT 52 52 P -> A (IN REF. 2).
FT CONFLICT 84 87 EATC -> AZCT (IN REF. 6).
SQ SEQUENCE 120 AA; 13616 MW; 99C153C5 CRC32;

Query Match 25.1%; Score 549; DB 1; Length 120;
Best Local Similarity 77.0%; Pred. No. 2.44e-115;
Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Db 34 GCEPEKLEENKFKSLGAPFYOCMCCFSRAVPTPARSKKTMVPRNITSEATCCVAF 93
QY 199 GCPECTLDENPFSGAPFILOCMGCCFSRAVPTPLRSKKTMLVQKNVTSSTCCVANST 258
DB 94 TKATVMGNVNHTECHSCSTCYHKS 120
QY 259 NRYVMGFKVENHTACHSCSTCYHKS 285

RESULT 9
ID GLHA_SHEEP STANDARD: PRT: 120 AA.
AC P01218;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.
GN CGA.
OS OVIS ARIES (SHEEP).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90098887.

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RA BELLO P.A., MOUNTFORD P.S., BRANDON M.R., ADAMS T.E.;  
RL NUCLEIC ACIDS RES. 17:10494-10494(1989).  
RN [2]  
RP SEQUENCE OF 25-120.  
RX MEDLINE: 7221144.  
RA LIU W.-K., NAHM H.S., SWEENEY C.M., LANKIN W.M., BAKER H.N.,  
RA WARD D.N.;  
RL J. BIOL. CHEM. 247:4351-4364(1972).  
RN [3]  
RP SEQUENCE OF 25-120.  
RX MEDLINE: 73190034.  
RA SAIRAM M.R., PAPKOFF H., LI C.H.;  
RL ARCH. BIOCHEM. BIOPHYS. 153:554-571(1972).  
RN [4]  
RP SEQUENCE OF 25-120.  
RX MEDLINE: 82113052.  
RA SAIRAM M.R.;  
RL BIOCHEM. J. 197:535-539(1981).  
RN [5]  
RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
RA CHUNG D., SAIRAM M.R., LI C.H.;  
RL ARCH. BIOCHEM. BIOPHYS. 159:678-682(1973).  
RN [6]  
RP STRUCTURE OF CARBOHYDRATES.  
RX MEDLINE: 91006170.  
RA WEISSHAAR G., HIYAMA J., REMICK A.G.C.;  
RL EUR. J. BIOCHEM. 192:741-751(1990).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
DR EMBL: X16977; G1366; -.  
DR PIR: A01483; TTRBA.  
DR PIR: A01484; UTSHA.  
DR PIR: S06935; S06935.  
DR PIR: S13200; S13200.  
DR HSSP: P01215; 1HCN.  
DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KM HORMONE; GLYCOPROTEIN; SIGNAL.  
FT FT CHAIN 1 24  
FT FT CHAIN 25 120  
FT FT DISULFID 35 59 GLYCOPROTEIN HORMONES ALPHA CHAIN.  
FT FT DISULFID 38 88 BY SIMILARITY.  
FT FT DISULFID 56 110 BY SIMILARITY.  
FT FT DISULFID 60 112 BY SIMILARITY.  
FT FT DISULFID 87 115 BY SIMILARITY.  
FT FT CARBOHYD 80 80  
FT FT CARBOHYD 106 106  
FT FT CONFLICT 27 27 D -> N (IN REF. 2).  
FT FT CONFLICT 29 29 E -> Q (IN REF. 2).  
FT FT CONFLICT 37 37 E -> Q (IN REF. 2 TO 4).  
FT FT CONFLICT 112 113 CS -> SC (IN REF. 3).  
SQ SEQUENCE 120 AA; 13588 MW; 13BADE1 CRC32;  
Query Match 25.1%; Score 549; DB 1; Length 120;  
Best Local Similarity 77.0%; Pred. No. 2.44e-15;  
Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
Db 34 GCPECKLENNKFSKLPAPYOCGCCFSRAYPTPARSKKTMVLPKNITSEATCCVAKAF 93  
QY 199 GCPECKLENNKFSKLPAPYOCGCCFSRAYPTPARSKKTMVLPKNITSEATCCVAKAF 93  
Db 94 TKATVGNARVENHTDCHSTCYTHKS 120  
QY 259 NRYTVMGFEVHTACHSTCYTHKS 285  
RESULT 10  
ID GLH1\_PAT STANDARD; PRT; 120 AA.  
AC P11962; P70516;  
DT 01-OCT-1989 (REL. 12, CREATED)  
DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE GLYCOPROTEIN HORMONES ALPHA CHAIN 1 PRECURSOR.  
OS RATIUS NORVEGICUS (RAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=PIUTITARY;  
RX MEDLINE: 82214055.  
RA GODINE J.E., CHIN W.W., HABENER J.F.;  
RL J. BIOL. CHEM. 257:8368-8371(1982).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 89196918.  
RA BURNSIDE J., BUCKLAND P.R., CHIN W.W.;  
RL GENE 70:67-74(1988).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WISTAR-IMAMICHI; TISSUE=ANTERIOR PITUITARY;  
RA KATO Y., EZASHI T., HIRAI T., KATO T.;  
RL ZOOL. SCI. 7:877-885(1990).  
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
DR EMBL: V01252; G56580; -.  
DR EMBL: J00757; G206111; -.  
DR EMBL: M25543; G204470; -.  
DR EMBL: M25544; G204471; -.  
DR EMBL: D00575; G220842; -.  
DR PIR: J04048; TTRTA.  
DR PIR: S27385; S27385.  
DR HSSP: P01233; 1HRP.  
DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
KM HORMONE; GLYCOPROTEIN; SIGNAL.  
FT FT CHAIN 1 24  
FT FT CHAIN 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN 1.  
FT FT DISULFID 35 59 BY SIMILARITY.  
FT FT DISULFID 38 88 BY SIMILARITY.  
FT FT DISULFID 56 110 BY SIMILARITY.  
FT FT DISULFID 60 112 BY SIMILARITY.  
FT FT DISULFID 87 115 BY SIMILARITY.  
FT FT CARBOHYD 80 80  
FT FT CARBOHYD 106 106 PROBABLE.  
FT FT CONFLICT 84 84 E -> Q (IN G206111).  
SQ SEQUENCE 120 AA; 13453 MW; 5E507A0D CRC32;  
Query Match 24.9%; Score 544; DB 1; Length 120;  
Best Local Similarity 78.2%; Pred. No. 5.64e-114;  
Matches 68; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
Db 34 GCPECKLENNKFSKLPAPYOCGCCFSRAYPTPARSKKTMVLPKNITSEATCCVAKAF 93  
QY 199 GCPECKLENNKFSKLPAPYOCGCCFSRAYPTPARSKKTMVLPKNITSEATCCVAKAF 93  
Db 94 TKATVGNARVENHTDCHSTCYTHKS 120  
QY 259 NRYTVMGFEVHTACHSTCYTHKS 285  
RESULT 11  
ID GLH1\_BALAC STANDARD; PRT; 96 AA.  
AC P37036;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE GLYCOPROTEIN HORMONES ALPHA CHAIN.  
GN CGA.  
OS BALAEONPTERA ACUTROSTRATA (MINKE WHALE) (LESSER RORQUAL).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; CETACEA.  
RN [1]  
RP SEQUENCE.

RA KARASEV V.S., PANKOV Y.A.;  
 RL BIOCHIMIA 50:1972-1986(1985).  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERNS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 DR PIR: P0138; P0138.  
 DR HSSP: P01215; 1HCN.  
 DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 KW HORMONE; GLYCOPROTEIN.  
 FT DISULFID 11 35 BY SIMILARITY.  
 FT DISULFID 14 64 BY SIMILARITY.  
 FT DISULFID 32 86 BY SIMILARITY.  
 FT DISULFID 36 88 BY SIMILARITY.  
 FT DISULFID 63 91 BY SIMILARITY.  
 FT CARBOHYD 56 56  
 FT CARBOHYD 82 82  
 SQ SEQUENCE 96 AA; 10720 MW; E2CD30DF CRC32;

Query Match 24.8%; Score 542; DB 1; Length 96;  
 Best Local Similarity 70.1%; Pred. No. 1,98e-113;  
 Matches 61; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

Db 10 GCPZCLAKZBKFSKLGAPILYZCMGCCFSRAYPTPARSKTMLVPRNITSZATCCYAKAF 69  
 QY 199 GCEPCLQENPFPSOGAPILQCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCYAKSY 258  
 Db 70 TRATVGNARVZHNTHCHSTCYHKS 96  
 QY 259 NRYTVMGKFEVNHHTACHSTCYHKS 285

RESULT 12  
 ID GLH2\_RAT STANDARD; PRT; 120 AA.  
 AC P1163;  
 DT 01-OCT-1989 (REL. 12, CREATED)  
 DT 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
 DE GLYCOPROTEIN HORMONES ALPHA CHAIN 2 PRECURSOR.  
 OS RATUUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE; 82214055.  
 RA GODINE J.E., CHIN W.W., HABENER J.F.;  
 RL J. BIOL. CHEM. 257:8368-8371(1982).  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERNS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 DR EMBL; V01253; G55583; -.  
 DR PIR; S27386; S27386.  
 DR HSSP; P01215; 1HCN.  
 DR PROSITE; PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE; PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 KW HORMONE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN 2.  
 FT DISULFID 35 59 BY SIMILARITY.  
 FT DISULFID 38 88 BY SIMILARITY.  
 FT DISULFID 56 110 BY SIMILARITY.  
 FT DISULFID 60 112 BY SIMILARITY.  
 FT DISULFID 87 115 BY SIMILARITY.  
 FT CARBOHYD 80 80 PROBABLE.  
 FT CARBOHYD 106 106  
 SQ SEQUENCE 120 AA; 13565 MW; 4EAFAB2E CRC32;

Query Match 24.8%; Score 542; DB 1; Length 120;  
 Best Local Similarity 77.0%; Pred. No. 1,98e-113;  
 Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;  
 Db 34 GCEPCLQENPFPSOGAPILQCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCYAKAF 93  
 QY 199 GCEPCLQENPFPSOGAPILQCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCYAKSY 258

QY 199 GCEPCLQENPFPSOGAPILQCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCYAKSY 258  
 Db 94 TRATVGNARVZHNTHCHSTCYHKS 120  
 QY 259 NRYTVMGKFEVNHHTACHSTCYHKS 285

RESULT 13  
 ID GLH2\_MOUSE STANDARD; PRT; 120 AA.  
 AC P01216;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.  
 GN CGA.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE; 82060239.  
 RA CHIN W.W., KRONENBERG H.M., DEE P.C., MALOOF F., HABENER J.F.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:5329-5333(1981).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE; 89170115.  
 RA GORDON D.F., WOOD W.M., RIDGWAY E.C.;  
 RL DNA 7:679-690(1988).  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERNS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 DR EMBL; J00643; G202180; -.  
 DR EMBL; V00852; G54799; -.  
 DR EMBL; M22991; -; NOT ANNOTATED\_CDS.  
 DR EMBL; M22992; G575520; -.  
 DR PIR; A01482; TTNSA.  
 DR PIR; A31598; A31598.  
 DR HSSP; P01215; 1HCN.  
 DR MGI; M6188390; CGA.  
 DR PROSITE; PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE; PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 KW HORMONE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN.  
 FT DISULFID 35 59 BY SIMILARITY.  
 FT DISULFID 38 88 BY SIMILARITY.  
 FT DISULFID 56 110 BY SIMILARITY.  
 FT DISULFID 60 112 BY SIMILARITY.  
 FT DISULFID 87 115 BY SIMILARITY.  
 FT CARBOHYD 80 80 PROBABLE.  
 FT CARBOHYD 106 106  
 SQ SEQUENCE 120 AA; 13565 MW; 86F1F31A CRC32;

Query Match 24.8%; Score 542; DB 1; Length 120;  
 Best Local Similarity 77.0%; Pred. No. 1,98e-113;  
 Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Db 34 GCEPCLQENPFPSOGAPILQCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCYAKAF 93  
 QY 199 GCEPCLQENPFPSOGAPILQCMGCCFSRAYPTPLRSKTKMLVQKNVTSSTCCYAKSY 258  
 Db 94 TRATVGNARVZHNTHCHSTCYHKS 120  
 QY 259 NRYTVMGKFEVNHHTACHSTCYHKS 285

RESULT 14  
 ID GLH2\_PIG STANDARD; PRT; 120 AA.  
 AC P01219;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR.

GN CGA.  
 OS SUS SCROFA (PIG).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; ARTIODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89325834.  
 RA HIRAI T., TAKIKAWA H., KATO Y.;  
 RL MOL. CELL. ENDOCRINOL. 63:209-217(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA KATO Y., EZASHI T., HIRAI T., KATO T.;  
 RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.  
 RN [3]  
 RP SEQUENCE OF 31-120.  
 RX MEDLINE; 74075725.  
 RA MAGHUIIN-ROGISTER G., COMBARNOUS Y., HENNEN G.;  
 RL EUR. J. BIOCHEM. 39:255-263(1973).  
 RN [4]  
 RP PRELIMINARY SEQUENCE OF 25-120.  
 RA CLOSSET J., MAGHUIIN-ROGISTER G., HENNEN G.;  
 RL ENDOCRINOL. EXP. 8:164(1974).  
 RN [5]  
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.  
 RX MEDLINE; 75093922.  
 RA COMBARNOUS Y., HENNEN G.;  
 RL BIOCHEM. SOC. TRANS. 2:915-917(1974).  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 DR EMBL; D00767; G217699; JOINED.  
 DR PIR; A01485; UPPGA.  
 DR PIR; A30339; A30339.  
 DR HSSP; P01215; 1HCN.  
 DR PROSITE; PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE; PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 KM HORMONE; GLYCOPROTEIN; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 120 GLYCOPROTEIN HORMONES ALPHA CHAIN.  
 FT DISULFID 35 59 BY SIMILARITY.  
 FT DISULFID 38 88 BY SIMILARITY.  
 FT DISULFID 56 110 BY SIMILARITY.  
 FT DISULFID 60 112 BY SIMILARITY.  
 FT DISULFID 87 115 BY SIMILARITY.  
 FT CARBOHYD 80 80  
 FT CARBOHYD 106 106  
 SQ SEQUENCE 120 AA; 13532 MW; 8749DBA5 CRC32;

Query Match 24.8%; Score 542; DB 1; Length 120;  
 Best Local Similarity 77.0%; Pred. No. 1.98e-113;  
 Matches 67; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Db 34 GCPECKLGENRFFSKGAPYQCGCCFSRAYPTLRKSKTMYLPKNITSEATCCVAKAF 93  
 QY 199 GCPECTIQENPFPSQPGAPILQCMGCCFSRAYPTLRKSKTMYLQKNVTSSTCCVAKSY 258  
 Db 94 TKATVMGNARVENHTCHCSTCYHKS 120  
 QY 259 NRYVTVMGKFVENHTACHCSTCYHKS 285

RESULT 15  
 ID GLHA\_STRCA STANDARD; PRT; 96 AA.  
 AC P80665;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
 DE GLYCOPROTEIN HORMONES ALPHA CHAIN.  
 OS STRUTHIO CAMELUS (OSTRICH).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES;  
 OC PALAEOGNATHAE; STRUTHIONIFORMES.  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE; 97025333.  
 RA KOIDE Y., PAPKOFF H., KAWAUCHI H.;  
 RL EUR. J. BIOCHEM. 240:262-267(1996).  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 DR PROSITE; PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE; PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 KM HORMONE; GLYCOPROTEIN.  
 FT DISULFID 11 35 BY SIMILARITY.  
 FT DISULFID 14 64 BY SIMILARITY.  
 FT DISULFID 32 86 BY SIMILARITY.  
 FT DISULFID 36 88 BY SIMILARITY.  
 FT DISULFID 63 91 BY SIMILARITY.  
 FT CARBOHYD 56 56  
 FT CARBOHYD 82 82 POTENTIAL.  
 SQ SEQUENCE 96 AA; 10781 MW; DDF7B4BB CRC32;

Query Match 24.7%; Score 539; DB 1; Length 96;  
 Best Local Similarity 74.7%; Pred. No. 1.30e-112;  
 Matches 65; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Db 10 GCPECKLGENRFFSKGAPYQCGCCFSRAYPTLRKSKTMYLPKNITSEATCCVAKAF 69  
 QY 199 GCPECTIQENPFPSQPGAPILQCMGCCFSRAYPTLRKSKTMYLQKNVTSSTCCVAKSY 258  
 Db 70 TKITLKDNRKVENHTCHCSTCYHKS 96  
 QY 259 NRYVTVMGKFVENHTACHCSTCYHKS 285

Search completed: Wed May 6 08:58:56 1998  
 Job time : 42 secs.

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DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).  
 GN TNFR-1.  
 OS FELIS SILVESTRIS CATUS (CAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; CARNIVORA.  
 RN  
 RP SEQUENCE FROM N.A.  
 RA DUTHIE S., NASIR L., ECKERSALL P.D.;  
 RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: U7344; G1613880; -.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 FT NON\_TER 1 1  
 FT SEQUENCE 180 AA; 20399 MW; 54524682 CRC32;  
 SQ  
 Query Match 43.2%; Score 943; DB 4; Length 180;  
 Best Local Similarity 85.3%; Pred. No. 1.42e-214;  
 Matches 116; Conservative 10; Mismatches 10; Indels 0; Gaps 0;  
 Db 45 CPQKRYHPQDNNISICCKCHKGYLYNDACGPGLDTCRECENGTFTASENYLRQCLSCS 104  
 QY 26 CPQKRYHPQDNNISICCKCHKGYLYNDACGPGQDTCRECESGSFTASENHLRCLSCS 85  
 Db 105 KCRKEMQVEISPCITYRDYTCGCRKNQYRYWSETHFQCLNGTNGVQISCKETON 164  
 QY 86 KCRKEMQVEISPCITYRDYTCGCRKNQYRYWSENLFOCCNCTLCINGTVHLSQEKON 145  
 Db 165 TVCTCHAGFFLRGNEC 180  
 QY 146 TVCTCHAGFFLRGNEC 161  
 RESULT 3 PRELIMINARY; PRT; 107 AA.  
 ID Q90286  
 AC 090286;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
 DE GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).  
 OS CARASSIUS AURATUS (GOLDFISH).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;  
 OC OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.  
 RN  
 RP SEQUENCE FROM N.A.  
 RA KOBAYASHI M., KATO Y., YOSHITURA Y., AIDA K.;  
 RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: D86551; G1469836; -.  
 FT NON\_TER 1 1  
 FT SEQUENCE 107 AA; 11959 MW; 8806840 CRC32;  
 SQ  
 Query Match 20.8%; Score 453; DB 12; Length 107;  
 Best Local Similarity 72.0%; Pred. No. 3.04e-85;  
 Matches 59; Conservative 7; Mismatches 15; Indels 1; Gaps 1;  
 Db 27 GCECKLKENNIFSKPGAPVYQCGCCFSRAYPTPLSKTKMTLVPKNTSEATCCVAKY 86  
 QY 199 GCEPCTIQENPFESQPGAPILQCGCCFSRAYPTPLSKTKMTLVQKNVTSSTCCVAKSY 258  
 Db 87 KRVLY-NDVRLVNHRTDCHGCTC 107  
 QY 259 NRYVTMGGFVKNHTACHGCTC 280  
 RESULT 4 PRELIMINARY; PRT; 108 AA.  
 ID Q90287  
 AC 090287;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)

DE GONADOTROPIN ALPHA SUBUNIT (FRAGMENT).  
 OS CARASSIUS AURATUS (GOLDFISH).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;  
 OC OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.  
 RN  
 RP SEQUENCE FROM N.A.  
 RA KOBAYASHI M., KATO Y., YOSHITURA Y., AIDA K.;  
 RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: D86552; G1469838; -.  
 FT NON\_TER 1 1  
 FT SEQUENCE 108 AA; 12129 MW; 82812212 CRC32;  
 SQ  
 Query Match 20.8%; Score 454; DB 12; Length 108;  
 Best Local Similarity 72.0%; Pred. No. 1.68e-85;  
 Matches 59; Conservative 7; Mismatches 15; Indels 1; Gaps 1;  
 Db 28 GCECKLKENNIFSKPGAPVYQCGCCFSRAYPTPLSKTKMTLVPKNTSEATCCVAKY 87  
 QY 199 GCEPCTIQENPFESQPGAPILQCGCCFSRAYPTPLSKTKMTLVQKNVTSSTCCVAKSY 258  
 Db 88 KRVLY-NDVRLVNHRTDCHGCTC 108  
 QY 259 NRYVTMGGFVKNHTACHGCTC 280  
 RESULT 5 PRELIMINARY; PRT; 119 AA.  
 ID Q91370  
 AC 091370;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE GONADOTROPIN ALPHA 1 SUBUNIT.  
 OS ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;  
 OC OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94197892.  
 RA GEN K., MARIYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.;  
 RL J. MOL. ENDOCRINOLOGY. 11:265-273(1993).  
 DR EMBL: S69273; G546258; -.  
 DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 SQ SEQUENCE 119 AA; 13131 MW; 2EE28F4 CRC32;  
 Query Match 20.7%; Score 452; DB 12; Length 119;  
 Best Local Similarity 67.8%; Pred. No. 5.48e-85;  
 Matches 59; Conservative 11; Mismatches 16; Indels 1; Gaps 1;  
 Db 34 GCECKLKENNIFSKPGAPVYQCGCCFSRAYPTPLSKTKMTLVPKNTSEATCCVAKY 93  
 QY 199 GCEPCTIQENPFESQPGAPILQCGCCFSRAYPTPLSKTKMTLVQKNVTSSTCCVAKSY 258  
 Db 94 ERY-VVDIKLTNHTBCWCNTCYHKS 119  
 QY 259 NRYVTMGGFVKNHTACHGCTCYHKS 285  
 RESULT 6 PRELIMINARY; PRT; 114 AA.  
 ID Q91371  
 AC 091371;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
 DE GONADOTROPIN ALPHA 2 SUBUNIT.  
 OS ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;  
 OC OSTEICHTHYES; ACTINOPTERYGII; SALMONIFORMES.  
 RN  
 RP SEQUENCE FROM N.A.

RA MEDLINE: 94197892.  
 RA GEN K., MARUYAMA O., KATO T., TOMIZAWA K., WAKABAYASHI K., KATO Y.,  
 J. MOL. ENDOCRINOLOGY. 11:265-273(1993).  
 DR EMBL: S69274; G546260; -;  
 DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 SQ SEQUENCE 114 AA; 12519 MW; 473D3C83 CRC32;

Query Match  
 Best Local Similarity 58.3%; Score 448; DB 12; Length 114;  
 Matches 67; Conservative 11; Mismatches 33; Indels 4; Gaps 2;

Db 4 LKSTGLSLIALVYADSPYNSDKTNGCECTKLPNTIF--PN--IIQCTCCFSRAY 59  
 QY 171 LECTKSLDPIEVKCTEDSGTAGAPGCEPTLOENPFSGPAPILQCMCCFSRAY 230  
 Db 60 PTPLRKSKTMLVPKNTSEATCCVAKGEGERYTKDGFVYTNHTECHSCFYHKS 114  
 QY 231 PTPLRKSKTMLVOKNTSESTCCVAKSYNRYVMGSGFKVENHTACHSCFYHKS 285

RESULT 7  
 ID Q91119 PRELIMINARY; PRT; 117 AA.

AC Q91119;  
 DT 01-NOV-1996 (TREMBLERL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLERL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLERL. 05, LAST ANNOTATION UPDATE)  
 DE GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR (GONADOTROPIN ALPHA CHAIN) (GH-ALPHA).  
 OS MORONE SAKATILIS (STRIPED BASS).  
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;  
 OC OSTEICHTHYES; ACTINOPTERYGII; PERCIFORMES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PITUITARY GLAND;  
 RX MEDLINE: 96020549.  
 RA HASSIN S., ELIZUR A., ZOHAR Y.;  
 RL J. MOL. ENDOCRINOLOGY. 15:23-35(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PITUITARY GLAND;  
 RA HASSIN S.;  
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- FUNCTION: INVOLVED IN GAMETOGENESIS AND STEROIDOGENESIS (BY SIMILARITY).

CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).

DR EMBL: L35071; G2322657; -;  
 DR PROSITE: PS00779; GLYCO\_HORMONE\_ALPHA\_1; 1.  
 DR PROSITE: PS00780; GLYCO\_HORMONE\_ALPHA\_2; 1.  
 KW HORMONE; GLYCOPROTEIN; SIGNAL.

FT SIGNAL 1 23  
 FT CHAIN 24 117  
 FT DISULFID 34 57  
 FT DISULFID 37 86  
 FT DISULFID 54 107  
 FT DISULFID 58 109  
 FT DISULFID 85 112  
 FT CARBOHYD 78 78  
 FT CARBOHYD 103 103  
 SQ SEQUENCE 117 AA; 13066 MW; CARB9DOC CRC32;

Query Match  
 Best Local Similarity 65.5%; Score 433; DB 12; Length 117;  
 Matches 57; Conservative 14; Mismatches 12; Indels 4; Gaps 4;

Db 33 GGECELRKNSVFSR-DRVYQCMGCCFSRAYPTPLKAKAKTMTIPKNTSEATCCYAKS 91  
 QY 199 GGECELRKNSVFSR-DRVYQCMGCCFSRAYPTPLKAKAKTMTIPKNTSEATCCYAKS 257  
 Db 92 YE-TEV-AGIKVNNHTDCHSCFYHKS 116  
 QY 258 YNRVYMGSGFKVENHTACHSCFYHKS 284

RESULT 8  
 ID Q62589 PRELIMINARY; PRT; 55 AA.

AC Q62589;  
 DT 01-NOV-1996 (TREMBLERL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLERL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLERL. 05, LAST ANNOTATION UPDATE)  
 DE ALPHA SUBUNIT OF GLYCOPROTEIN HORMONES (FRAGMENT).  
 OS PHOOPUS SUNGORUS (STRIPED HAIRY-FOOTED HAMSTER) (DJUNGARIAN HAMSTER).  
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PITUITARY;  
 RX MEDLINE: 96198779.  
 RA BOCKMANN J., BOCKERS T.M., VENNEMANN B., NIKLOWITZ P., MULLER J.,  
 RA WITKOWSKI W., SABEL B., KREUTZ M.R.;  
 RL ENDOCRINOLOGY 137:1804-1813(1996).  
 DR EMBL: X90776; E195634; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 55 AA; 6047 MW; E5A80F8 CRC32;

Query Match  
 Best Local Similarity 76.4%; Score 334; DB 10; Length 55;  
 Matches 42; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 1 PTPLRKSKTMLVPKNTSEATCCVAKGEGERYTKDGFVYTNHTECHSCFYHKS 55  
 QY 231 PTPLRKSKTMLVOKNTSESTCCVAKSYNRYVMGSGFKVENHTACHSCFYHKS 285

RESULT 9  
 ID 014866 PRELIMINARY; PRT; 277 AA.

AC 014866;  
 DT 01-JAN-1998 (TREMBLERL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBLERL. 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLERL. 05, LAST ANNOTATION UPDATE)  
 DE SOLUBLE DEATH RECEPTOR 3 BETA.  
 GN DR3.

OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA WAROCHA K., RIBETRO P., RENARD N., CHARLOT C., COIFFIER B.,  
 RA SALES G.;  
 RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF026071; G2570833; -;  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 SQ SEQUENCE 277 AA; 29111 MW; 06E165C7 CRC32;

Query Match  
 Best Local Similarity 11.4%; Score 249; DB 2; Length 277;  
 Matches 57; Conservative 31; Mismatches 76; Indels 15; Gaps 11;

Db 13 AALLLV-LLG-ARAGGRSPRCAGDF-HKIGLPCRCRCPAGHYAKATEPCGNS 68  
 QY 3 TSLLAFLGLCLPWLQEGSADSVCP-QGKYIHPNNSICTCTCHGTLYLNDCCPGGODT 61  
 Db 69 TGLVCPDPTFLAMENHNSEACACQACDQASOVALENCASAVADPRCGCKPGMEVDCQVS 128  
 QY 62 DRECESSGFTASSENHLR-HCLSCSKCRKEMGOVELSCTVDYRDYCGCKRKNQRIYV-S 119  
 Db 129 QCVSSPFYQPCDLCGALHRTFLIC-SRDPDGTCLPGFYERHGDGCVSCPPTPSSL 186  
 QY 120 ENLFOC-FNCTICLN-GTVH---LSCQEKQNTVC-TCHAGFLLENCEVSCSNCKSL 171

RESULT 10  
 ID 014865 PRELIMINARY; PRT; 426 AA.

AC 014865;  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE DEATH RECEPTOR 3 BETA.  
DN DR3.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA VARZIOHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,  
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: AF026070; G2570831; -  
DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
SQ SEQUENCE 426 AA; 45950 MW; 87E00821 CRC32;

Query Match 11.4%; Score 249; DB 2; Length 426;  
Best Local Similarity 31.8%; Pred. No. 1.12e-34;  
Matches 57; Conservative 31; Mismatches 76; Indels 15; Gaps 11;

Db 13 ALLLV--LLG-ARAOGGTRSPRCDCAGDF-HKKIGLFCRCGCPAGHYLAKPCTEPCGNS 68  
QY 3 TSLLAAGLCLPWLQSGSADSVCP-OGKYIHPONNISICTCKHKGYLYLNDGPGQDT 61  
DB 69 TCLVCPDPTFLAMENHNHNSCARQACDEQASOYALENCASVADTRGCGKPGWFEQCVS 128  
QY 62 DCRCEGSGFTASFNHNR-HCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQRYHW-S 119  
Db 129 QCVSSPFYQPCDLCGALHRTLLC-SRRDTCGCTLPGFYHGGCVSCP 186  
QY 120 ENLFQC-FNCTLCIN-GTVH----LSCQEKQNTVC-TCHAGFFLENECVSCSKKSL 171

RESULT 11  
ID 000276 PRELIMINARY; PRT; 253 AA.

AC 000276;  
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)  
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE LIMPLOCYTE ASSOCIATED RECEPTOR OF DEATH 2.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA SREATION G., XU X.N., OLSEN A., COMPER A., TAN R., MCMICHAEL A.,  
RA BELL J.;  
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U94503; G2071953; -  
DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
SQ SEQUENCE 253 AA; 26934 MW; A21C863E CRC32;

Query Match 11.3%; Score 247; DB 2; Length 253;  
Best Local Similarity 31.8%; Pred. No. 3.31e-34;  
Matches 55; Conservative 31; Mismatches 72; Indels 15; Gaps 11;

Db 13 ALLLV--LLG-ARAOGGTRSPRCDCAGDF-HKKIGLFCRCGCPAGHYLAKPCTEPCGNS 68  
QY 3 TSLLAAGLCLPWLQSGSADSVCP-OGKYIHPONNISICTCKHKGYLYLNDGPGQDT 61  
DB 69 TCLVCPDPTFLAMENHNHNSCARQACDEQASOYALENCASVADTRGCGKPGWFEQCVS 128  
QY 62 DCRCEGSGFTASFNHNR-HCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQRYHW-S 119  
Db 129 QCVSSPFYQPCDLCGALHRTLLC-SRRDTCGCTLPGFYHGGCVSCP 180  
QY 120 ENLFQC-FNCTLCIN-GTVH----LSCQEKQNTVC-TCHAGFFLENECVSCS 165

RESULT 12  
ID 000280 PRELIMINARY; PRT; 380 AA.

AC 000280;  
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)  
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE LIMPLOCYTE ASSOCIATED RECEPTOR OF DEATH 9.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA SREATION G., XU X.N., OLSEN A., COMPER A., TAN R., MCMICHAEL A.,  
RA BELL J.;  
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U94510; G2071967; -  
DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
SQ SEQUENCE 380 AA; 41192 MW; 17992A14 CRC32;

Query Match 11.3%; Score 247; DB 2; Length 380;  
Best Local Similarity 31.8%; Pred. No. 3.31e-34;  
Matches 55; Conservative 31; Mismatches 72; Indels 15; Gaps 11;

Db 13 ALLLV--LLG-ARAOGGTRSPRCDCAGDF-HKKIGLFCRCGCPAGHYLAKPCTEPCGNS 68  
QY 3 TSLLAAGLCLPWLQSGSADSVCP-OGKYIHPONNISICTCKHKGYLYLNDGPGQDT 61  
DB 69 TCLVCPDPTFLAMENHNHNSCARQACDEQASOYALENCASVADTRGCGKPGWFEQCVS 128  
QY 62 DCRCEGSGFTASFNHNR-HCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQRYHW-S 119  
Db 129 QCVSSPFYQPCDLCGALHRTLLC-SRRDTCGCTLPGFYHGGCVSCP 180  
QY 120 ENLFQC-FNCTLCIN-GTVH----LSCQEKQNTVC-TCHAGFFLENECVSCS 165

RESULT 13  
ID 000275 PRELIMINARY; PRT; 418 AA.

AC 000275;  
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)  
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE LIMPLOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA SREATION G., XU X.N., OLSEN A., COMPER A., TAN R., MCMICHAEL A.,  
RA BELL J.;  
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL: U94502; G2071951; -  
DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
SQ SEQUENCE 418 AA; 45456 MW; 3D04954A CRC32;

Query Match 11.3%; Score 247; DB 2; Length 418;  
Best Local Similarity 31.8%; Pred. No. 3.31e-34;  
Matches 55; Conservative 31; Mismatches 72; Indels 15; Gaps 11;

Db 13 ALLLV--LLG-ARAOGGTRSPRCDCAGDF-HKKIGLFCRCGCPAGHYLAKPCTEPCGNS 68  
QY 3 TSLLAAGLCLPWLQSGSADSVCP-OGKYIHPONNISICTCKHKGYLYLNDGPGQDT 61  
DB 69 TCLVCPDPTFLAMENHNHNSCARQACDEQASOYALENCASVADTRGCGKPGWFEQCVS 128  
QY 62 DCRCEGSGFTASFNHNR-HCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQRYHW-S 119  
Db 129 QCVSSPFYQPCDLCGALHRTLLC-SRRDTCGCTLPGFYHGGCVSCP 180  
QY 120 ENLFQC-FNCTLCIN-GTVH----LSCQEKQNTVC-TCHAGFFLENECVSCS 165



RESULT	ID	PRELIMINARY;	PRT;	348 AA.
	Q85407			
AC	Q85407;			
DT	01-NOV-1996 (TREMREL. 01, CREATED)			
DT	01-NOV-1996 (TREMREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMREL. 05, LAST ANNOTATION UPDATE)			
DE	HOMOLOG OF VACCINIA VIRUS COS B28R.			
GN	G2R.			
OS	VARIOLA VIRUS.			
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPXVIRINAE;			
OC	ORTHOPOXVIRUSES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BANGLADESH-1975;			
RX	MEDLINE; 94088747.			
RA	MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,			
RA	KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;			
RL	NATURE 366:748-751(1993).			
DR	EMBL: L22579; G439102; -.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.			
SO	SEQUENCE 348 AA; 35075 MW; 2A911AF6 CRC32;			

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Db 513 AGCTGCTCCAAATGCCGAAAGAAATGGGTCAAGGTGAGATCTCTTTGACACAGTGAC 572  
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Qy 525 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTTTGACACAGTGAC 584  
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Db 573 CGGGACACCGGTGTGGCGGAGAGAAACAGTACCGGCATTTATTTGGATGAAAACTT 632  
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Qy 585 CGGGACACCGGTGTGGCGGAGAGAAACAGTACCGGCATTTATTTGGATGAAAACTT 644  
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Qy 765 TCCTGTAGTAATGTGAAGAAAAAGCTGGAGTGCAGAGATTTGGCTTACCCAGATTGAG 824  
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Db 813 AATGTTAAGGCATGAGACTCAGCACCACAG 846  
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Qy 825 AATGTTAAGGCATGAGACTCAGCACCACAG 858  
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RESULT 2  
LOCUS A29098 1368 bp DNA PAT 03-JUL-1995

DEFINITION Synthetic DNA for TNF-receptor from patent EP0393438.

ACCESSION A29098  
NID g1248892

KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1368)

AUTHORS Hauptmann,R., Himmeler,A., Maurer-Fogy,I. and Stratowa,C.

TITLE TNF-receptor, TNF-binding protein and DNA coding therefor

JOURNAL Patent: EP 0393438-A 48 24-OCT-1990;  
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

FEATURES  
Location/Qualifiers

source 1..1368  
/organism="unidentified"  
/db\_xref="taxon:32644"

source 1..1368  
/organism="artificial sequence"  
/db\_xref="taxon:29278"

BASE COUNT 293 a 424 c 375 g 276 t

ORIGIN

Query Match 39.5%; Score 514; DB 25; Length 1368;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATTAATTCATTTGCTGTACC 180  
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Qy 345 GATAGTGTGTGTCGCCAAGAAATATATATCCACCTCAAAATTAATTCATTTGCTGTACC 404  
| | | | |  
Db 181 AAGTCCCAAGAAACCTACTTGTATGATGATGCTGCCAGCGCGGGGAGATACGGAC 240  
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Qy 405 AAGTCCCAAGAAACCTACTTGTATGATGATGCTGCCAGCGCGGGGAGATACGGAC 464  
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Db 241 TGCAGGAGTGTGAGAGCGGCTCTTACCGGTTGAGAAACACACTCAGACACTGCTC 300  
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Qy 465 TGCAGGAGTGTGAGAGCGGCTCTTACCGGTTGAGAAACACACTCAGACACTGCTC 524  
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Db 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGTGCTTCTTTCACAGTGAGAC 360  
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Qy 525 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGTGCTTCTTTCACAGTGAGAC 584  
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Db 361 CGGGACACCGGTGTGGCTGCGAGGAAACGATCGGCAATTTATTTGATGAAAACTT 420  
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Qy 585 CGGGACACCGGTGTGGCTGCGAGGAAACGATACCGGCATTTATTTGAGTGAACCTT 644  
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Db 421 TTCCAGTGTTCATATTTGACAGCTTGCCTCAATGGGACCGTGCACCTCTCTGCCAGAG 480  
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Qy 645 TTCCAGTGTTCATATTTGACAGCTTGCCTCAATGGGACCGTGCACCTCTCTGCCAGAG 704  
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Db 481 AAACGAAACACCGGTGTGCACCTGCATGCAAGGTTCTTTCTAAGAAAAAGAGTGTGC 540  
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Qy 705 AAACGAAACACCGGTGTGCACCTGCATGCAAGGTTCTTTCTAAGAAAAAGAGTGTGC 764  
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Db 541 TCCTGTAGTAATGTGAAGAAAAAGCTGGAGTGCAGAGATTTGGCTTACCCAGATTGAG 600  
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Qy 765 TCCTGTAGTAATGTGAAGAAAAAGCTGGAGTGCAGAGATTTGGCTTACCCAGATTGAG 824  
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Db 601 AATGTTAAGGCATGAGACTCAGCACCACAG 634  
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Qy 825 AATGTTAAGGCATGAGACTCAGCACCACAG 858  
| | | | |

RESULT 3  
LOCUS HUMTNFRP 2050 bp mRNA PRI 11-OCT-1991

DEFINITION Human tumor necrosis factor receptor(TNF) mRNA, complete cds.

ACCESSION M60275 M37764  
NID g339759

KEYWORDS  
TNF receptor; transmembrane receptor; tumor necrosis factor receptor.

SOURCE Human placenta, CDNA to mRNA.

ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

REFERENCE 1 (bases 1 to 2050)  
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Gray,P.W., Barrett,R.J., Chantry,D., Turner,M. and Feldman,M.

TITLE Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384 (1990)  
91017509

COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by P.W.Gray, 13-Aug-1990.

FEATURES  
Location/Qualifiers

source 1..2050  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

sig\_peptide 155..274  
/tissue="placenta"

CDS 155..274  
/gene="TNF receptor"  
/codon\_start=1

product="TNF receptor"

/db\_xref="PID:g339760"

/translation="MGLSTVPDLLPLVLELVGIVPSGVIGLVPHLGDREKRDVSC  
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KQNTVCTCHAEFLRENECVSCSKSLKSLVCKSLKLPQIENVKGTESGTVLPLVI  
FFGLCLSLFLIGLIRYORWKSLSIVCKSLPEKGELEGTTLKPLAPSPSP  
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LLR"

gene 155..274  
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mat\_peptide 275..1513  
/product="TNF receptor"

BASE COUNT 429 a 611 c 566 g 444 t

ORIGIN

Query Match 39.5%; Score 514; DB 27; Length 2050;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 275 GATAGTGTGTGTCGCCAAGAAATATATCCACCTCAAAATTAATTCATTTGCTGTACC 334  
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QY 345 GATAGTGTGTGTCGCCAAGGAAATATATATCCACCCTCAAAATATGATTTGCTTACC 404  
Db 335 AAGTGCACAAAGGAACTTCTTGTACATGACGTCAGGCGCGGGGAGATACGAG 394  
QY 405 AAGTGCACAAAGGAACTTCTTGTACATGACGTCAGGCGCGGGGAGATACGAG 464  
Db 395 TGCAGGAGTGTGAGACGGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 454  
QY 465 TGCAGGAGTGTGAGACGGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 524  
Db 455 AGCTGCTCCAAATGCCGAAAGAAATGGTCAAGTGAATCTCTTTCGACAGTGGAC 514  
QY 525 AGCTGCTCCAAATGCCGAAAGAAATGGTCAAGTGAATCTCTTTCGACAGTGGAC 584  
Db 515 CGGGACACCGTGTGTGCTCAGAGAACCAACGATATTTGAGAGTGAACCTT 574  
QY 585 CGGGACACCGTGTGTGCTCAGAGAACCAACGATATTTGAGAGTGAACCTT 644  
Db 575 TTCCAGTGTCAATTGCTCAGCCTCTGCTCAATGGAGACCGTCACTCTCTGCGAGAG 634  
QY 645 TTCCAGTGTCAATTGCTCAGCCTCTGCTCAATGGAGACCGTCACTCTCTGCGAGAG 704  
Db 635 AAACAGAACACCGTGTGCTCAGCCTCTGCTCAATGGAGAACGAGTGTGTC 694  
QY 705 AAACAGAACACCGTGTGCTCAGCCTCTGCTCAATGGAGAACGAGTGTGTC 764  
Db 695 TTCTGTGTACCTGTATAGAAAAAGCTTGAGTGCACGAAATGTGTGCTTACCCAGATTGAG 754  
QY 765 TTCTGTGTACCTGTATAGAAAAAGCTTGAGTGCACGAAATGTGTGCTTACCCAGATTGAG 824  
Db 755 AATGTTAAGGCACTGAGACTCAGGACCAACAG 788  
QY 825 AATGTTAAGGCACTGAGACTCAGGACCAACAG 858

RESULT 4  
LOCUS A21522 2062 bp RNA PAT 26-JUL-1994  
DEFINITION TNF alpha gene.  
ACCESSION A21522  
NID 9579599  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
AUTHORS Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
JOURNAL 1 (bases 1 to 2062)  
FEATURES  
Patent: GB 2246569-A 1 05-FEB-1992;  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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FGLCLSLFLIGLRYORWKSILYSIVGKSPKEGELGEGTTRKPLAPNSFSP  
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BASE COUNT 429 a 617 c 573 g 443 t  
ORIGIN  
Query Match 39.5%; Score 514; DB 25; Length 2062;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 275 GATAGTGTGTGTCGCCAAGGAAATATATCCACCCTCAAAATATGATTTGCTTACC 334  
QY 345 GATAGTGTGTGTCGCCAAGGAAATATATCCACCCTCAAAATATGATTTGCTTACC 404  
Db 335 AAGTGCACAAAGGAACTTCTTGTACATGACGTCAGGCGCGGGGAGATACGAG 394  
QY 405 AAGTGCACAAAGGAACTTCTTGTACATGACGTCAGGCGCGGGGAGATACGAG 464  
Db 395 TGCAGGAGTGTGAGACGGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 454  
QY 465 TGCAGGAGTGTGAGACGGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 524  
Db 455 AGCTGCTCCAAATGCCGAAAGAAATGGTCAAGTGAATCTCTTTCGACAGTGGAC 514  
QY 525 AGCTGCTCCAAATGCCGAAAGAAATGGTCAAGTGAATCTCTTTCGACAGTGGAC 584  
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QY 585 CGGGACACCGTGTGTGCTCAGAGAACCAACGATATTTGAGAGTGAACCTT 644  
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QY 645 TTCCAGTGTCAATTGCTCAGCCTCTGCTCAATGGAGACCGTCACTCTCTGCGAGAG 704  
Db 635 AAACAGAACACCGTGTGCTCAGCCTCTGCTCAATGGAGAACGAGTGTGTC 694  
QY 705 AAACAGAACACCGTGTGCTCAGCCTCTGCTCAATGGAGAACGAGTGTGTC 764  
Db 695 TTCTGTGTACCTGTATAGAAAAAGCTTGAGTGCACGAAATGTGTGCTTACCCAGATTGAG 754  
QY 765 TTCTGTGTACCTGTATAGAAAAAGCTTGAGTGCACGAAATGTGTGCTTACCCAGATTGAG 824  
Db 755 AATGTTAAGGCACTGAGACTCAGGACCAACAG 788  
QY 825 AATGTTAAGGCACTGAGACTCAGGACCAACAG 858

RESULT 5  
LOCUS I43805 2062 bp DNA PAT 10-JUL-1997  
DEFINITION Sequence 24 from patent US 5633145.  
ACCESSION I43805  
NID 92468903  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2062)  
AUTHORS Feldmann, M., Gray, P.W., Turner, M.J.C. and Brennan, F.M.  
JOURNAL TNF alpha receptor binding protein  
Patent: US 5633145-A 24 27-MAY-1997;  
FEATURES  
Location/Qualifiers  
source  
1..2062  
/organism="unknown"  
BASE COUNT 429 a 617 c 573 g 443 t  
ORIGIN

Query Match 39.5%; Score 514; DB 25; Length 2062;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 275 GATAGTGTGTGTCGCCAAGGAAATATATCCACCCTCAAAATATGATTTGCTTACC 334  
QY 345 GATAGTGTGTGTCGCCAAGGAAATATATCCACCCTCAAAATATGATTTGCTTACC 404  
Db 335 AAGTGCACAAAGGAACTTCTTGTACATGACGTCAGGCGCGGGGAGATACGAG 394  
QY 405 AAGTGCACAAAGGAACTTCTTGTACATGACGTCAGGCGCGGGGAGATACGAG 464  
Db 395 TGCAGGAGTGTGAGACGGGCTCTTACCGCTTCAGAAAAACCACTCAGACACTGCTC 454

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QY 465 TGCAGGAGTGTGAGAGCGGCTCTACCGCTTCAGAAACACCTCAGACATGCTTC 524  
Db 455 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGCAGATCTCTTTCAGCAGTGCAG 514  
QY 525 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGCAGATCTCTTTCAGCAGTGCAG 584  
Db 515 CGGAGACCGGTGTGTGGTGCAGAGAAACAGATCCGCAATTTATGGATGAAAACTTT 574  
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LOCUS  
DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION M33294  
NID 9339744  
KEYWORDS cell surface receptor; tumor necrosis factor receptor.  
SOURCE Human placenta, cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Eukaryota; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 2087)  
Schall, T.J., Lewis, M., Koller, K.J., Lee, A.L., Rice, G.C., Wong, G.H., Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Kohn, W.J. and Goeddel, D.V.  
Molecular cloning and expression of a receptor for human tumor necrosis factor  
Cell 61, 361-370 (1990)  
JOURNAL 90235285  
MEDLINE  
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by T.Schall, 26-MAR-1990.  
FEATURES  
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LOCUS  
DEFINITION cDNA for (55Kd TNF-BP) tumor necrosis factor binding protein from  
patent EP0417563.  
ACCESSION A26412  
NID 9904968  
KEYWORDS unidentified.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2111)  
Brockhaus, M., Dembic, Z., Gentz, R., Lesslauer, W., Loetscher, H. and Schlaeger, E.J.  
TNF-binding proteins  
Patent: EP 0417563-A 24 20-MAR-1991;  
JOURNAL F. HOFMANN-IA ROCHE AG  
MEDLINE  
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LOCUS A43873 2175 bp DNA PAT 06-MAR-1997  
DEFINITION Sequence 1 from Patent EP0657536.  
ACCESSION A43873  
NID 92299022  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2175)  
AUTHORS Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.  
TITLE Proteases capable of shedding the soluble TNF-receptor and TNF-R  
derived peptides and antibodies against the proteases inhibiting  
the shedding  
Patent: EP 0657536-A 14-JUN-1995;  
JOURNAL XEDA RES & DEV (IL) 9407962 951121  
COMMENT other publication ZA 9407962 951121  
other publication JP 7194376 950801  
other publication AU 7574294 950504  
other publication CA 2133872 950413.  
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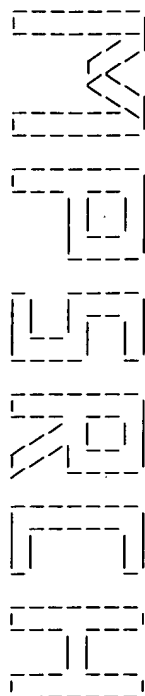
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ACCESSION I64751  
NID 92481645  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2175)  
AUTHORS Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.  
TITLE Molecules influencing the shedding of the TNF receptor, their  
preparation and their use  
Patent: US 5665859-A 1 09-SEP-1997;  
JOURNAL location/Qualifiers  
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Query Match 39.5% Score 514; DB 25; Length 2175;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 13 A19907 2176 bp DNA PAT 04-OCT-1994  
LOCUS  
DEFINITION Synthetic nucleotide sequence Type I TNF receptor gene.  
ACCESSION A19907  
KEYWORDS 9641222  
NID  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 2176)  
AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.  
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TNF-I)  
JOURNAL Patent: EP 0433900-A 28-26-JUN-1991;  
FEATURES  
source YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED  
location/Qualifiers  
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ORIGIN  
Query Match 39.5%; Score 514; DB 25; Length 2176;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
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ACCESSION 126928  
KEYWORDS 91606798  
NID  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 6889)  
AUTHORS Crowley,C.W.  
TITLE Method for selecting high-expressing host cells  
JOURNAL Patent: US 5561053-A 2 01-OCT-1996;  
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location/Qualifiers  
BASE COUNT 1729 a 1826 c 1681 g 1653 t  
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Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Msrch.n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 15:05:10 1998; Maspar time 167.20 Seconds

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Description: (1-1301) from US08804166.seq  
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Comp: GAGCTTACGAGATGTCATTT.....GTGTATTCCTCAGGAGCTC

Scoring table: TABLE default  
Gap 6

Mismatch STD : Dbase 0; Query 0

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Post-processing: Minimum Match 0%  
Listing first 45 summaries

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Statistics: Mean 9.269; Variance 5.321; scale 1.742

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	514	39.5	2062	4	Q24440	Encodes TNF-alpha 55k	0.00e+00
4	514	39.5	2062	3	Q20973	TNF-alpha binding pro	0.00e+00
5	514	39.5	2088	2	Q10883	30kD TNF inhibitor pr	0.00e+00
6	514	39.5	2111	2	Q10955	Encodes human 55kD TN	0.00e+00
7	514	39.5	2175	15	Q90513	p55 TNF-R gene.	0.00e+00
8	514	39.5	6889	18	T15931	DHFR/Inttron (WTtrassp)	0.00e+00
9	512	39.4	2141	1	Q06285	Human Tumour Necrosis	0.00e+00
10	512	39.4	2176	2	Q12215	Type I TNF receptor.	0.00e+00
11	510	39.2	2170	9	Q50870	p55 Tumour necrosis f	0.00e+00
12	478	36.7	608	4	Q24441	Encodes truncated TNF	0.00e+00
13	416	32.0	579	9	Q14800	Human chorionic gonad	6.61e-279
14	415	31.9	836	17	T03212	Single chain gonadotr	3.64e-278
15	415	31.9	836	17	T03243	Single chain gonadotr	3.64e-278

16	411	31.6	575	17	T03240	Human CG beta-subunit	3.34e-275
17	383	29.4	504	4	Q24445	Encodes truncated TNF	1.75e-254
18	354	27.2	474	4	Q24442	Encodes truncated TNF	4.64e-233
19	321	24.7	743	17	T03219	Single chain gonadotr	9.76e-209
20	304	23.4	2771	31	T76770	Rat FcBp1 gut-specific	3.12e-196
21	303	23.3	2160	33	T62826	Human growth hormone	1.69e-195
22	296	22.8	436	6	Q41459	Human growth hormone	2.35e-190
23	285	21.9	426	2	N60524	Sequence encoding hum	2.78e-182
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26	282	21.7	752	17	T03229	Single chain gonadotr	4.41e-180
27	276	21.2	744	17	T03221	Single chain gonadotr	1.10e-175
28	267	20.5	752	17	T03227	Single chain gonadotr	4.31e-169
29	259	19.9	2173	1	Q06284	Rat Tumour Necrosis F	3.07e-163
30	257	19.8	477	4	Q24444	Encodes truncated TNF	8.89e-162
31	221	17.0	462	4	Q24443	Encodes truncated TNF	1.58e-135
32	215	16.5	525	1	Q03844	Bovine beta LH subun	3.57e-131
33	213	16.4	540	1	Q03851	Porcine beta LH subun	1.01e-129
34	208	16.0	2660	4	N30032	Sequence encoding dog	4.28e-126
35	188	14.5	496	2	N60523	Sequence encoding dog	1.28e-111
36	185	14.2	611	1	Q03848	Equine beta LH subun	1.84e-109
37	132	10.1	1027	2	Q10878	Partial sequence of c	1.41e-71
38	101	7.8	114	2	N60522	Sequence encoding am	7.09e-50
39	99	7.6	138	13	Q80819	LH-beta -5 to 41 frag	1.71e-48
40	79	6.1	1047	2	Q10572	Human Natrluxetic pep	7.76e-35
41	73	5.6	1047	2	Q10572	Human Natrluxetic pep	8.20e-31
42	72	5.5	114	6	Q34669	DNA encoding hCG beta	3.81e-30
43	71	5.5	651	2	N71239	Sequence encoding hum	1.76e-29
44	71	5.5	700	2	N60678	Sequence encoding pre	1.76e-29
45	71	5.5	3557	2	N60801	Human pro-growth horm	1.76e-29

ALIGNMENTS

RESULT 1	ID	Q06282	standard; DNA; 1334 BP.
AC	Q06282;		
DT	29-JAN-1991	(first entry)	
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OS	Human sapiens.		
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PN	EP-393438-A.		
PD	24-OCR-1990.		
PE	06-APR-1990; 106624.		
PR	21-APR-1989; DE-913101.		
PR	21-JUN-1989; DE-920282.		
PA	(BOEH ) BOEHRINGER INGELHEIMINT.		
PI	Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;		
DR	WPI: 90-321987/43.		
DR	P-PSDB: R07449.		
PT	DNA encoding TNF binding protein and TNF- receptor - used in		
PT	tumour treatment and to understand mechanisms to TNF action		
PS	Disclosure; Fig 1(1-3); 51pp; German.		
CC	TNF-BP15 is one of 30 positives clones in a screened cDNA library		
CC	from induced TNF-induced fibrosarcoma cells. A TNF-BP had been		
CC	isolated from the urine of patients with uraemia and probes/primers		
CC	were constructed from the determined amino acid sequence.		
CC	to produce a vector expressing a soluble form of TNF-binding		
CC	protein, this plasmid was cut with XbaI, amplified by PCR and the		
CC	amplified DNA cut with BamHI and EcoRI.		
CC	The resulting 0.75 kb DNA fragment was inserted into pT73 alpha-19		
CC	(BRL) cut with the same enzymes to recover pTNF-BP. This was cut		
CC	with BamHI and EcoRI, and the recovered fragment inserted into		
CC	pMD-CMV1 (Q06283) to give the required plasmid pMDTNF-BP.		
CC	See also Q06282-Q06285.		
SO	Sequence	1334 BP; 299 A; 409 C; 342 G; 284 T;	
Query Match	39.5%;	Score 514;	DB 1; Length 1334;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

333 gatagctgtgtcccaaggaataatataccaccctcaaaataatcagattgctgtacc 392  
|||||  
345 GATAGCTGTGTGTCCTCCAGGAAAATATATCCACCCCTCAAAATATTCGATTCTGTACC 404  
|||||  
393 aagtcacacaaagaaactactgttacaatgactgtccagcccgaggcagaaacagac 452  
405 AAGTGCACACAAAGAAACCTCTGTACAAATGATGTCAGGCCCGGGGAGATACGAGAC 464  
|||||  
453 tgaaggagatgtgaaggagcgtctctccacgcgtcttcagaaacacactcagacgtctc 512  
|||||  
465 TGAAGGAGAGTGAAGAGCGGCTCTTACCGCTTCAGAAAAACACCTCAGACACTGCTTC 524  
|||||  
513 agctgtctccaaatgcgcaaaagaaatggtcaggtgagagatctctcttcacaggtgac 572  
|||||  
525 AGCTGCTCCAAATGCCGAAAAGAAATGGCTCAGGTGAGATCTCTTTCACACAGTGGAC 584  
|||||  
573 cggagacacgctgtgtgctgcaggaagaaacagtaaccgcatatttggagtgaaaaactt 632  
585 CCGGACACCGCTGTGTGCTGCAGGAAGAACCATACCGGATATTGAGTGAATGAACTT 644  
|||||  
633 ttccagtgcttaattgacagctctctcctcaatgagacgctgacactctctcgcagagag 692  
|||||  
645 TTCAGTGTCTCAATTGACACCTCTGCTCAATGGGACCTGTGACCTCTCTGCGCAGAG 704  
|||||  
693 aaacagaaacacgctgtgcacctgcacatgcaggtttcttctaagagaaacagatgtgtc 752  
|||||  
705 AAACAGAACACCTGTGACCTGCTGCATGACAGTTCCTTTTAAGAGAAAAAGATGTGTC 764  
|||||  
753 tctgtagtaactgttaagaaagcctgtgagtgacagaaagtgtgctaccacagattgag 812  
765 TCCTGTAGTAACGTGAAGAAAGCCTGAGATGACGAAAGTTGTGCTTACCCAGATTGAG 824  
|||||  
813 aatgttaaggacactgagacactcagagaccacag 846  
|||||  
825 AATGTTAAGGGCACTGAGACTCAGGCACACACAG 858  
|||||

RESULT 2  
ID 049932 standard: cDNA to mRNA: 1368 BP.  
AC 049932;  
DT 29-APR-1994 (first entry)  
DE Lambda-derived TNF-R cDNA.  
KW Human: tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;  
IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;  
rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;  
pulmonary fibrosis; silicosis; allograft; xenograft; rejection;  
graft versus host disease; sepsis; inflammation; allergy;  
KW autoimmune dysfunction; ss.  
OS Homo sapiens.  
FH Lambda-gt10-7-ctnfbp.  
FT Key Location/Qualifiers  
FT CDS 1..1366  
FT /\*tag= a  
FT /product= htnf-R  
FT sfg\_peptide 1..120  
FT /\*tag= b  
FT mac\_peptide 121..1363  
FT /\*tag= c  
FT MO9319777-A.  
PD 14-OCT-1993.  
PE 26-MAR-1993: 002938.  
PR 30-MAR-1992: US-860710.  
PA (IMVY ) IMMUNEX CORP.  
PI Smith CA:  
DR WPI: 93-336592/42.  
DR P-PSDB: R42059.  
PT New fusion protein tumour necrosis factor and human interleukin-1  
PT receptor: useful in therapy, diagnosis and assays of e.g.  
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.  
PS Disclosure; Page 57-59; 85bp; English.

CC The sequences given in 049931-32 encode human tumour necrosis factor  
CC receptor (TNF-R) and the sequences in 049933-34 encode human  
CC interleukin-1 receptor (IL-1R). These sequences were used in the  
CC production of a fusion protein which conformed to one of the  
CC formulae:  
CC TNF-R-linker-TNF-R-linker-IL-1R  
CC IL-1R-linker-TNF-R-linker-TNF-R or  
CC TNF-R-linker-TNF-R  
CC The linker may comprise 5-100 amino acids selected from Gly, Asp,  
CC Ser, Thr and Ala. These linkers separate the individual moieties  
CC by such a distance that each component of the fusion protein is  
CC capable of folding into the secondary or tertiary structure required  
CC for its biological activity. These fusion proteins may be used in  
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
CC particularly in conditions in which both TNF and IL-1 play a causative  
CC role. They may be used to treat cachexia, rheumatoid arthritis,  
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
CC cerebral malaria, allograft and xenograft rejection in graft versus  
CC host disease, sepsis, septic shock, inflammation, allergies and  
CC autoimmune dysfunction.  
SQ Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T;

Query Match 39.5%; Score 514; DB 8; Length 1368;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 121 gatagctgtgtcccaaggaataatataccaccctcaaaataatcagattgctgtacc 180  
345 GATAGCTGTGTGTCCTCCAGGAAAATATATCCACCCCTCAAAATATTCGATTCTGTACC 404  
|||||  
DB 181 aagtcacacaaagaaactactgttacaatgactgtccagcccgaggcagaaacagac 240  
405 AAGTGCACACAAAGAAACCTCTGTACAAATGATGTCAGGCCCGGGGAGATACGAGAC 464  
|||||  
DB 241 tgaaggagatgtgaaggagcgtctctcctcaacgcgtcttcagaaacacactcagacgtctc 300  
465 TGAAGGAGAGTGAAGAGCGGCTCTTACCGCTTCAGAAAAACACCTCAGACACTGCTTC 524  
|||||  
DB 301 agctgtctccaaatgcgcaaaagaaatggttcaggtgagtgagatctctcttcacagtgagac 360  
525 AGCTGCTCCAAATGCCGAAAAGAAATGGCTCAGGTGAGATCTCTTTCACACAGTGGAC 584  
|||||  
DB 361 cggagacacgctgtgtgctgcaggaagaaacagtaaccgcatatttggagtgaaaaactt 420  
585 CCGGACACCGCTGTGTGCTGCAGGAAGAACCATACCGGATATTGAGATGAAAACTT 644  
|||||  
DB 421 ttccagtgcttaattgacagcctctcctcaatgagacggtgacactctctcgcaggag 480  
645 TTCAGTGTCTCAATTGACACCTCTGCTCAATGGGACCTGTGACCTCTCTCCAGGAG 704  
|||||  
DB 481 aaacagaaacacgctgtgcacctgcacatgcaggtttcttctaagagaaacagatgtgtc 540  
705 AAACAGAACACCTGTGACCTGCTGCATGACAGTTCCTTTTAAGAGAAAAAGATGTGTC 764  
|||||  
DB 541 tctgtagtaactgttaagaaagcctgtgagtgacagaaagtgtgctaccacagattgag 600  
765 TCCTGTAGTAACGTGAAGAAAGCCTGAGATGACGAAAGTTGTGCTTACCCAGATTGAG 824  
|||||  
DB 601 aatgttaaggacactgagacactcagagacacacag 634  
825 AATGTTAAGGGCACTGAGACTCAGGCACACACAG 858  
|||||

RESULT 3  
ID 024440 standard: DNA: 2062 BP.  
AC 024440;  
DT 05-NOV-1992 (first entry)  
DE Encodes TNF-alpha 55kd receptor.  
KW tumour necrosis factor alpha; extracellular binding domain;  
treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.



Db	455	agctgcgtcccaaatgcgcgaagaagaaatggtgtcaggctggaagatctcttcttcagacagtggac	514
Oy	525	agctgcgtcccaatgcccgaagaaatgggtgcaggtggagatctcttcttcagacagctggac	584
Db	515	cggagcacccggtgtgtgctgcaggaagaacacagacacggaattatggagtggaaacctc	574
Oy	555	cgggacacccggtgtgtgctgcaggaagaacacagacacggaattatggagtggaaacctc	644
Db	575	ttccagtgcttcaaatgtgagccctctgcctcaatgtgagacgctgcacctctccctgcagag	634
Oy	645	ttccagtgcttcaaatgtgagccctctgcctcaatgtgagacgctgcacctctccctgcagag	704
Db	635	aaacagaaacacccggtgtgcacctgcacatgcaggttctcttctaagagaanaacgagtgctc	694
Oy	705	aaacagaaacacccggtgtgcacctgcacatgcaggttctcttctaagagaanaacgagtgctc	764
Db	695	tcctgtatgtaatctgtaaagaaaaagcctgtgagtgcacggaagtgtgtcctaacccagattgag	754
Oy	765	tcctgtatgtaatctgtaaagaaaaagcctgtgagtgcacggaagtgtgtcctaacccagattgag	824
Db	755	aatgttaagggcactgcagagactgcagagacacacag	788
Oy	825	aatgttaagggcactgcagagactgcagagacacacag	858

RESULT	5	
ID	Q10863	standard; cDNA; 2088 BP.
AC	Q10863;	
DT	13-MAY-1991	(first entry)
DE	30kD TNF inhibitor precursor gene in lambda-gt10-7ctnfbp.	
KW	Tumour necrosis factor; inhibitor; ss.	
OS	Homo sapiens.	
FX	Key	
FT	CDS	Location/Qualifiers
FT	/*tag-a	171..1536
PN	AU0958975-A.	
PD	24-JAN-1991.	
PF	16-JUL-1990; 058976.	
PR	18-JUL-1989; US-381080.	
PR	11-DEC-1989; US-450329.	
PR	07-FEB-1990; US-479661.	
PA	(SYNE-) SYNERGEN INC.	
DR	WPI; 91-073847/11.	
DR	P-PSDS; R10986.	
PT	Tumour necrosis factor inhibitor - for suppression of TNF-alpha	
PT	and -beta, useful as therapeutic agent.	
PS	disclosure; Fig 21: 142pp; English.	
CC	The sequence encodes the entire 30 kD TNF inhibitor. The clone from	
CC	which the sequence was obtd. was isolated from a cDNA library	
CC	prepd. from RNA from U937 cells treated with PMA/PHA. The whole	
CC	gene can be inserted into expression vectors for prepn. of TNF	
CC	inhibitor for use in the treatment of inflammatory and degenerative	
CC	diseases.	
CC	See also Q10878, Q10864 and Q10907.	
Q0	Sequence	2088 BP; 439 A; 626 C; 578 G; 445 T;

```
Query Match      39.5%; Score 514; DB 2; Length 2088;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches      514; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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Db	289	gaagtagtgtgtccccaaaggaaatataatcacccctcaaaataattgatttgcgtaac	348
Oy	345	gatatgtgtgtccccaagaaanaatwtccaccctcaaaataattgatttgcgtaac	404
Db	349	aagttccacaaaggaaactactttgacatgactcgtccaggtccggggcaggataagac	408
Oy	405	aagttccacaaaggaaactactttgacatgactcgtccaggtccggggcaggataagac	464
Db	409	tgcaggagagttgaaagaggtctccttcacgcttcagaaaaaacacccacagcaactgctc	468
Oy	465	tgcaggagagttgaaagaggtctccttcacgcttcagaaaaaacacccacagcaactgctc	524

Db	469	agtgcttccaatgcccgaagaagaaatggtctcaggtgaaatctctcttcttcacacagtgagc	528
Oy	525	AGCTGCTCCAATATCCGAAAGAAATAGGTCTAGGTGAAGATCTCTTTTCCACAGTGAGC	584
Db	529	cggagcacccgtgtgtgcgtgcagaaagaaacagagccggacatctatggatgaaaacctc	588
Oy	585	CGGACACCCGTGTGTGCTGACGAAGAAGACCATGACCGGCATTTTGGATGAAAACTT	644
Db	589	ttccagtgcttcaattgcagcctcttgctccaatgatggaacgltgcacctctcctccagag	648
Oy	645	TTCCAGTGCTTCAATTGAGGCTCTGCCTCAATGGAGACGAGACCTCTCCTGCAGAG	704
Db	649	aaacagaacacccgtgtgcacctgcctgcctgcaggtctcttcttaagagaaacaggtgtc	708
Oy	705	AAACGAACACCCGTGTGCACCTGCCATGCAAGTTCCTTTAAGAGAAAAAGAGTGCTC	764
Db	709	tcctctagtaactctgaagaagaagccttgagatgacgaagtgttgccacccaagattgag	768
Oy	765	TCTCTATATACTGAAGAAAAAGCCTGGAGTGCAGGAAGTTGTGCTTACCCAGATTGAG	824
Db	769	aatgttaaggccactgagagcctcagggcacccacag	802
Oy	825	AATGTTAAGGCACCTGAGAGCATCAGGACCCAC	858

RESULT	6
ID	Q10955 standard; cDNA; 2111 BP.
AC	O10955;
DT	24-MAY-1991 (first entry)
DE	Encodes human 55kD TNF-binding protein.
KW	Tumour Necrosis Factor; binding proteins; septic shock;
KW	Autoimmune glomerulonephritis; lymphokine; cytokine.
FH	key Location/Qualifiers
FT	/sig_peptide 187..273
FT	/tag_a
FT	mat_peptide 274..1551
FT	/tag_b
FT	/product= 55kD TNF-BP
PD	EP-417563-A.
PD	20-MAR-1991.
PF	31-AUG-1990; 116707.
PR	12-SEP-1989; CH-003319.
PR	08-MAR-1990; CH-000746.
PR	20-APR-1990; CH-001347.
PA	(HOFF) HOFFMANN-LA ROCHE AG.
P1	Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotzschler H;
P1	Schlaeger EJ;
DR	WPI: 91-081851/12.
DR	P-PDSB: R11082.
PT	Insoluble tumour necrosis factor binding proteins - and DNA
PT	procdn them, useful in pharmaceutical prods. and for antibody
PS	prodn.
PS	Claim 4; Fig 1; 26pp; German.
CC	Partial amino acid sequences were determined for the 55 and 75kD
CC	TNF-BPs (see R11072-R11081) and oligonucleotide primers were
CC	synthesised based on these partial sequences. The primers were used
CC	to produce a cDNA fragment for use as aprobe to screen a human
CC	placental cDNA bank constructed in lambda gt11. Positive clones were
CC	identified and sequenced. DNA constructs comprising the TNF-BP coding
CC	sequence may also contain a fragment encoding a human Ig domain.
CC	Recombinant constructs are used to transform cells to confer
CC	improved TNF-binding properties.
SC	See also Q10956.
SC	Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;

```

Query Match      39.5%; Score 514; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 307 gatagtgtgtgtccccaagaaataataccaccctcaaaataattcgattgctgtacc 366  
OY 345 GATAGTGTGTGTCCCAAGAAATAATATCCACCTCAAAATAATTGATTGCTGTACC 404



Db 367 aagtcacacaaagaaacctactgttacaatgactgtccaggcccgaggcagagatcagac 426  
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 Qy 405 AAGTGCACAAAGAAAGAACTCTGTACAAATGACTGTCCAGGCCGGGGAGATACGAC 464  
 Db 427 tgcaggagatgtgtagagcggcctccctcaacgcttcagaacacactcagactgctc 486  
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 Qy 465 TGCAGGAGAGTGAAGAGCGGCTCTTCACCGCTTCACAAAACACACCTCAACACACTGCCTC 524  
 Db 487 agctgtcccaatgcccgaagaagaatggtcagagtgtagatctctttccacagtgagc 546  
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 Qy 525 AGCTGTCCAAATGCGCAAAAGAAATGGTGTACAGTGGAGATCTCTTTCACACAGTGGAC 584  
 Db 547 cgggaacacgctgtgtgctgcaggaagaacacagatccagatattatgagtgaaacctc 606  
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 Qy 585 CGGGACACCGCTGTGTGGCTCTCAGGAAGAACACAGACCGCATTAATGATGAAAACTT 644  
 Db 607 ttccagtgcttcaatgacagctctcctcaatgagacgctgcacctcctcgcaggag 666  
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 Db 667 aacagagaacacgctgtgacactgcctcagcaggtttcttctaagagaacagagtgctc 726  
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 Qy 705 AAACAGAACACCGTGTGCTACCTGCACAGGTTCTTCTTAAGAGAAACGAGTGTCTC 764  
 Db 727 tctctgtagtaactgttaagaaagcctgagtgacagagttgtcctaccacagattgag 786  
 |||||||  
 Qy 765 TCTGTGTAGTAAGTGAAGAAAGCTGTGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 824  
 Db 787 aatgttaaggacactgagagactcaagcaccag 820  
 |||||||  
 Qy 825 AATGTTAAGGGCACTGAGACTCAGGCACACAG 858

RESULT 7  
090513 standard; DNA; 2175 BP.

AC 090513;  
 DT 19-JAN-1996 (first entry)  
 DE p55 TNF-R gene.  
 KM p55: tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
 KM epidermal growth factor receptor; EGF-R; protease; inhibitor;  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 256..1623  
 FT /tag= a  
 FT /product= p55 TNF-R  
 FT /misc\_signal 2143..2149  
 FT /tag= b  
 FT /note= "possible poly-A signal"  
 PN A09475742-A.  
 PD 04-MAY-1995.  
 PE 11-OCT-1994; 075742.  
 PR 12-OCT-1993; IL-107268.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI Belkin M, Brakebusch C, Varfolomeev E, Wallach D;  
 DR MPI: 95-194342/26.  
 DR P-PSDB; R75084.  
 PT New protease capable of cleaving soluble tumour necrosis factor  
 PT (TNF) receptor - from cell-bound TNF- receptor, useful for  
 PT antaonising deleterious effects of TNF.  
 PS Disclosure: Fig 1: 40pp; English.  
 CC This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.  
 CC expression of this receptor is regulated by shedding of the extracellular  
 CC receptor fragment. The p55 TNF-R can be shed in response to different  
 CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell  
 CC type. The only region of the receptor whose structure affects the  
 CC shedding response is the spacer region (see R75012) in the extracellular  
 CC domain. This region is located close to a site of cleavage of the  
 CC molecule, and links the Cys rich module to the transmembrane domain. The  
 CC spacer region of the encoded protein was used to create the chimeras  
 CC between human p55 TNF-R and murine epidermal growth factor receptor  
 CC (EGF-R) that are represented by R75007-11. This spacer region was  
 CC subjected to deletion mutations (R75013-25) and substitutions

CC (R75026-47): Of the spacer region, the most important residues are  
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most  
 CC important of these. The shedding of the receptor is independent of the  
 CC side chain identity of these residues, with the exception of a limited  
 CC dependence on the identity of Val 173. Mutations which alter the  
 CC conformation of the protein adversely effect the shedding process. The  
 CC mutations shown in R75013-47 were introduced in order to create an  
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R  
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in  
 CC R75017-9, R75023, R75033-5 and R75042-3. These protease inhibitors can  
 CC be used for enhancing TNF function.  
 SQ Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T;

Query Match 39.58; Score 514; DB 15; Length 2175;  
 Best Local Similarity 100.08; Pred. No. 0.00e+00;  
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 376 gatagtgtgtgtccccaaggaataatataccaccctcaataatcogattgtctgacc 435  
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 Qy 345 GATAGTGTGTGTCCCAAGGAATAATATATCCACCTCAATAATATGATTGTCTGTACC 404  
 Db 436 aagtcacacaaagaaacctactgttacaatgactgtccaggcccgaggcagagatcagac 495  
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 Qy 405 AAGTGCACAAAGAAAGAACTCTGTACAAATGACTGTCCAGCCCGGGGAGATACGAC 464  
 Db 496 tgcaggagatgtgtagagcggcctcctcaccgcttcaagaacacactcagacactgctc 555  
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 Qy 465 TGCAGGAGTGTGAAGAGCGGCTCTTCACCGCTTCAGAAAAACACCTCAACACTGCTC 524  
 Db 556 agctgtcccaatgcccgaagaagaatggtcagagtgagatctcttccacagtgagc 615  
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 Qy 525 AGCTGTCCAAATGCGCAAAAGAAATGGTGTACAGTGGAGATCTCTTTCACACAGTGGAC 584  
 Db 616 cgggaacacgctgtgtgctgcaggaagaacacagatccgagattatggagtgaaacctc 675  
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 Qy 585 CGGGACACCGTGTGTGGCTCTCAGGAAGAACACAGTACCGCATTAATGAGTGAACCTT 644  
 Db 676 ttccagtgcttaatgacagcctcctcctcaatgagacgctgtgacactctctccaggag 725  
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 Qy 645 TTCACAGTCTTCAATTGACACCTCTCGCTCAATGGAGCCGTGACCTCTCTCCAGAG 704  
 Db 736 aacagagaacacgctgtgacactgcctcagcaggtttcttctaagagaacagagtgctc 795  
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 Qy 705 AAACAGAACACCGTGTGCTACCTGCACAGGTTCTTCTTAAGAGAAACGAGTGTCTC 764  
 Db 796 tctctgtagtaactgttaagaaagcctgagtgacagagttgtcctaccacagattgag 855  
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 Qy 765 TCTGTGTAGTAAGTGAAGAAAGCTGTGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 824  
 Db 856 aatgttaaggacactgagagactcaagcaccag 889  
 |||||||  
 Qy 825 AATGTTAAGGGCACTGAGACTCAGGCACACAG 858

RESULT 8  
115931 standard; DNA; 6889 BP.

AC 115931;  
 DT 20-JUN-1996 (first entry)  
 DE DHFR/Inttron (WTRASSD)-TNF-R IgG dicistronic vector.  
 KM Recombinant host cell; dihydrofolate reductase; selectable marker;  
 KM DHFR: ras splice donor; dicistronic vector; gene expression;  
 KM Immunoadhesin; TNF-R; tumour necrosis factor; ds.  
 OS Synthetic.  
 PN W09604391-A1.  
 PD 15-FEB-1996.  
 PE 28-JUL-1995; 009576.  
 PR 05-AUG-1994; US-286740.  
 PA (GENT ) GENENTECH INC.  
 PI Crowley CW;  
 DR MPI: 96-129407/13.  
 PT Improved process for the selection of recombinant host cells  
 PT expressing high level of a desired product - uses eukaryotic host  
 PT cells contg. a DNA construct comprising a selectable gene



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FT /note= "may be 2 codons shorter or a few codons
FT longer"
FT misc.feature 376..414
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FT misc.RNA 889..957
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FT /label= transmembrane.domain
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FT /number= 1
FT repeat_unit 505..633
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FT /number= 2
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FT /tag= k
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FT repeat_unit 757..858
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FT polyA_signal 2145..2150
FT /tag= m
FT EP-433900-A.
FT 26-JUN-1991.
FT 13-DEC-1990: 124133.
FT 13-DEC-1989: IL-092697.
FT 12-JUL-1990: IL-095064.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
FT Aderka D;
FT WPI: 91-186774/26.
FT P-PSDB; R12550.
FT Recombinant tumour necrosis factor binding protein I - prepd. by
FT transfecting eukaryotic cells with vector contg. deoxyribonucleic
FT acid encoding human type I TNF receptor or soluble domain
FT PS Disclosure: Fig 1(D): 30pp; English.
FT The Tumour Necrosis Factor Binding Protein I is the soluble form of
FT type I TNF-receptor and constitutes a fragment of the cell surface
FT form of this receptor, corresp. to its extracellular domain.
FT There is no characteristic poly(A) addition signal near the 3' end
FT of the cDNA. The sequence ACTAA (tag m) may serve as an
FT alternative to this signal, but with low efficiency.
FT See also Q1212-15.
FT CC
FT Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T;
SO
Query Match 39.4%; Score 512; DB 2; Length 2176;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 585 CCGGACACCGCTGTGCTCAGAGAAACACGACGAGATATTGATGAACCTT 644
DB 676 ttcaagtgttcaatgtcagcctctgcctcaatggaacgttgcacctctccaggag 735
QY 645 TTCAGTGTCTTCAATTGACCTCTGCTCAATGGAGCCCTGACACCTCTCTGACAGAG 704
DB 736 aaacagaaacacgtgtgcacctgcacatgacaggtttctttaaagaaacaggtgtc 795
QY 705 AAACAGAAACACCGTGTGCTCAGATGACAGTTCCTTCTTAAGAGAAACGAGTGTCTC 764
DB 796 tccgtgtacgttaagaaacgtgtgagtgcaagaagttgtccaccacagatgag 855
QY 765 TCCTGTGTACTACTGTAGAAAGAGCTGAGTGCAGAGAGTTGTGCTTCCACCATTTGAG 824
DB 856 aatgttaaggcaactgagacccaagcaccag 889
QY 825 AATGTTAAGGGCACTGAGACTCAGCACCACAG 858

RESULT 11
ID Q50870 standard; DNA; 2170 BP.
AC Q50870;
DT 13-MAY-1994 (first entry)
DE p55 Tumour necrosis factor receptor coding sequence.
KW TNF, tumour necrosis factor; receptor; disease; autoimmunity;
KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 256..1623
FT /tag= a
FT /product= p55 Tumour necrosis factor receptor.
FT EP-568925-A.
FT 10-NOV-1993.
FT 29-APR-1993: 106981.
FT 03-MAY-1992: IL-101769.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT PI Brakebusch C, Wallach D;
FT WPI: 93-353057/45.
FT P-PSDB; R42197.
FT DR P-PSDB; R42197.
FT Modulating activity of tumour necrosis factor receptor - using
FT peptide(s), antibodies, etc. which interact with critical regions
FT of receptor or effector protein, for controlling auto-immune
FT disease, septic shock, etc.
FT PS Claim 2; Figure 1; 17pp; English.
FT CC Modification of the tumour necrosis factor receptor by mutation or
FT deletion modulates signal transduction and/or cleavage effected by
FT the receptor. This modulation of activity can also be achieved
FT using effector proteins which interact with the TNF receptor.
FT CC Molecules which interact with the TNF receptor or the effector
FT proteins can be used to treat or prevent diseases associated with
FT CC TNF activity e.g. autoimmune disease; Rheumatoid arthritis; graft
FT rejection; graft vs. host disease or septic shock. They can also
FT be used to treat overdoes of exogenous TNF.
FT CC
FT Sequence 2170 BP; 474 A; 657 C; 384 G; 455 T;
SO
Query Match 39.2%; Score 510; DB 9; Length 2170;
Best Local Similarity 99.6%; Pred. No. 0.00e+00;
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```



```
QY 870 CCACGGTGGCCGCCATCATGACCCCTGCTGTGAGAGAGGGCTCCCCGTGTGC 929
Db 164 ataccgtcaaacaccacacatctgtccggtactgtcccaaccatgaccgctgtcag 223
QY 930 ATACCGCTCAACACACACATCTGTGCGGCTACTGCCCCACATGACCCCGTGTGAG 989
Db 224 ggggtgtccgcggccctgtccctcagtggtgtgcaactacgcagatgtgtcagtc 283
QY 990 GGGGTCTGCGGCGCCCTGCTCAGGTGTGTGCAATACCGCATGTGCGCTTCGATCC 1049
Db 284 atccggtccctgtgtcgcgcgcgcgcgtgaaccgctgtctcctcagcgtgtc 343
QY 1050 ATCCGGTCTCCTGTGCTGCGCGCGGCGGTGACCCCTGTGTCTCTACGCGGTGCTC 1109
Db 344 agctgtcaatgtgtactgtcgcgcgcgcgcacactgtcgtgtgtgtcccaaggacac 403
QY 1110 AGCTGTCAATGTGTACTCTGCGCGGACACACTACTGCGGGGTCCCAAGACAC 1169
Db 404 cccttgacctgtatgaccccgcttcacgaactcctctcctcaaaaggccctccccc 463
QY 1170 CCCTGACCTGTATGATGACCCCGCTTCAGAGACTCTCTCTCAAGGCGCCCTCCCC 1229
Db 464 agccttcaagccatcccgactcccggtggtccctcgagacaccccgatcctccacaataa 523
QY 1230 AGCCTTCAAGCCCATCCGACTCCCGGGCGCTCGGACACCCCGATCTCCCATTA 1289

RESULT 14
ID T03212 standard; cDNA; 836 BP.
AC T03212;
DE 26-APR-1996 (first entry)
KW Single chain gonadotropin analogue 1 coding sequence.
KW alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW inhibits; stimulate; increase; lutropin; luteinizing hormone; LH;
KW follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 33..830
FT /tag- a Location/Qualifiers
FT /transl_except- pos:240..242, aa:Arg
FT sig_peptide 33..92
FT /tag- b
FT mat_peptide 93..827
FT /tag- c
FT /label- Analogue_1
FT /note- "nucleotides 93..527 encode amino acids
FT 1-145 of hCG beta-subunit; nucleotides
FT 528..551 encode a (Gly-Ser)4 linker and
FT nucleotides 552..827 encode amino acids
FT 1-92 of gonadotropin alpha-subunit"
FT misc_feature 1..26
FT /tag- d
FT /label- sticky_end
FT /note- "single-strand overhang. The complementary
FT strand also has a single-strand overhang at
FT its 5'-end; the sequence of the overhang is
FT 5'-TCGGATTAGTTGATGATGATCC-3'"
FT 5-TCGGATTAGTTGATGATGATCC-3'"
PN W09523240-AL.
PD 24-AUG-1995.
PR 17-FEB-1995; 002067.
PR 18-FEB-1994; US-199382.
PA (SENS-) SENS1-TEST.
PI Moyle WR;
DR MPI; 95-302553/39.
DR P-PSDB; R86247.
PT Methods for altering fertility in mammals, esp. humans - e.g.
PT stimulating fertility by reducing the activity and/or levels of
PT circulating glyco/protein hormones having lutropin activity
CC Example 12; Fig 6; 10pp; English.
CC Analogue 1 (human CG-beta(1-145)-linker-human CG-alpha(1-92)) is a
CC specific example of a single chain gonadotropin having a chorionic
CC gonadotropin (CG) beta-subunit at the N-terminus and a CG alpha-
```

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CC subunit at the C-terminus, joined by a linker of 1-16 amino acids.
CC The analogue has luteinizing hormone (lutropin) activity and is
CC useful for inducing ovulation and increasing male fertility.
CC The sequences coding for analogue 1 were cloned from a human
CC placental cDNA library using strand overlap extension PCR.
SQ Sequence 836 BP; 166 A; 282 C; 222 G; 166 T;

Query Match 31.9%; Score 415; DB 17; Length 836;
Best Local Similarity 99.8%; Pred. No. 3,64e-278;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 111 ccaagtgccgcgccatcaatgtccacccctgtgtgagaaggaggtgtcccggtgtc 170
QY 870 CCACGGTGGCCGCCATCATGACCCCTGCTGTGAGAGAGGGCTCCCCGTGTGC 929
Db 171 ataccgtcaaacaccacacatctgtccggtactgtcccaaccatgacgcgtgtcag 230
QY 930 ATACCGCTCAACACACACATCTGTGCGGCTACTGCCCCACATGACCCCGTGTGAG 989
Db 231 ggggtctcgcggccctgtccctcagtggtgtgcaactacgcagatgtgtcgtcagtc 290
QY 990 GGGGTCTGCGGCGCCCTGCTCAGGTGTGTGCAATACCGCATGTGCGCTTCGATCC 1049
Db 291 atccggtccctgtgtcgcgcgcgcgcgtgaaccgctgtctcctcagcgtgtc 350
QY 1050 ATCCGGTCTCCTGTGCTGCGCGCGGCGGTGACCCCGTGTCTCTACGCGGTGCTC 1109
Db 351 agctgtcaatgtgtactgtcgcgcgcgcgcacacactgtcgtgtgtgtcccaaggacac 410
QY 1110 AGCTGTCAATGTGTACTCTGCGCGGACACACTACTGCGGGGTCCCAAGACAC 1169
Db 411 cccttgacctgtatgaccccgcttcacgaactcctctcctcaaaaggccctccccc 470
QY 1170 CCCTGACCTGTATGATGACCCCGCTTCAGAGACTCTCTCTCAAGGCGCCCTCCCC 1229
Db 471 agccttcaagccatcccgactcccggtggtccctcgagacaccccgatcctcccca 527
QY 1230 AGCCTTCAAGCCCATCCGACTCCCGGGCGCTCGGACACCCCGATCTCCCATTA 1286


RESULT 15
ID T03243 standard; cDNA; 836 BP.
AC T03243;
DE 08-MAY-1996 (first entry)
KW Single chain gonadotropin analogue 1a coding sequence.
KW alpha; beta; subunit; analogue; glycoprotein hormone; fertility;
KW inhibits; stimulate; increase; lutropin; luteinizing hormone; LH;
KW follicle stimulating hormone; FSH; vaccine; contraceptive; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 33..830
FT /tag- a Location/Qualifiers
FT /transl_except- pos:240..242, aa:Arg
FT sig_peptide 33..92
FT /tag- b
FT mat_peptide 93..827
FT /tag- c
FT /label- Analogue_1a
FT /note- "nucleotides 93..527 encode amino acids
FT 1-145 of hCG beta-subunit; nucleotides
FT 528..551 encode a (Gly-Ser)4 linker and
FT nucleotides 552..827 encode amino acids
FT 1-92 of gonadotropin alpha-subunit lacking
FT the glycosylation sites at amino acid
FT positions 52 and 78"
FT misc_difference 705..707
FT /tag- d
FT /note- "wild-type Asn 52 codon has been changed to a
FT Gln codon to remove a glycosylation site"
FT misc_difference 783..785
FT /tag- e
FT /note- "wild-type Asn 78 codon has been changed to a
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```
FT Gln codon to remove a glycosylation site"
FT misc_feature 1..26
FT /lag- f
FT /label= sticky_end
FT /note= "single-strand overhang. The complementary
FT strand also has a single-strand overhang at
FT its 5'-end; the sequence of the overhang is
FT 5'-TCCGATTACCTTGATGATGATCC-3'."
PN MO9522340-A1.
PD 24-AUG-1995.
PF 17-FEB-1995; U02067.
PR 18-FEB-1994; US-199382.
PA (SENS-) SENSIT-TEST.
PI Moyle WR;
DR WPI; 95-302553/39.
DR P-PSDB; R86259.
PT Methods for altering fertility in mammals, esp. humans - e.g.
PT stimulating fertility by reducing the activity and/or levels of
PT circulating glyco-protein hormones having luteotropin activity
PT Example 23; Fig 18; 102pp; English.
CC Analogue 1a (human CG-beta(1-145)-linker-human CG-alpha(1-92) [N53Q,
CC N78Q]) is a specific example of a single chain gonadotropin having
CC a chorionic gonadotropin (CG) beta-subunit at the N-terminus and a
CC CG alpha-subunit at the C-terminus, joined by a linker of 1-16 amino
CC acids. The analogue 1a was derived from analogue 1 by removing the
CC two glycosylation sites from the alpha-subunit. The analogue has
CC anti-luteinizing hormone (lutropin) activity and can be used for
CC facilitating ovulation, terminating pregnancy and reducing androgen
CC secretion. The present sequence codes for analogue 1a.
SQ Sequence 836 BP; 166 A; 282 C; 222 G; 166 T;

Query Match 31.9%; Score 415; DB 17; Length 836;
Best Local Similarity 99.8%; Pred. No. 3,64e-278;
Matches 416; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 111 ccagggtccggcccatcatccaccctggctgtggaagagggtgccccctgtgtc 170
OY 870 CCACGGTCCGCCCATCATCATGACCCCTGGCTGTGAGAAAGAGGCTGCCCGGTGTC 929
Db 171 atcacggtaaacacacacacatctgtccggctactgccccacatgaccccgctgtcag 230
OY 930 ATCACGGTCAACACACACCATCTGTGCGGCTACTGCCCCACATGACCCGCGTGTGACG 989
Db 231 ggggtccctgcggccctgcctcagggtgtgtgcaactacccgcatgtgccttcgagtc 290
OY 990 GGGGTCTCTGCGCCCTGCTCAGGTGTGTCACACTACCGCATGTGCGCTTCGAGTCC 1049
Db 291 atccggctccctggctgcccgcggcggtgaaccccggtgtctcctacgcgtgtgcttc 350
OY 1050 ATCCGGCTCCTGGCTGCGCCGCGCGGCGTGAACCCCGTGTCTCTACCCCGTGGCTTC 1109
Db 351 agctgtcaatgtgcaactctgcgcgcgcgcacacactgactgagggtgtcccaaggaccac 410
OY 1110 AGCTGTCAATGTGCACTCTGCGCGCGCGACACACTGACTGCGGGGTTCCTCAAGGACAC 1169
Db 411 cccctgacctgtgatacaccgccgcttccaggaactcctcttcccaaaaggccctccccc 470
OY 1170 CCCTTGACCTGTGATGACCCCGGCTTCAGGACTCTCTTCTCAAGGCCCTCTCCCCC 1229
Db 471 agccttcaagcccatcccgactccgggggacctggagacaccgcgatacctcccacaa 527
OY 1230 AGCCTTCAAGCCCATCCCGACTCCCGGGGCCCTCGAGACCCCGATCTCTCCACAA 1286
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Search completed: Wed May 6 15:08:03 1998  
Job time : 173 secs.

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 (TM)  
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Release 3.0.5AA John F. Collins, Biocomputing Research Unit.  
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 Distribution rights by Oxford Molecular Ltd

Mpsrch.n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed May 6 14:44:44 1998; MasPar time 1191.25 Seconds

Tabular output not generated. 1327.720 Million cell updates/sec

Title: >US-08-804-166-7  
 Description: (1-1301) from US08804166.seq  
 Perfect Score: 1301  
 N.A. Sequence: 1 CTCGAGATGCTACAGCTA.....CACATAGAGATCCTCGAG 1301  
 Comp: GAGCTCTACCGATGTCATT.....GTGTTATTCCTAGGAGCTC

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1610801 seqs, 607859669 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

embl-est  
 1:em-est1 2:em-est2 3:em-est3 4:em-est4 5:em-est5  
 6:em-est6 7:em-est8 8:em-gss 9:em-est13  
 genbank-est

10:gb-est1 11:gb-est2 12:gb-est3 13:gb-est4 14:gb-est5  
 15:gb-est6 16:gb-est7 17:gb-est8 18:gb-est9 19:gb-est10  
 20:gb-est11 21:gb-est12 22:gb-est13 23:gb-est14 24:gb-est15  
 25:gb-est16 26:gb-est17 27:gb-est18 28:gb-est19  
 29:gb-est20 30:gb-est21 31:gb-est22

Statistics: Mean 11.285; Variance 2.123; scale 5.317

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	Match	Length	DB	ID	Description	Pred. No.
c 1	397	30.5	601	13	N32759	YW91B05.s1 Homo sapien	0.00e+00
c 2	391	30.1	537	13	N30276	YW69804.s1 Homo sapien	0.00e+00
c 3	387	29.7	564	13	N32804	YW95603.s1 Homo sapien	0.00e+00
c 4	385	29.6	548	13	N30036	YW80B11.s1 Homo sapien	0.00e+00
c 5	383	29.4	593	13	N29130	YW78H03.s1 Homo sapien	0.00e+00
c 6	379	29.1	442	13	N32233	YW81F08.s1 Homo sapien	0.00e+00
c 7	379	29.1	473	13	N27302	YW71F12.s1 Homo sapien	0.00e+00
c 8	379	29.1	566	13	N30831	YW70B04.s1 Homo sapien	0.00e+00
c 9	377	29.0	563	13	N31955	YW89607.s1 Homo sapien	0.00e+00
c 10	376	28.7	479	13	N30684	YW77H04.s1 Homo sapien	0.00e+00
c 11	373	28.7	473	25	AA400910	zt71H09.s1 Soares test	0.00e+00
c 12	371	28.5	446	13	N31616	YW84602.s1 Homo sapien	0.00e+00
c 13	367	28.2	526	28	AA644163	af62808.s1 Soares NHM	0.00e+00

c 14	356	27.4	400	25	AA32905	zr46G04.s1 Soares NHM	0.00e+00
c 15	351	27.0	419	16	H95374	YW60B03.s1 Soares plac	0.00e+00
c 16	350	26.9	531	16	W71989	zdB6B03.s1 Soares feta	0.00e+00
c 17	335	25.7	403	13	N26397	YW76G11.s1 Homo sapien	0.00e+00
c 18	331	25.4	441	13	N30741	YW74B04.s1 Homo sapien	0.00e+00
c 19	332	24.8	422	11	R23214	Yh28A03.s1 Homo sapien	0.00e+00
c 20	319	24.5	404	13	N30833	YW70B08.s1 Homo sapien	0.00e+00
c 21	319	24.5	515	13	N30608	YW72C07.s1 Homo sapien	0.00e+00
c 22	317	24.4	386	13	N30822	YW65H07.s1 Homo sapien	0.00e+00
c 23	315	24.2	367	11	R68815	Y143C05.s1 Homo sapien	0.00e+00
c 24	307	23.6	329	12	H12587	YJ12G11.s1 Homo sapien	0.00e+00
c 25	305	23.4	367	16	H94466	YW55F02.s1 Soares plac	0.00e+00
c 26	300	23.1	352	13	H87464	YW17E12.s1 Homo sapien	0.00e+00
c 27	298	22.9	380	13	N30290	YW69F05.s1 Homo sapien	0.00e+00
c 28	297	22.8	526	25	AA393716	zt71H09.r1 Soares test	0.00e+00
c 29	285	22.7	427	13	N27111	YW75H12.s1 Homo sapien	0.00e+00
c 30	283	22.5	386	16	H94451	YW55G08.s1 Soares plac	0.00e+00
c 31	285	22.5	319	13	H87631	YW17E12.s1 Homo sapien	0.00e+00
c 32	280	21.9	329	13	H87156	YW15B04.s1 Homo sapien	0.00e+00
c 33	276	21.2	311	10	T47334	Yb10E11.s1 Homo sapien	0.00e+00
c 34	273	21.0	284	13	H93656	YW55E11.s1 Homo sapien	0.00e+00
c 35	268	20.6	303	13	H86993	YW15B10.s1 Homo sapien	0.00e+00
c 36	259	19.9	291	10	T90191	Yd38G09.s1 Homo sapien	0.00e+00
c 37	251	19.3	266	13	H93668	YW55G12.s1 Homo sapien	0.00e+00
c 38	245	18.8	251	19	AA330413	EST34462 Embryo, 6 wee	0.00e+00
c 39	239	18.4	278	10	T49170	Yb09G02.r1 Homo sapien	0.00e+00
c 40	240	18.4	519	23	C18044	Human placenta cdna 5	0.00e+00
c 41	235	18.1	248	16	H95381	YW60B07.s1 Soares plac	0.00e+00
c 42	230	17.7	412	12	T29543	EST83815 Homo sapiens	0.00e+00
c 43	224	17.2	244	16	H94107	YW58H09.s1 Soares plac	0.00e+00
c 44	224	17.2	360	14	HSC32B021	H. sapiens partial cdn	0.00e+00
c 45	219	16.8	255	11	R63352	Y107H10.s1 Homo sapien	0.00e+00

#### ALIGNMENTS

RESULT	LOCUS	1	N32759	601 bp	mRNA	EST	10-JAN-1996
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DEFINITION YW91B05.s1 Homo sapiens CDNA clone 259569 3' similar to gb:J00117  
 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);

ACCESSION N32759  
 GI153158

KEYWORDS

SOURCE

human clone-259569 primer-m13 -40 forward library-Soares placenta  
 809weeks 2NDHP8CO9W vector-p173D (Pharmacia) with a modified  
 polylinker host-DH10B (ampicillin resistant) Raitel-Not I  
 Raitel2-Eco RI two placentae: one from 8 weeks and another from 9  
 weeks post conception. 1st strand cdna was primed with a Not I -  
 Oligo(dT) primer  
 [5'-TGTACCACCTGACGTGAGCGCGCGGCGGATTTTCTTTT-3']  
 double-stranded cdna was size selected, ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I and Eco  
 RI sites of a modified pT73 vector (Pharmacia). Library  
 constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
 Eutheria; Archonta; Primates; Cetartihini; Homnidae; Homo.  
 1 (bases 1 to 601)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Holtman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rolfing,T., Soares,M., Tan,F.,  
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.

TITLE The Washu-Merck EST Project  
 JOURNAL Unpublished (1995)  
 COMMENT

Contact: Wilson RK  
 Washu-Merck EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence stops: 387  
Source: IMAGE Consortium, LNLN  
This clone is available royalty-free through LNLN; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
location/Qualifiers

FEATURES  
source 1. .601  
/organism="Homo sapiens"  
/clone="259569"

BASE COUNT 112 a 154 c 219 g 110 t 6 others  
ORIGIN

Query Match 30.5%; Score 397; DB 13; Length 601;  
Best Local Similarity 97.9%; Pred. No. 0.00e+00;  
Matches 411; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Db 17 TTATTGTGGAGGATCGGGGTGTCCGAGGGCCCGGAGTCGGATGGCTTGAAGGCT 76  
|||||  
CP 1289 TTATTGTGGAGGATCGGGGTGTCCGAGGGCCCGGAGTCGGATGGCTTGAAGGCT 1230  
|||||  
Db 77 GGGGGGAGGGCCCTTTAGAGAGAGAGAGTCTGGAAGCGGGGGTCATCAGAGTCAAGG 136  
|||||  
CP 1229 GGGGGGAGGGCCCTTTAGAGAGAGAGAGTCTGGAAGCGGGGGTCATCAGAGTCAAGG 1170  
|||||

Db 137 GTGTCCTTGGGAGCCG-GCAGTCAGTGTGCTCGGCGGCGAGAGTCAGATTTACAGCT 195  
|||||  
CP 1169 GTGTCCTTGGGAGCCCGCGAGTCAGTGTGCTCGGCGGCGAGAGTCAGATTTACAGCT 1110  
|||||

Db 196 GAGAGCCAGCGCGTAGAGAGACACAGGGGTTCCAGCCCGCGGCGAGCCAAAGGAGCCGAT 255  
|||||  
CP 1109 GAGAGCCAGCGCGTAGAGAGACACAGGGGTTCCAGCCCGCGGCGAGCCAAAGGAGCCGAT 1050  
|||||

Db 256 GGACTCGAAGCGCATCGCGGTAGTTGCACACCACTGAGGCGGCGGCAAGCC 315  
|||||  
CP 1049 GGACTCGAAGCGCATCGCGGTAGTTGCACACCACTGAGGCGGCGGCAAGCC 990  
|||||

Db 316 TTGCAGACGCGGGGTATGAGGGGGAGTAGCGGGGACAGATGGTGGTTGAGAGGTGAT 375  
|||||  
CP 989 CTGCAGACGCGGGGTATGAGGGGGAGTAGCGGGGACAGATGGTGGTTGAGAGGTGAT 930  
|||||

Db 376 GCACACGCGGCGCGCTCTCTCTCCACAGCCAGGGTGGCATTTGATGGGGCGCACCGTGG 435  
|||||  
CP 929 GCACACGCGGCGCGCTCTCTCTCCACAGCCAGGGTGGCATTTGATGGGGCGCACCGTGG 870  
|||||

RESULT 2 N30276 537 bp mRNA EST 05-JAN-1996  
LOCUS  
DEFINITION YW69404.s1 Homo sapiens cDNA clone 257479 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.  
ACCESSION N30276  
NID 91148796  
KEYWORDS  
SOURCE human clone=257479 primer=m13 -40 forward library=Soares placenta  
800weeks 2bhp8to9w vector=PT73D (Pharmacia) with a modified  
polylinier host-DH10B (ampicillin resistant) Ks1tel-Not I  
Ks1tel-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
019g(dt) primer  
[5'-TGTTACCACTGGAAGTGGAGCGGCGGATTTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library  
constructed by Bento Soares and M. Fatima Bernaldo.

## ORGANISM

Homo sapiens  
Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 537)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Merre, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)

## TITLE

CONTACT: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
High quality sequence stops: 313  
Source: IMAGE Consortium, LNLN  
This clone is available royalty-free through LNLN; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
location/Qualifiers

FEATURES  
source 1. .537  
/organism="Homo sapiens"  
/clone="257479"

BASE COUNT 98 a 145 c 201 g 90 t 3 others  
ORIGIN

Query Match 30.1%; Score 391; DB 13; Length 537;  
Best Local Similarity 96.2%; Pred. No. 0.00e+00;  
Matches 426; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

Db 17 TTATTGTGGAGGATCGGGGTGTCCGAGGGCCCGGAGTCGGATGGCTTGAAGGCT 76  
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CP 1289 TTATTGTGGAGGATCGGGGTGTCCGAGGGCCCGGAGTCGGATGGCTTGAAGGCT 1230  
|||||

Db 77 GGGGGGAGGGCCCTTTAGAGAGAGAGAGTCTGGAAGCGGGGGTCATCAGAGTCAAGG 136  
|||||  
CP 1229 GGGGGGAGGGCCCTTTAGAGAGAGAGAGTCTGGAAGCGGGGGTCATCAGAGTCAAGG 1170  
|||||

Db 137 GTGTCCTTGGGAGCCG-GCAGTCAGTGTGCTCGGCGGCGAGAGTCAGATTTACAGCT 195  
|||||  
CP 1169 GTGTCCTTGGGAGCCCGCGAGTCAGTGTGCTCGGCGGCGAGAGTCAGATTTACAGCT 1110  
|||||

Db 196 GAGAGCCAGCGCGTTAGAGACACAGGGGTTCCAGCCCGCGGCGAGCCAAAGGAGCCGAT 254  
|||||  
CP 1109 GAGAGCCAGCGCGTTAGAGACACAGGGGTTCCAGCCCGCGGCGAGCCAAAGGAGCCGAT 1051  
|||||

Db 255 TGGACTGGAAGCGCATCGCGGTAGTTGCACACCACTGAGGCGGCGGCAAGCC 314  
|||||  
CP 1050 TGGACTGGAAGCGCATCGCGGTAGTTGCACACCACTGAGGCGGCGGCAAGCC 991  
|||||

Db 315 CCTCGACACGCGGGGTGATGTGGGCGAGTAAACCGGACAGATGTGTGTGACGGTG 374  
|||||  
CP 990 CC-TGCAGCACAGCGGGGTGATGTGGGCGAGTAAACCGGACAGATGTGTGTGACGGTG 932  
|||||

Db 375 ATGCACAGGGGGAGCGCTCTCTCTCCACAGCCAGGGTGGCATTTGAGGGCGGCAAGCT 434  
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CP 931 ATGCACAGGGGGAGCGCTCTCTCTCCACAGCCAGGGTGGCATTTGAGGGCGGCAAGCT 872  
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Db 435 GGCNAACGCGCTCTTGGATGCC 457  
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CP 871 GGCNAACGCGCTCTTGGATGCC 849  
|||||

RESULT 3 N32604 564 bp mRNA EST 10-JAN-1996  
LOCUS  
DEFINITION YW95403.s1 Homo sapiens cDNA clone 259973 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.  
ACCESSION N32604  
NID 91153003  
KEYWORDS  
SOURCE human clone=259973 primer=m13 -40 forward library=Soares placenta



8to9weeks 2Nbp8to9w vector-pT73D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) RstetI-Not I Rstet2-Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cDNA was primed with a Not I - 0190(dT) primer  
 [5'-TGTACCAATCTGAAGTGGAGCGGCCGCGATTCTTTTCTTTTCTTTT-3'],  
 double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

## REFERENCE

1 (bases 1 to 564)

Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

## TITLE

The WashU-Merck EST Project

## JOURNAL

Unpublished (1995)

## COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

High quality sequence stops: 364

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Location/Qualifiers

1. 564

/organism="Homo sapiens"

/clone="25973"

&lt;1. &gt;564

MRNA

BASE COUNT

103 a 148 c 206 g 99 t 8 others

ORIGIN

Query Match

Best Local Similarity 97.28; Score 387; DB 13; Length 564;

Matches 413; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

Db

17 TTATTGTGGAGATGGGGTGTCCGAGGGCCCGGGAGTCGGATGTGGAAGGCT 76

CP 1289 TTTATTGGAGATGGGGTGTCCGAGGGCCCGGGAGTCGGATGTGGAAGGCT 1230

Db

77 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCTGGAAGCGGGGCTCATCAAGTCAAGG 136

CP 1229 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCTGGAAGCGGGGCTCATCAAGTCAAGG 1170

Db

137 GTGGTCTTTGGACCCC-GCAGTCAGTGTGCTGCGGGCGGACAGTGCACATTGACAGCT 195

CP 1169 GTGGTCTTTGGACCCC-GCAGTCAGTGTGCTGCGGGCGGACAGTGCACATTGACAGCT 1110

Db

196 GAGAGCCAGGGGCTAG 255

CP 1109 GAGAGCCAGGGGCTAG 1050

Db

256 GGAAGTGAAG 315

CP 1049 GGAAGTGAAG 990

Db

316 CTTCGAG 374

CP 989 CT-GCAG 931

Db

375 TGCACAGGGGAG 434

CP 930 TGCACAGGGGAG 871

Db 435 GCCNA 439

CP 870 GACCA 866

RESULT 4

LOCUS N30036 548 bp mRNA EST 05-JAN-1996

DEFINITION yw80b11.s1 Homo sapiens cDNA clone 258525 3' similar to gb:U00117

CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN);

ACCESSION N30036

KEYWORDS NID

SOURCE EST

human clone-258525 primer-m13 -40 forward library--Soares placenta

8to9weeks 2Nbp8to9w vector-pT73D (Pharmacia) with a modified

polylinker host-DH10B (ampicillin resistant) RstetI-Not I

Rstet2-Eco RI two placentae: one from 8 weeks and another from 9

weeks post conception. 1st strand cDNA was primed with a Not I -

0190(dT) primer

[5'-TGTACCAATCTGAAGTGGAGCGGCCGCGATTCTTTTCTTTTCTTTT-3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters

(Pharmacia), digested with Not I and cloned into the Not I and Eco

RI sites of a modified pT73 vector (Pharmacia). Library

constructed by Bento Soares and M. Fatima Bonaldo.

Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 548)

Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

CONTACT: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

High quality sequence stops: 333

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Location/Qualifiers

1. 548

/organism="Homo sapiens"

/clone="258525"

<1. >548

MRNA

BASE COUNT

99 a 143 c 206 g 93 t 7 others

ORIGIN

Query Match

Best Local Similarity 97.68; Score 385; DB 13; Length 548;

Matches 413; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

Db

18 TTATTGTGGAGATGGGGTGTCCGAGGGCCCGGGAGTCGGATGTGGAAGGCT 77

CP 1289 TTTATTGGAGATGGGGTGTCCGAGGGCCCGGGAGTCGGATGTGGAAGGCT 1230

Db

78 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCTGGAAGCGGGGCTCATCAAGTCAAGG 137

CP 1229 GGGGGAGGGGCTTTGAGAGAGAGAGTCTCTGGAAGCGGGGCTCATCAAGTCAAGG 1170

Db

138 GTGGTCTTTGGACCCC-GCAGTCAGTGTGCTGCGGGCGGACAGTGCACATTGACAGCT 196

CP 1169 GTGTCCTTGGAGACCCCGGACATCAGTGTGCTGCGGCGGACAGATGCAATTGACAGCT 1110

Db 197 GAGAGCCACGGCGTAGAGACACGGGGTTCACGGCGCGGCAAGCCATGGAGCCGGA 256  
|||||  
CP 1109 GAGAGCCACGGCGTAGAGACACGGGGTTCACGGCGCGGCAAGCCGGA 1051  
|||||

Db 257 TGGAGTCGAAGCGGCATCGGGGTAGTTGACACACCACTGAGGGCGCGGCAAGACCN 316  
|||||  
CP 1050 TGGATTCGAAGCGGCATCGGGGTAGTTGACACACCACTGAGGGCGCGGCAAGACCC 991  
|||||

Db 317 CCTGACAGACGGGGGTATGTTGGGGAGTAGAGGGGCAAGATGGTGTGACAGT 376  
|||||  
CP 990 CCT-GCA-GCACGCGGGATGTTGGGGAGTAGAGGGGCAAGATGGTGTGACAGT 933  
|||||

Db 377 GATGACACGGGGGACCGCTCTCTCCACAGCCAGGGTGGCATTTGATGGGGCGGACCG 436  
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CP 932 GATGACACGGGGGACCGCTCTCTCCACAGCCAGGGTGGCATTTGATGGGGCGGACCG 873  
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Db 437 TGG 439  
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CP 872 TGG 870

RESULT 5  
LOCUS N29730 593 bp mRNA EST 05-JAN-1996

DEFINITION yw78h03.a1 Homo sapiens cDNA clone 258389 3' similar to gb:J00117  
CHORIGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN).  
N29730  
g1148250

ACCESSION  
NID  
KEYWORDS  
SOURCE

human clone-258389 primer-m13 -40 forward library-Soares placenta  
8to9weeks 2NBHP8to9W vector-pT73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) RsfI-e1-Not I  
RsfI-e2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCGCGGATTTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library  
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
I (bases 1 to 593)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The Washu-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Contact: Wilson RK  
Washu-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel.: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 368  
Source: IMAGE Consortium, LBNL  
This clone is available royalty-free through LBNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Location/Qualifiers  
1..593  
/organism="Homo sapiens"  
/clone="258389"  
<1..>593

FEATURES  
source

BASE COUNT 109 a 151 c 216 g 111 t 6 others

ORIGIN

Query Match 29.4%; Score 383; DB 13; Length 593;  
Best Local Similarity 95.3%; Pred. No. 0.00e+00;  
Matches 422; Conservative 0; Mismatches 17; Indels 4; Gaps 4;

Db 18 TTATTTGGAGAGATCGGGGTGTCGAGGGCCCGGAGTGGGATGGCTTGAAGGCT 77  
|||||  
CP 1289 TTATTTGGAGAGATCGGGGTGTCGAGGGCCCGGAGTGGGATGGCTTGAAGGCT 1230  
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Db 78 GGGGGGAGGGGCTTTGAGAAAGAGAGTCTTGAAAGGGGGGTTCATACAGTCAAGG 137  
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CP 1239 GGGGGGAGGGGCTTTGAGAAAGAGAGTCTTGAAAGGGGGGTTCATACAGTCAAGG 1170  
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Db 138 GTGGCTCTTGGAGACCC-GCAGTCAGTGTGCTGGGGGGGAGAGTGCATTGACAGT 196  
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CP 1169 GTGTCCTTGGAGACCCCGGACATGATGTTCTGCGGGGCAAGATGCAATTGACAGT 1110  
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Db 197 GAGAGCCACGGCGTAGAGACACGGGGTTCACGCCCGGNGG-CAGCCAGGAGCCGAGT 255  
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CP 1109 GAGAGCCACGGCGTAGAGACACGGGGTTCACGCCCGGNGG-CAGCCAGGAGCCGAGT 1050  
|||||

Db 256 GGACTCGAAGCGGCATCGCGGTAGTTGCACACCACTGAGGAGGGCGCAAGCCAC 315  
|||||  
CP 1049 GGACTCGAAGCGGCATCGCGGTAGTTGCACACCACTGAGGAGGGCGGCAAGCCAC 990  
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Db 316 CTGACAGCAGGGGGGTATGTTGGGGAGTAGAGCGGCAAGATGGTGTGACGGTGA 375  
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CP 989 CTGACAGCAGGGGGGTATGTTGGGGAGTAGAGCGGCAAGATGGTGTGACGGTGA 931  
|||||

Db 376 TGCACACGGGGGACCGCTCTCTCCACAGCCAGTGGCATTTGATGGGGCGGACCGT 435  
|||||  
CP 930 TGCACACGGGGGACCGCTCTCTCTCCACAGCCAGTGGCATTTGATGGGGCGGACCGT 872  
|||||

Db 436 GCCCAGCGGCTCTTGGATGCC 458  
|||||  
CP 871 GGACCAGCCACGATGTGTGCC 849  
|||||

RESULT 6  
LOCUS N32233 442 bp mRNA EST 10-JAN-1996

DEFINITION yw81f08.a1 Homo sapiens cDNA clone 258663 3' similar to gb:J00117  
CHORIGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN).  
N32233  
g1152632

ACCESSION  
NID  
KEYWORDS  
SOURCE

human clone-258663 primer-m13 -40 forward library-Soares placenta  
8to9weeks 2NBHP8to9W vector-pT73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) RsfI-e1-Not I  
RsfI-e2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCGCGGATTTTTTTTTTTTTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT73 vector (Pharmacia). Library  
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.  
I (bases 1 to 442)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The Washu-Merck EST Project  
Unpublished (1995)

TITLE  
JOURNAL  
COMMENT

Contact: Wilson RK

Washu-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu

High quality sequence stops: 364  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Location/Qualifiers

source  
1. .442  
/organism="Homo sapiens"  
/clone="258663"

BASE COUNT 85 a 110 c 174 g 68 t 5 others  
ORIGIN

Query Match 29.1%; Score 379; DB 13; Length 442;  
Best Local Similarity 94.6%; Pred. No. 0.00e+00;  
Matches 402; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

Db 17 TTATTGTGGAGATCGGGTGTCCAGAGGCCCGGAGTCCGGATGAGCTTGGAGGCT 76  
|||||  
Cp 1289 TTATTGTGGAGATCGGGTGTCCAGAGGCCCGGAGTCCGGATGAGCTTGGAGGCT 1230  
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Db 77 GGGGGGGGGGCTTTAGAGAGAGAGTCTGGAGAGGGGGCTCATCAGTCAAGG 136  
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Cp 1229 GGGGGGGGGGCTTTAGAGAGAGAGTCTGGAGAGGGGGCTCATCAGTCAAGG 1170  
|||||

Db 137 GTGGTCTTGGAGAGCCCGCAAGTGTGGTGTGGGGGAGAGTGCACATTGAGACG 196  
|||||

Cp 1169 GTGGTCTTGGAGAGCCCGCAAGTGTGGTGTGGGGGAGAGTGCACATTGAGACG 1111  
|||||

Db 197 TGAGAGCCAGGGGTAGAGACCAAGGGGTTCACGCCGCGAGCAGCANGAGAGCCGGA 256  
|||||

Cp 1110 TGAGAGCCAGGGGTAGAGACCAAGGGGTTCACGCCGCGAGCAGCANGAGAGCCGGA 1091  
|||||

Db 257 TGGACTGGAAGCCGACATCGCGGTAGTTGCACACACCTGAGGAGGCGCAAGACAC 316  
|||||

Cp 1050 TGGACTGGAAGCCGACATCGCGGTAGTTGCACACACCTGAGGAGGCGCGAGACCC 991  
|||||

Db 317 CCGGACGAGCGGGGTATGATGGGGAGTAAACGGGACAGAGTGTGTGACGGTNA 376  
|||||

Cp 990 CCGGACGAGCGGGGTATGATGGGGAGTAAACGGGACAGAGTGTGTGACGGTGA 931  
|||||

Db 377 TGCACAGGGGAGCCCTCTTCACACAGCAGAGTGGATGATGGGGCGAGGCTG 436  
|||||

Cp 930 TGCACAGGGGAGCCCTCTTCACACAGCAGAGTGGATGATGATGGGGCGAGGCTG 871  
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Db 437 GCCCA 441  
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Cp 870 GACCA 866  
|||||

RESULT 7  
LOCUS N27302 473 bp mRNA EST 29-DEC-1995

DEFINITION yw71f12.s1 Homo sapiens cDNA clone 257711 3' similar to gb:J00117  
CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);.

ACCESSION N27302  
MID 91141650  
KEYWORDS  
SOURCE

human clone-257711 primer-m13 -40 forward library-Soares placenta  
8c9yweeks 2mbp8c10m vector-PT73D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) Rstrel-Not I  
Rstrel2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTTACCAATCTGAGTGGAGCGGCCGATTTTGTTTT-3']  
double-stranded cDNA was size selected, ligated to Eco RI adapters  
(Pharmacia), digested with Not I and cloned into the Not I and Eco  
RI sites of a modified pT773 vector (Pharmacia). Library

## ORGANISM

constructed by Bento Soares and M. Fatima Bonaldo.  
Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 473)

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Ritzlin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Woldmann, P. and  
Wilson, R.

TITLE  
JOURNAL  
COMMENT  
The Washu-Merck EST Project  
Unpublished (1995)

## COMMENT

Contact: Wilson RK  
Washu-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu

High quality sequence stops: 225  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.

## FEATURES

## source

1. .473  
/organism="Homo sapiens"  
/clone="257711"

BASE COUNT 87 a 122 c 182 g 76 t 6 others  
ORIGIN

Query Match 29.1%; Score 379; DB 13; Length 473;  
Best Local Similarity 95.5%; Pred. No. 0.00e+00;  
Matches 402; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

Db 18 TTATTGTGGAGATCGGGTGTCCAGAGGCCCGGAGTCCGGATGAGCTTGGAGGCT 77  
|||||

Cp 1289 TTATTGTGGAGATCGGGTGTCCAGAGGCCCGGAGTCCGGATGAGCTTGGAGGCT 1230  
|||||

Db 78 GGGGGGGGGGCTTTAGAGAGAGAGTCTGGAGAGGGGGGTCATCAGTCAAGG 137  
|||||

Cp 1229 GGGGGGGGGGCTTTAGAGAGAGAGTCTGGAGAGGGGGGTCATCAGTCAAGG 1170  
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Db 138 GTGGTCTTGGAGAGCCCGCAAGTGTGGTGTGGGGGAGAGTGCACATTGAGACG 197  
|||||

Cp 1169 GTGGTCTTGGAGAGCCCGCAAGTGTGGTGTGGGGGAGAGTGCACATTGAGACG 1110  
|||||

Db 198 GAGAGCCAGGGGTAGAGACCAAGGGGTTCACGCCGCGGCGG -CAGCAGGAGGCGGAT 256  
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Cp 1109 GAGAGCCAGGGGTAGAGACCAAGGGGTTCACGCCGCGGCGGCGGAGGCGGAT 1050  
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Db 257 GGAATCAAGCCAGATCGGGGTAGTTCACACACCACTGAGGAGGCGGCAAGACAC 316  
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Cp 1049 GGAATCAAGCCAGATCGGGGTAGTTCACACACCACTGAGGAGGCGGCAAGACAC 990  
|||||

Db 317 TTGACAGCCCGGGTATGATGGGGAGTANCCGGGACAGATGGTGTNNACGGTGA 376  
|||||

Cp 989 TTGACAGCCCGGGTATGATGGGGAGTANCCGGGACAGATGGTGTNNACGGTGA 931  
|||||

Db 377 TGCACAGGGGAGCCCGCTTTCACACAGCAGAGTGGATGATGGGGCGGACCGCTN 436  
|||||

Cp 930 TGCACAGGGGAGCCCGCTTTCACACAGCAGAGTGGATGATGGGGCGGACCGCTG 871  
|||||

Db 437 G 437  
|||||

Cp 870 G 870  
|||||

RESULT 8  
LOCUS N30831 566 bp mRNA EST 05-JAN-1996

DEFINITION yw70b04.s1 Homo sapiens cDNA clone 257551 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN); .  
ACCESSION N30831  
NID g1149351  
KEYWORDS EST.  
SOURCE human clone-257551 primer-m13 -40 forward library-Soares placenta  
8to9weeks 2NDHP8to9W vector-p173D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) Ralte1-Not I  
Ralte2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTTCACATCTCAAGTGGAGCGCCGCGCATTTTCTTTTCTTTT-3']  
(Pharmacia), digested with Not I and ligated into the Not I and Eco  
RI sites of a modified p173 vector (Pharmacia). Library  
constructed by Bento Soares and M. Fatima Bonaldo.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 566)  
Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Merri, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence stops: 400  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source  
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/organism="Homo sapiens"  
/clone="257551"  
BASE COUNT 103 a 148 c 209 g 100 t 6 others  
ORIGIN  
Query Match 29.1%; Score 379; DB 13; Length 566;  
Best Local Similarity 96.7%; Pred. No. 0.00e+00;  
Matches 408; Conservative 0; Mismatches 11; Indels 3; Gaps 3;  
Db 17 TTATTGTGGAGAGTGGGGTGTCCAGAGGCCCGGAGTGGGATGACTTGAAGGCT 76  
CP 1289 TTATTGTGGAGAGTGGGGTGTCCAGAGGCCCGGAGTGGGATGACTTGAAGGCT 1230  
Db 77 GGGGGAGGGGCTTGAAGAGAGAGTCTTGAAGCGGGGGTCTATCAGAGTCAAGG 136  
CP 1229 GGGGGAGGGGCTTGAAGAGAGAGTCTTGAAGCGGGGGTCTATCAGAGTCAAGG 1170  
Db 137 GTGTGCTTGGG-CGCCCGAGTCACTGTGTGTGGGGGAGAGAGTCACTTGAAGGCT 195  
CP 1169 GTGTGCTTGGGAGCCCGGAGTCACTGTGTGTGGGGGAGAGAGTCACTTGAAGGCT 1110  
Db 196 GAGAGCCAGGCTTGAAGAGAGAGAGGAGTCACTTGAAGCGGGGAGAGAGAGGAGAGG 255  
CP 1109 GAGAGCCAGGCTTGAAGAGAGAGAGGAGTCACTTGAAGCGGGGAGAGAGGAGAGG 1051  
Db 256 TGGAGTCAAG 315  
CP 1050 TGGAGTCAAG 992

Db 316 CCTGCAGACAGCGGGTCACTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375  
CP 991 CCTGCAGACAGCGGGTCACTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 932  
Db 376 ATGCACAGCGGGAG 435  
CP 931 ATGCACAGCGGGAG 872  
Db 436 GG 437  
CP 871 GG 870  
RESULT 9  
LOCUS N31955 563 bp mRNA EST 10-JAN-1996  
DEFINITION yw89a07.s1 Homo sapiens cDNA clone 259380 3' similar to gb:J00117  
CHORIOGNADOTROPIN BETA CHAIN PRECURSOR (HUMAN); .  
ACCESSION N31955  
NID g1152354  
KEYWORDS EST.  
SOURCE human clone-259380 primer-m13 -40 forward library-Soares placenta  
8to9weeks 2NDHP8to9W vector-p173D (Pharmacia) with a modified  
polylinker host-DH10B (ampicillin resistant) Ralte1-Not I  
Ralte2-Eco RI two placentae: one from 8 weeks and another from 9  
weeks post conception. 1st strand cDNA was primed with a Not I -  
oligo(dT) primer  
[5'-TGTTCACATCTCAAGTGGAGCGCCGCGCATTTTCTTTTCTTTT-3']  
(Pharmacia), digested with Not I and ligated into the Not I and Eco  
RI sites of a modified p173 vector (Pharmacia). Library  
constructed by Bento Soares and M. Fatima Bonaldo.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;  
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;  
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;  
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 563)  
Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Merri, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence stops: 335  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source  
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/organism="Homo sapiens"  
/clone="259380"  
BASE COUNT 101 a 148 c 208 g 103 t 3 others  
ORIGIN  
Query Match 29.0%; Score 377; DB 13; Length 563;  
Best Local Similarity 97.4%; Pred. No. 0.00e+00;  
Matches 418; Conservative 0; Mismatches 5; Indels 6; Gaps 6;  
Db 17 TTATTGTGGAGAGTGGGGTGTCCAGAGGCCCGGAGTGGGATGAGGCTTGAAGGCT 76  
CP 1289 TTATTGTGGAGAGTGGGGTGTCCAGAGGCCCGGAGTGGGATGAGGCTTGAAGGCT 1230

DEFINITION	LOCUS	10	bp	EST	05-JAN-1996
CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN):	N30684	479	bp	EST	05-JAN-1996
Accession	N30684				
KeyWords	g1149204				
Source	human clone-258295 primer-m13 -40 forward library-Soares placenta				
ORGANISM	homo sapiens				
REFERENCE	15-757TTCACATCGTGAAGTGGAGCGCGCGCATTTTCTTTTCTTTT-3'}				
AUTHORS	Haller, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Merri, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.				
TITLE	The WashU-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence stops: 333 Source: IMAGE Consortium, LNLN This clone is available royalty-free through LNLN; contact the				

FEATURES	IMAGE Consortium (info@image.llnl.gov) for further information.
SOURCE	location/Qualifiers 1..479 /organism="Homo sapiens" /clone="258295"
MRNA	<1..>479
BASE COUNT	86 a 122 c 184 g 79 t 8 others
ORIGIN	
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Best Local Similarity	96.0%; Pred. No. 0.00e+00;
Matches	403; Conservative 0; Mismatches 14; Indels 3; Gaps 3
Db	17 TTATTGTGGAGAGATCGGGGTGTCTCCGAGGGCCCCGGGAGTGGGATGGGCTTGGAAAGCT 76
Cp	1289 TTATTGTGGAGAGATCGGGGTGTCTCCGAGGGCCCCGGGAGTGGGATGGGCTTGGAAAGCT 1230
Db	77 GGGGGGAGGGGCGCTTTGAGGAAGAGAGATCCCTGGAAAGGGGGGGTCAATCAGACGTAAAGG 136
Cp	1229 GGGGGGAGGGGCGCTTTGAGGAAGAGAGATCCCTGGAAAGGGGGGGTCAATCAGACGTAAAGG 1170
Db	137 GTGGCTCTTGGGACCCC-GCAGTCAGTGTGTCTGGCGGCGAGAGTGCACATTGACAGCT 195
Cp	1169 GTGGCTCTTGGGAGACCCCGGAGTCAAGTGTGTGTGGGGCGAGAGTGCACATTGACAGCT 1110
Db	196 GAGAGCCAGCGCNTAGAGACCAAGGGGTTACAGCCCGCGGCGAGCCAGCCAGAGCCCGGAT 255
Cp	1109 GAGAGCCAGCGCGTGTAGAGACCAAGGGGTTACAGCCCGCGGCGAGCCAGAGCCCGGAT 1050
Db	256 GGACTCGAAGGCGCANTATCGCGTATTTCCACACACCTGAGGCAGAGGC-GCGAGACCCC 314
Cp	1049 GGACTCGAAGGCGCAGATCGCGTATTTCCACACACCTGAGGCAGAGGC-CGCGAGAGCCCC 990
Db	315 TTGCAGCAGCGGGGTCATGTGGGGCAGTAGCGGCGACAGATGTGTGTAAAGGTGAT 374
Cp	989 CTGCAGCAGCGGGGTCATGTGGGGCAGTAGCGGCGACAGATGTGTGTAAAGGTGAT 930
Db	375 GCACAGGGGGGAGCCCTCTCTCCACAGCCAGGGGTGGNATTTGATGGGGCGGCACNTTG 434
Cp	929 GCACAGGGGGGAGCCCTCTCTCTCCACAGCCA-GGGTGGCATTGATGGGGCGGCACCGTG 871
RESULT	11
LOCUS	AA400910 473 bp mRNA EST 12-AUG-1997
DEFINITION	z711h09.s1 Soares testis NHT Homo sapiens cDNA clone 727841 3' similar to gb:J00117 CHORIOGNADOTROBIN BETA CHAIN PRECURSOR (HUMAN);
ACCESSION	AA400910
NID	92054783
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 473) Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S., Knabe,T., Lacy,M., Le,N., Lennon,G., Marr,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
TITLE	Washington University School of Medicine
JOURNAL	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
COMMENT	Tel: 314 286 1800 Fax: 314 286 1810 Email: est@atson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 640 Std Error: 0.00



RESULT 13  
LOCUS AA644163 526 bp mRNA EST 27-OCT-1997

DEFINITION af62d08.s1 Soares Nhmpu S1 Homo sapiens cDNA clone 1046607 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);

ACCESSION AA644163  
NID 92569381  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 526)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project Unpublished (1997)

TITLE JOURNAL  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40m13 fwd. ET from Amerisham  
High quality sequence stop: 335.  
Location/Qualifiers  
1.526  
/organism="Homo sapiens"  
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI. Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NBHPV, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."  
/db\_xref="taxon:9606"  
/clone\_lib="Soares Nhmpu S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"  
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BASE COUNT 100 a 140 c 201 g 85 t

ORIGIN

Query Match 28.2%; Score 367; DB 28; Length 526;  
Best Local Similarity 97.1%; Pred. No. 0.00e+00;  
Matches 409; Conservative 0; Mismatches 6; Indels 6; Gaps 6;

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CP 1289 TTTATTTGGAGAGATGGGGTGTCCGAGGAGCCCGGAGTGCAGTGGAGGCT 1230  
|||||  
DB 76 GGCAGAGAGGGGCTTTAAGAGAGAGAGTCTCGAAGCGGGGGTTCATCAGAGTCAAGG 135  
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CP 1229 GGGGAGAGGGGCTTTGAGAGAGAGAGTCTCGAAGCGGGGGTTCATCAGAGTCAAGG 1170  
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DB 136 GTGGTCTCTTGGGAGCCCGAGAGTCAAGTGTCTGGCGGCGGAGAGTGCACATTTGACAGCT 195  
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CP 1169 GTGGTCTCTTGGGAGCCCGAGAGTCAAGTGTCTGGCGGCGGAGAGTGCACATTTGACAGCT 1110  
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DB 196 GAGAGCCAGCGGCTAGAGAGAGAGGAGTTCAGCGCGCGCGG-G-CAGCCAGAGAGCGGAGT 254

CP 1109 GAGAGCCAGCGGCTAGAGAGACCAAGCGGGGTTACAGCCCGCGGCGGAGCGCGGAT 1050  
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DB 255 GGACTCGAAGCGGACATCGCGGAGTGTTCAGACACACCTAGAGGAGCGG-C-GCAGAGACCC 313  
|||||  
CP 1049 GGACTCGAAGCGGACATCGCGGAGTGTTCAGACACACCTAGAGGAGCGCGGAGCGCC 990  
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DB 314 -TGACAGCGCGGCTATGTGTGGGAGTAGC-GGCACAGATGTGTGTGAGGAT 371  
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CP 989 CTGACAGCGCGGCTATGTGTGGGAGTAGC-GGCACAGATGTGTGTGAGGAT 930  
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DB 372 GGCACAGCGGCGGAGCGGCTCTCTCCACAGCGGAGGATGATGAGGCGG-ACCAGT 430  
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CP 929 G-CACAGCGGCGGAGCGGCTCTCTCCACAGCGGAGGATGATGAGGCGGAGCGG 871  
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DB 431 G 431  
CP 870 G 870

RESULT 14  
LOCUS AA232905 400 bp mRNA EST 06-AUG-1997

DEFINITION z146C04.s1 Soares Nhmpu S1 Homo sapiens cDNA clone 666438 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);

ACCESSION AA232905  
NID 9185917  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 400)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-Merck EST Project 1997 Unpublished (1997)

TITLE JOURNAL  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
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High quality sequence stop: 361.  
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/db\_xref="taxon:9606"  
/clone\_lib="Soares Nhmpu S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
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Best Local Similarity 97.4%; Pred. No. 0.00e+00;
Matches 376; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

D 17 TTATGTGGAGAGATCGGGGTGTCCGAGGGCCCGGAGTCGGATGGCTTGAAGCT 76
Cp 1289 TTATGTGGAGAGATCGGGGTGTCCGAGGGCCCGGAGTCGGATGGCTTGAAGCT 1230
D 77 GGGGGAGATGGCTTGTGAAGAGAGAGTCTGGAAGCGGGGGTCATCAGAGCAAGG 136
Cp 1229 GGGGGAGAGTGGCTTGTGAAGAGAGAGTCTGGAAGCGGGGGTCATCAGAGCAAGG 1170
D 137 GTGGTCTTGGAGACACCCGAGTCACTGTGTGTGGGGGGGAGGACATTCAGAGCT 196
Cp 1169 GTGGTCTTGGAGACACCCGAGTCACTGTGTGTGGGGGGGAGGACATTCAGAGCT 1110
D 197 GAGAGCCACGCGGTGAGAGACACGAGGGGTTCAGCGCGCGGGGAGCCAGAGGAGCGGAT 256
Cp 1109 GAGAGCCACGCGGTGAGAGACACGAGGGGTTCAGCGCGCGGGGAGCCAGAGGAGCGGAT 1050
D 257 GGAATCGAAGCGCAGATCGCGGTAGTTGCACACACCTGAGGAGGCGGTGAG-AGCCC 315
Cp 1049 GGAATCGAAGCGCAGATCGCGGTAGTTGCACACACCTGAGGAGGCGGTGAGAGAGCC 990
D 316 CTGCAGCAGCGCGGTGATGTTGGGGCAGTACG-GGCAGCAGATGTTGTGTACGGTGTAT 374
Cp 989 CTGCAGCAGCGCGGTGATGTTGGGGCAGTACGAGCAGATGTTGTGTACGGTGTAT 930
D 375 GCACAGGGGGCAGCCCTCTCTCCA 400
Cp 929 GCACAGGGGGCAGCCCTCTCTCCA 904

RESULT 15
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DEFINITION yv60b03.s1 Soares placenta 8to9weeks 2NHP8to9W Homo sapiens cDNA
            clone 256589.3 similar to gb:J00117 CHORIOGNADOTROBIN BETA CHAIN
            PRECURSOR (HUMAN);.
ACCESSION      H95374
NID      91103007
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
            Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
            1 (bases 1 to 419)
REFERENCE      1 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
AUTHORS      Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevisakis,E., Waterston,R., Williamson,A., Woldmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)

TITLE      The WashU-Merck EST Project
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence stops: 297
Source: IMAGE Consortium, LNLN.
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1014 Std Error: 0.00
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FEATURES
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      /note="Organ: placenta; Vector: pRT73D (Pharmacia) with a
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      strand cDNA was primed with a Not I - oligo(dT) primer [5'
      TGTATCCAAATCTGAAGTGGAGGCGCGCCGAGATTTTTTTTTTTT 3'],
      double-stranded cDNA was size selected, ligated to Eco RI
      adapters (Pharmacia), digested with Not I and cloned into
      the Not I and Eco RI sites of a modified pRT73 vector
      (Pharmacia). Library constructed by Bento Soares and
      M. Felicia Bonaldo."
      /db_xref="taxon:9606"
      /clone_id="256589"
      /dev_stage="two placentae: one from 8 weeks and another
      from 9 weeks post conception"
      /lab_host="DH10B (ampicillin resistant)"
      complement(<1..>419)
BASE COUNT      73 a 109 c 168 g 63 t 6 others
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Query Match      27.0%; Score 351; DB 16; Length 419;
Best Local Similarity 95.6%; Pred. No. 0.00e+00;
Matches 390; Conservative 0; Mismatches 13; Indels 5; Gaps 5;

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Cp 1266 CCGAGGGCCCGGGAGTGGGATGAGTGTGAAGGCTGGGGGAGGGGCTTTGAAGAG 1207
D 61 AGGAGCCCTGGAAGCGGGGGTCACTACAGTCAAGGGGTGTCTTGGAGACCCCGCAGT 120
Cp 1206 AGGAGTCTGGAAGCGGGGGTCACTACAGTCAAGGGGTGTCTTGGAGACCCCGCAGT 1147
D 121 CAGTGTCTCTGGCGGGCGNGAGTGCACATTGCACAGTCAAGAGCCAGCGGTGAGAGACCA 180
Cp 1146 CAGTGTCTCTGGCGGGCGNGAGTGCACATTGCACAGTCAAGAGCCAGCGGTGAGAGACCA 1087
D 181 CGGGGTTCAGCGCGCGGNGAGCCAGCCAGGAGCGGATGAGTCCGAAGGCGCATGCGGCT 240
Cp 1086 CGGGGTTCAGCGCGCGGNGAGCCAGCCAGGAGCGGATGAGTCCGAAGGCGCATGCGGCT 1027
D 241 TAGTTGACACACCACTGAGGAGGCGCCAGAGACNCCCTGACAGCAGCGGTTTCATGG 300
Cp 1026 -AGTTGACACACCACTGAGGAGGCGCGGCGGAGAGC-CCCTGACAGCAGCGGCT-CATGG 970
D 301 TGGGCACTAGCGGNCACAGATGTTGTGTGANGTATGCACACGGGGGACGCGCTCTCT 360
Cp 969 TGGGCACTAGCGGNCACAGATGTTGTGTGANGTATGCACACGGGGGACGCGCTCTCT 910
D 361 TNCCTCAGCAGCGAGGTGGCTTGTATGGGCGGCGGACCGTGGCCAGC 408
Cp 909 T-CTTCACAGCGCAGGTGGCATGTAT-GGGGCGGCGCAGCGTGGACAGC 864

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Search completed: Wed May 6 15:04:47 1998  
Job time : 1203 secs.



\*\*\*\*\*  
M P E R E H  
(TM)  
\*\*\*\*\*

Release 3.0.5AA John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

MPearch\_dp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed May 6 09:06:59 1998; Maspar time 10.23 Seconds  
Tabular output not generated.

Title: >US-08-804-166-8  
Description: (1-336) from US08804166.pep  
Perfect Score: 2541  
Sequence: 1 SRTSLLAFLGCLCPWLOEG.....PSLSPSPRLPGSPDPPIIPQ 336

Scoring table: PAM 150  
Gap 11

Searched: 120837 seqs, 14945562 residues

Post-processing: Minimum Match 08  
Listing first 45 summaries

Database:

a-geneseq1  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26

Statistics: Mean 32.744; Variance 136.204; scale 0.240

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
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2	2022	79.6	307	26	W33358 TBP(20-161)/hCG-beta	7.11e-192
3	1505	59.2	285	26	W33359 TBP(20-190)/hCG-alpha	8.93e-139
4	1322	52.0	371	2	R07449 Tumour Necrosis Factor	4.69e-120
5	1321	52.0	451	13	R70107 TNF-R-GBP 130 fusion	5.93e-120
6	1322	52.0	455	4	R24000 TNF-alpha 55KD receptor	4.69e-120
7	1322	52.0	455	14	R75084 p55 TNF-R	4.69e-120
8	1322	52.0	455	4	R20787 TNF-alpha binding protein	4.69e-120
9	1322	52.0	455	8	R42059 Lambda derived TNF-R	4.69e-120
10	1322	52.0	455	2	R10986 30KD TNF inhibitor protein	4.69e-120
11	1322	52.0	455	2	R11082 Human 55KD TNF-binding	4.69e-120
12	1321	52.0	900	13	R70103 TNF-R-GBP 130 fusion	5.93e-120
13	1319	51.9	309	13	R70108 TNF-R-GBP fusion protein	9.50e-120
14	1319	51.9	455	2	R07451 Human Tumour Necrosis	9.50e-120
15	1319	51.9	547	13	R70104 TNF-R-GBP fusion protein	9.50e-120
16	1319	51.9	1604	13	R70105 TNF-R-EBA 175 fusion	9.50e-120
17	1317	51.8	1245	13	R70106 TNF-R-p1. viVax Duffy	1.52e-119
18	1313	51.7	433	8	R51032 Mutant p55 tumour nec	3.89e-119
19	1313	51.7	443	8	R51033 Mutant p55 tumour nec	3.89e-119

ID	W33360	standard	Protein	336	AA.
AC	W33360				
DT	19-MAR-1998	(first entry)			
DE	TBP(20-190)/hCG-beta fusion protein.				
KW	Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;				
KM	beta subunit; hCG-beta.				
OS	Homo sapiens.				
PN	W09730161-A1.				
PD	21-AUG-1997.				
PF	20-FEB-1997; U02315.				
PR	20-FEB-1996; US-011936.				
PA	(1STP) ARS APPLIED RES SYSTEMS HOLDING NV.				
PI	Campbell RK, Chappel SC, Jameson BA;				
DR	WPI; 97-425036/39.				
DR	N-PSDB; T94022.				
PT	Hybrid dimeric protein comprising two co-expressed units - each				
PT	based on receptor or ligand and a subunit of a heterodimeric				
PS	Example: Pages 39-40; 60pp; English.				
CC	A novel fusion protein comprises 2 dimer forming co-expressed amino				
CC	acid sequences, each consisting of a homodimeric or heterodimeric				
CC	receptor chain or ligand, with ligand-receptor binding activity,				
CC	bound directly or via a peptide linker to a subunit of a				
CC	heterodimeric protein hormone capable of forming a heterodimer with				
CC	the hormone's other subunits. The fusion protein, e.g. the				
CC	thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit				
CC	(hCG-beta) fusion protein denoted by the present sequence,				
CC	significantly increases the biological activity of the hormone				
CC	component, reducing the requirement for hormone itself and the				
CC	number of injections needed.				
SQ	Sequence 336 AA;				

## ALIGNMENTS

RESULT 1  
ID W33360 standard; Protein; 336 AA.  
AC W33360;  
DT 19-MAR-1998 (first entry)  
DE TBP(20-190)/hCG-beta fusion protein.  
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;  
KM beta subunit; hCG-beta.  
OS Homo sapiens.  
PN W09730161-A1.  
PD 21-AUG-1997.  
PF 20-FEB-1997; U02315.  
PR 20-FEB-1996; US-011936.  
PA (1STP) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Campbell RK, Chappel SC, Jameson BA;  
DR WPI; 97-425036/39.  
DR N-PSDB; T94022.  
PT Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PS Example: Pages 39-40; 60pp; English.  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit  
CC (hCG-beta) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.  
SQ Sequence 336 AA;  
Query Match 100.0%; Score 2541; DB 26; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2.22e-145;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 strslilaflgclcpwloegsadvcpqgkyihpqnmslctckhstylyndpgpgd 60  
1 strslilaflgclcpwloegsadvcpqgkyihpqnmslctckhstylyndpgpgd 60  
61 tdcecgsgftasenhllrlcscskckemgvelsscvdtdtvgcgkngrhyvse 120

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QY 61 TDCRESESSFTASENHLHCLSCSKCKREMGVEISCTVDRTVCGCKRKNQRYHWSE 120
DB 121 nlfqcfncalcngtvtvhlscqekqntvctchagfflirencvscsnokkslectkiclpq 180
QY 121 NFFOCFNCISCLNGTNGVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKSLBECTKICLPQ 180
DB 181 lenvxtedsagttagagprrcrpinalavekegcpvcltnttcagcyptmtrvlgvyl 240
QY 181 IENVKGTEDSGTTAGAGPRCRPINALAVEKEGCPVCLTNTTICAGCYPTMTRVLOGVYL 240
DB 241 palpvyvcmrdrvfesirllpgcprgvnpvsvayavalscgcalcrsttdcgspkdhplt 300
QY 241 PALPQVVCNTRDVRFSIRLLPGCPRGVNPVSVAYAVALSCGALCRNSTITDCGSPKDHPLT 300
DB 301 cddprfqsassakpppslpspsrllpgpadtlpqp 336
QY 301 CDDPRFQDSSSSKAPPPSLPSPSRLLPGPSDTPILPQ 336

RESULT 2
ID W33358 standard; Protein: 307 AA.
AC W33358;
DT 19-MAR-1998 (first entry)
DE TBP(20-161)/hcg-beta fusion protein.
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;
KW beta subunit; hcg-beta.
OS Homo sapiens.
PI Campbell RK, Chappel SC, Jameson BA;
PI MPI: 97-425036/39.
DR N-PSDB: T94008.
PT Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation
PS Example: Pages 34-35; 60pp; English.
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein hormone capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotropin-beta subunit
CC (hcg-beta) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed.
SQ Sequence 307 AA.
```

```
Query Match 79.6%; Score 2022; DB 26; Length 307;
Best Local Similarity 91.4%; Pred. No. 7,11e-192;
Matches 307; Conservative 0; Mismatches 0; Indels 29; Gaps 1;
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```
DB 1 srtslilaflgllclpwlqgsadsavcpqgkyihpqmsicctckhkytlyndcpqpgd 60
QY 1 SRTSLILAFGLCLPWLQGSADSVCPQGRKYIHPQNSICCTCKHKGTYLYNDCCPGPD 60
DB 61 tdcreecsqsfasenhhlhclscskckremgveisctvdrtvccgckrknqryhwse 120
QY 61 TDCRECESSFTASENHLHCLSCSKCKREMGVEISCTVDRTVCGCKRKNQRYHWSE 120
DB 121 nlfqcfncalcngtvtvhlscqekqntvctchagfflirencvsc----- 164
QY 121 NFFOCFNCISCLNGTNGVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKSLBECTKICLPQ 180
DB 165 -----agagprrcrpinalavekegcpvcltnttcagcyptmtrvlgvyl 211
QY 165 -----agagprrcrpinalavekegcpvcltnttcagcyptmtrvlgvyl 211
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QY 181 IENVKGTEDSGTTAGAGPRCRPINALAVEKEGCPVCLTNTTICAGCYPTMTRVLOGVYL 240
DB 212 palpvyvcmrdrvfesirllpgcprgvnpvsvayavalscgcalcrsttdcgspkdhplt 271
QY 241 PALPQVVCNTRDVRFSIRLLPGCPRGVNPVSVAYAVALSCGALCRNSTITDCGSPKDHPLT 300
DB 272 cddprfqsassakpppslpspsrllpgpadtlpqp 307
QY 301 CDDPRFQDSSSSKAPPPSLPSPSRLLPGPSDTPILPQ 336
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```
RESULT 3
ID W33359 standard; Protein: 285 AA.
AC W33359;
DT 19-MAR-1998 (first entry)
DE TBP(20-190)/hcg-alpha fusion protein.
KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotropin;
KW alpha subunit; hcg-alpha.
OS Homo sapiens.
PI Campbell RK, Chappel SC, Jameson BA;
PI MPI: 97-425036/39.
DR N-PSDB: T94021.
PT Hybrid dimeric protein comprising two co-expressed units - each
PT based on receptor or ligand and a subunit of a heterodimeric
PT hormone, especially FSH, for inducing follicular maturation
PS Example: Pages 37-38; 60pp; English.
CC A novel fusion protein comprises 2 dimer forming co-expressed amino
CC acid sequences, each consisting of a homodimeric or heterodimeric
CC receptor chain or ligand, with ligand-receptor binding activity,
CC bound directly or via a peptide linker to a subunit of a
CC heterodimeric protein hormone capable of forming a heterodimer with
CC the hormone's other subunits. The fusion protein, e.g. the
CC thrombopoietin (TPO)/human chorionic gonadotropin-alpha subunit
CC (hcg-alpha) fusion protein denoted by the present sequence,
CC significantly increases the biological activity of the hormone
CC component, reducing the requirement for hormone itself and the
CC number of injections needed.
SQ Sequence 285 AA;
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```
Query Match 59.2%; Score 1505; DB 26; Length 285;
Best Local Similarity 98.0%; Pred. No. 8,93e-139;
Matches 196; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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DB 1 srtslilaflgllclpwlqgsadsavcpqgkyihpqmsicctckhkytlyndcpqpgd 60
QY 1 SRTSLILAFGLCLPWLQGSADSVCPQGRKYIHPQNSICCTCKHKGTYLYNDCCPGPD 60
DB 61 tdcreecsqsfasenhhlhclscskckremgveisctvdrtvccgckrknqryhwse 120
QY 61 TDCRECESSFTASENHLHCLSCSKCKREMGVEISCTVDRTVCGCKRKNQRYHWSE 120
DB 121 nlfqcfncalcngtvtvhlscqekqntvctchagfflirencvscsnokkslectkiclpq 180
QY 121 NFFOCFNCISCLNGTNGVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKSLBECTKICLPQ 180
DB 181 lenvxtedsagttagagapgc 200
QY 181 IENVKGTEDSGTTAGAGPRC 200
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```
RESULT 4
ID R07449 standard; Protein: 371 AA.
AC R07449;
DT 29-JAN-1991 (first entry)
DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
KW Tumour necrosis factor-binding protein; TNF-BP; TNF-receptor;
KW pTNF-BP15; infectious disease; parasitic disease; cachexia;
KW autoimmune disease; shock.
```

OS Homo sapiens.  
PN EP-393438-A.  
PD 24-OCT-1990.  
PR 06-APR-1990; 106624.  
PR 21-APR-1989; DE-913101.  
PR 21-JUN-1989; DE-920282.  
PA (BOEH) BOEHRINGER INGELHEIMINT.  
PI Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;  
DR WPI: 90-321987/43.  
DR N-PSDB: Q06282.  
PT DNA encoding TNF binding protein and TNF-receptor - used in  
PT tumour treatment and to understand mechanism to TNF action  
PS Disclosure; Fig 1(1-3); 51pp; German.  
CC Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of  
CC e.g. COS7 cells. The expressed proteins are useful  
CC prophylactically and therapeutically to control disorders which  
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
CC respiratory distress syndrome etc., or side effects of treatment with  
CC TNF-alpha). They can also be used as diagnostic reagents for  
CC assaying TNF and in study of TNF-receptor interactions.  
CC See also 006282-006285.  
SQ Sequence 371 AA:

Query Match 52.0%; Score 1322; DB 2; Length 371;  
Best Local Similarity 100.0%; Pred. No. 4,69e-120;  
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 41 davepgkxlyhpnmsicctckhkytlyndcpgpqqdtdcreesgftaenhlrhl 100  
AC ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 23 DSVCPQKXIHPONNISICTCKCHKGYLYNDGPGQDTRCCEGSGFTASENHLRHL 82  
DB 101 scskcrkmgvyeisctdrtdtvcgcrngryhwsenlfqfncslngtvhsce 160  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 83 SCSKCRKMGVYEISCTDRDVTCCGCRNQRHYSEMLFCFNCSLDNGTVHLSCE 142  
DB 161 kqntvctchagfflrenevscsnckslccklclpqlenkytedsgtt 211  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 143 KQNTVCTCHAGFFLRENEVCSCNCKSLCCKRLCLPQLENKGTEDSGTT 193

RESULT 5  
ID R70107 standard; Protein; 451 AA.  
AC R70107:  
DT 10-NOV-1995 (first entry)  
DE TNF-R-GBP 130 fusion protein.  
KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
KW red blood cell; cytokine receptor; glycophorin binding peptide 130;  
KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.  
OS Chimeric Homo sapiens.  
OS Chimeric Plasmodium falciparum.  
PN WO9506737-A.  
PN 09-MAR-1995.  
PR 01-SEP-1994; G01900.  
PR 03-SEP-1993; GB-018350.  
PR 23-AUG-1994; GB-017021.  
PA (PREN/) PRENDERGAST K F.  
PI Prendergast KF;  
DR WPI: 95-115452/15.  
DR New hybrid peptide(s) for binding cytokine(s) - comprising a  
PT malaria parasite peptide capable of binding a red blood cell and  
PT a receptor peptide.  
PS Example A: Page 53-54; 93pp; English.  
CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples  
CC of these hybrid peptides. R70107 is a fusion of tumour necrosis factor  
CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
CC and glycophorin binding protein (GBP) 130. The use of cytokine  
CC receptors not normally found on RBCs means that the cytokine can bind  
CC harmlessly to the RBC without deleterious effect. The RBC protects the  
CC hybrid peptides from excretion from the kidney, and due to steric  
CC hindrance prevents the cytokines binding to a receptor in another cell.

CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides  
CC used, others include ERA 175 (175 kDa erythrocyte binding antigen),  
CC PMMA (pre major merozoite surface antigen) and the Duffy binding  
CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on  
CC the surface of RBCs. The hybrid peptides are thus used to lower  
CC the levels of free cytokines in the circulation to reduce pathological  
CC damage.  
SQ Sequence 451 AA:

Query Match 52.0%; Score 1321; DB 13; Length 451;  
Best Local Similarity 99.4%; Pred. No. 5,93e-120;  
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 20 davepgkxlyhpnmsicctckhkytlyndcpgpqqdtdcreesgftaenhlrhl 79  
AC ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 23 DSVCPQKXIHPONNISICTCKCHKGYLYNDGPGQDTRCCEGSGFTASENHLRHL 82  
DB 80 scskcrkmgvyeisctdrtdtvcgcrngryhwsenlfqfncslngtvhsce 139  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 83 SCSKCRKMGVYEISCTDRDVTCCGCRNQRHYSEMLFCFNCSLDNGTVHLSCE 142  
DB 140 kqntvctchagfflrenevscsnckslccklclpqlenkytedsgtt 191  
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 143 KQNTVCTCHAGFFLRENEVCSCNCKSLCCKRLCLPQLENKGTEDSGTT 194

RESULT 6  
ID R24000 standard; Protein; 455 AA.  
AC R24000:  
DT 05-NOV-1992 (first entry)  
DE TNF-alpha 55kd receptor.  
KW tumour necrosis factor alpha; extracellular binding domain;  
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
KW malaria; viral meningitis; graft versus host disease;  
KW autoimmune disease; rheumatoid arthritis.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT peptide 1..40  
FT /label= signal peptide  
FT modified\_site 54..56  
FT /label= N linked glycosylation site  
FT /note= "potential"  
FT modified\_site 145..147  
FT /label= N linked glycosylation site  
FT /note= "potential"  
FT modified\_site 151..153  
FT /label= N linked glycosylation site  
FT /note= "potential"  
FT domain 212..234  
FT /label= transmembrane domain  
PN WO9207076-A.  
PN 30-APR-1992.  
PD 18-OCT-1991; G01826.  
PR 18-OCT-1990; GB-022648.  
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.  
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;  
DR WPI: 92-167156/20.  
DR N-PSDB: Q24440.  
PT New polypeptide capable of binding human TNF alpha - comprises  
PT first three cysteine-rich subdomains of TNF alpha receptor for  
PT treating autoimmune disease, septic shock, HIV etc.  
PS Example; Fig 1; 43pp; English.  
CC This sequence was deduced from human TNF-alpha cDNA isolated as in  
CC Q24440. The first 35 amino acids are generally quite hydrophobic  
CC and probably represent a signal sequence. Residues 35-40 are highly  
CC charged (DNEKR) and this is not normally found in secretory  
CC signal sequences. It is possible the receptor is processed by  
CC proteolysis after residue 40 which contains a dibasic cleavage site  
CC (KR). Hydrophathy analysis of this sequence predicts a single  
CC transmembrane domain of 23 amino acids, dividing the sequence into  
CC an extracellular domain of 171 residues and a cytoplasmic domain of  
CC 221 residues. The sequence contains a large number of cysteine

CC residues, the arrangement of which is similar to that of other cell  
 CC surface proteins, suggesting the TNF-alpha receptor is structurally  
 CC related to a family of receptors.  
 CC NOTE: - Residues 371,2 given in the sequence as T,L, are encoded by  
 CC TGG (W) and AAG (K).  
 CC See also Q24440-51, R24000, R24080-84, R27585, Q29236-8  
 SQ Sequence 455 AA;

Query Match 52.0%; Score 1322; DB 4; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.69e-120;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 41 dsvcpgkylhpgnmslccckhkgtylyndcpypgqdtcreceagsftasenhrlhcl 100  
 QY 23 DSVCPQKTYHPQNNISICCTCKHKGTLYNDCPGPGDTCRECESGSFTASENHLRCL 82  
 DB 101 scscrtremgveisctvdtdtvcgcrkngryhyseanlfqcfncslcngtyhlsce 160  
 QY 83 SCSCREKREMGVEISCTVDYDTCGCRKNQRYHYSENLFCFCNCSLCNGTYHLSCOE 142  
 DB 161 kqntvcchagffirencvscnckslcctkiclcpqienvkgtedsqtt 211  
 QY 143 KQNTVCTCHAGFFIRENDCVSCSNCKSLCCTKICLPQIENVKGTEDSGTT 193

RESULT 7  
 ID R75084 standard; Protein; 455 AA.

AC R75084; (first entry)

DE p55 TNF-R.

KW p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;  
 KM epidermal growth factor receptor; EGF-R; protease; inhibitor;  
 OS Homo sapiens.

FT key Location/Qualifiers

FT peptide 41..53 /note= "N terminus of soluble p55 TNF-R"

FT modified\_site 54..56 /note= "glycosylation site"

FT modified\_site 145..147 /note= "glycosylation site"

FT modified\_site 161..163 /note= "glycosylation site"

FT peptide 193..210 /note= "glycosylation site"

FT region 198..210 /note= "peptide used in creation of chimeras"

FT misc\_difference 201 /note= "spacer region"

FT misc\_difference 202 /note= "major C terminus for soluble p55 TNF-R"

FT misc\_difference 203 /note= "essential for shedding reaction"

FT misc\_difference 212..234 /note= "minor C terminus for soluble p55 TNF-R"

FT region 212..234 /note= "transmembrane region"

PN A09475742-A.

PD 04-MAY-1995.

PF 11-OCT-1994; 075742.

PR 12-OCT-1993; II-107268.

PA (YEDA ) YEDA RES & DEV CO LTD.

PI Backlin M, Brakebusch C, Varfolomeev E, Wallach D;

DR N-PSDB; 090513.

PT New protease capable of cleaving soluble tumour necrosis factor

PT (TNF) receptor from cell-bound TNF- receptor, useful for

PT antagonising deleterious effects of TNF.

PS Disclosure; Fig 1; 40pp; English.

CC This sequence represents human p55 tumour necrosis factor (TNF-R).

CC Expression of this receptor is regulated by shedding of the extracellular

CC receptor fragment. The p55 TNF-R can be shed in response to different

CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell

CC type. The only region of the receptor whose structure affects the

CC shedding response is the spacer region (see R75012) in the extracellular

CC domain. This region is located close to a site of cleavage of the  
 CC molecule, and links the Cys rich module to the transmembrane domain. The  
 CC spacer region of the encoded protein was used to create the chimeras  
 CC between human p55 TNF-R and murine epidermal growth factor receptor  
 CC (EGF-R) that are represented by R75007-11. This spacer region was  
 CC subjected to deletion mutations (R75013-25) and substitutions  
 CC (R75026-47). Of the spacer region, the most important residues are  
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most  
 CC important of these. The shedding of the receptor is independent of the  
 CC side chain identity of these residues, with the exception of a limited  
 CC dependence on the identity of Val 173. Mutations which alter the  
 CC conformation of the protein adversely effect the shedding process.  
 CC The mutations shown in R75013-47 were introduced in order to create an  
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R  
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in  
 CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can  
 SQ be used for enhancing TNF function.

Query Match 52.0%; Score 1322; DB 14; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.69e-120;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 41 dsvcpgkylhpgnmslccckhkgtylyndcpypgqdtcreceagsftasenhrlhcl 100  
 QY 23 DSVCPQKTYHPQNNISICCTCKHKGTLYNDCPGPGDTCRECESGSFTASENHLRCL 82  
 DB 101 scscrtremgveisctvdtdtvcgcrkngryhyseanlfqcfncslcngtyhlsce 160  
 QY 83 SCSCREKREMGVEISCTVDYDTCGCRKNQRYHYSENLFCFCNCSLCNGTYHLSCOE 142  
 DB 161 kqntvcchagffirencvscnckslcctkiclcpqienvkgtedsqtt 211  
 QY 143 KQNTVCTCHAGFFIRENDCVSCSNCKSLCCTKICLPQIENVKGTEDSGTT 193

RESULT 8

ID R20787 standard; Protein; 455 AA.

AC R20787; (first entry)

DE 11-MAY-1992 (first entry)

KW TNF-alpha binding protein.

KM Tumour necrosis factor alpha; autoimmune diseases; cachectin;

OS Homo sapiens.

FT key Location/Qualifiers

FT peptide 1..40 /note= "signal peptide"

FT peptide 41..455 /note= "mature peptide"

FT domain 30..199 /note= "extracellular domain"

FT domain 212..234 /note= "transmembrane domain"

FT modified\_site 145..147 /note= "potential N-glycosylation site"

FT modified\_site 151..153 /note= "potential N-glycosylation site"

PN G82246569-A.

PD 05-FEB-1992.

PF 15-JUN-1990; 013410.

PR 15-JUN-1990; GB-013410.

PA (CHAR-) CHARING CROSS SUNDLE.

PI Feldman M, Gray P, Turner M, Brennan F;

DR WPI; 92-043613/06.

PT New tumour necrosis factor alpha binding protein and polypeptide

PT - useful in treating cachexia, sepsis and auto immune diseases

PS Disclosure; Fig 1; 25pp; English.

CC The amino acid sequence is that of tumour necrosis factor alpha

CC binding protein which contains the extracellular domain of human TNF

CC alpha receptor. It is soluble and can be used in the regulation of

CC TNF-mediated responses by binding and sequestering the cytokine. It



FH Key Location/Qualifiers  
 FT modified\_site 54  
 FT /label= putative N-glycosylation site  
 FT modified\_site 145  
 FT /label= putative N-glycosylation site  
 FT modified\_site 151  
 FT /label= putative N-glycosylation site  
 FT modified\_site 270  
 FT /label= putative N-glycosylation site  
 FT region 212..230  
 FT /label= transmembrane region  
 FT peptide 1..28  
 FT /label= signal peptide  
 FT EP-417563-A.  
 PD 20-MAR-1991.  
 PF 31-AUG-1990; 116707.  
 PR 12-SEP-1989; CH-003319.  
 PR 08-MAR-1990; CH-000746.  
 PR 20-APR-1990; CH-001347.  
 PR (HOPE) HOFFMANN-LA ROCHE AG.  
 PA Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
 PI Schlaefer EJ;  
 DR MPI: 91-081851/12.  
 DR N-PSDB: Q10955.  
 PT Insoluble tumour necrosis factor binding proteins - and DNA  
 PT encoding them, useful in pharmaceutical prods. and for antibody  
 PT prodn.  
 PS Claim 1: Fig 1: 26pp: German.  
 CC Partial amino acid sequences were determined for the 55 and 75kd  
 CC TNF-BPs (see R11072-R11081) and oligonucleotide primers were  
 CC synthesised based on these partial sequences. The primers were used  
 CC to produce a cDNA fragment for use as a probe to screen a human  
 CC placental cDNA bank constructed in lambda gfil. Positive clones were  
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding  
 CC sequence may also contain a fragment encoding a human Ig domain.  
 CC Recombinant constructs are used to transform cells to confer  
 CC improved TNF-binding properties.  
 CC Sequence 455 AA;  
 SQ  
 Query Match 52.0%; Score 1332; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4,69e-120;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 41 dsvcpqgkylhpnmsicctckhkgtylyndcpqgqdtcdccesgsftasehlrhl 100  
 |||||||  
 Qy 23 dsvcpqgkylhpnmsicctckhkgtylyndcpqgqdtcdccesgsftasehlrhl 82  
 Db 101 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfcncslclngtlvsqge 160  
 |||||||  
 Qy 83 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfcncslclngtlvsqge 142  
 |||||||  
 Db 161 knvtctchagfflrenecvscnckleclclpqlenkygredgtt 211  
 |||||||  
 Qy 143 knvtctchagfflrenecvscnckleclclpqlenkygredgtt 193  
 |||||||  
 RESULT 12  
 ID R70103 standard; Protein; 900 AA.  
 AC R70103.  
 DT 02-NOV-1995 (first entry)  
 DE TNF-R-GBP 130 fusion protein.  
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
 KW red blood cell; cytokine receptor; glycophorin binding peptide 130;  
 KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A.  
 OS Chimeric Homo sapiens.  
 OS Chimeric Plasmodium falciparum.  
 PN WO9506737-A.  
 PD 09-MAR-1995.  
 PF 01-SEP-1994; G01900.  
 PR 03-SEP-1993; GB-018350.  
 PR 23-AUG-1994; GB-017021.  
 PA (PREN) PRENDERGAST K F.  
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PT malaria parasite peptide capable of binding a red blood cell and  
 PT a receptor peptide.  
 PS Example A: Page 46-47; 93pp: English.  
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples  
 CC of these hybrid peptides. R70103 is a fusion of tumour necrosis factor  
 CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
 CC and glycophorin binding protein (GBP) 130. The use of cytokine  
 CC receptors not normally found on RBCs means that the cytokine can bind  
 CC harmlessly to the RBC without deleterious effect. The RBC protects the  
 CC hybrid peptides from excretion from the kidney, and due to steric  
 CC hindrance prevents the cytokines binding to a receptor in another cell.  
 CC GBP 130 or GBPH (GBP homologue) are the pred. malaria parasite peptides  
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
 CC PMMSA (pre major merozoite surface antigen) and the Duffy binding  
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
 CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on  
 CC the surface of RBCs. The hybrid peptides are thus used to lower  
 CC the levels of free cytokines in the circulation to reduce pathological  
 CC damage.  
 SQ Sequence 900 AA;  
 Query Match 52.0%; Score 1321; DB 13; Length 900;  
 Best Local Similarity 99.4%; Pred. No. 5,93e-120;  
 Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 20 dsvcpqgkylhpnmsicctckhkgtylyndcpqgqdtcdccesgsftasehlrhl 79  
 |||||||  
 Qy 23 dsvcpqgkylhpnmsicctckhkgtylyndcpqgqdtcdccesgsftasehlrhl 82  
 Db 80 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfcncslclngtlvsqge 139  
 |||||||  
 Qy 83 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfcncslclngtlvsqge 142  
 |||||||  
 Db 140 knvtctchagfflrenecvscnckleclclpqlenkygredgtt 191  
 |||||||  
 Qy 143 knvtctchagfflrenecvscnckleclclpqlenkygredgtt 194  
 |||||||  
 RESULT 13  
 ID R70108 standard; Protein; 309 AA.  
 AC R70108.  
 DT 10-NOV-1995 (first entry)  
 DE TNF-R-GBP fusion protein.  
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
 KW red blood cell; cytokine receptor; glycophorin binding peptide 130;  
 KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;  
 KW tumour necrosis factor receptor; TNF-R.  
 OS Chimeric Homo sapiens.  
 OS Chimeric Plasmodium falciparum.  
 PN WO9506737-A.  
 PD 09-MAR-1995.  
 PF 01-SEP-1994; G01900.  
 PR 03-SEP-1993; GB-018350.  
 PR 23-AUG-1994; GB-017021.  
 PA (PREN) PRENDERGAST K F.  
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PT malaria parasite peptide capable of binding a red blood cell and  
 PT a receptor peptide.  
 PS Example A: Page 54-55; 93pp: English.  
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood

PI Prendergast KF;  
 DR MPI: 95-115452/15.  
 PR New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PR malaria parasite peptide capable of binding a red blood cell and  
 PR a receptor peptide.  
 PS Example A: Page 46-47; 93pp: English.  
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples  
 CC of these hybrid peptides. R70103 is a fusion of tumour necrosis factor  
 CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
 CC and glycophorin binding protein (GBP) 130. The use of cytokine  
 CC receptors not normally found on RBCs means that the cytokine can bind  
 CC harmlessly to the RBC without deleterious effect. The RBC protects the  
 CC hybrid peptides from excretion from the kidney, and due to steric  
 CC hindrance prevents the cytokines binding to a receptor in another cell.  
 CC GBP 130 or GBPH (GBP homologue) are the pred. malaria parasite peptides  
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
 CC PMMSA (pre major merozoite surface antigen) and the Duffy binding  
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
 CC bind to pref. glycophorin A, B and C, sialo glycoproteins, found on  
 CC the surface of RBCs. The hybrid peptides are thus used to lower  
 CC the levels of free cytokines in the circulation to reduce pathological  
 CC damage.  
 SQ Sequence 900 AA;  
 Query Match 52.0%; Score 1321; DB 13; Length 900;  
 Best Local Similarity 99.4%; Pred. No. 5,93e-120;  
 Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 20 dsvcpqgkylhpnmsicctckhkgtylyndcpqgqdtcdccesgsftasehlrhl 79  
 |||||||  
 Qy 23 dsvcpqgkylhpnmsicctckhkgtylyndcpqgqdtcdccesgsftasehlrhl 82  
 Db 80 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfcncslclngtlvsqge 139  
 |||||||  
 Qy 83 scskcrkemgveissctvdrtvcgcrknqyrhysenlfcfcncslclngtlvsqge 142  
 |||||||  
 Db 140 knvtctchagfflrenecvscnckleclclpqlenkygredgtt 191  
 |||||||  
 Qy 143 knvtctchagfflrenecvscnckleclclpqlenkygredgtt 194  
 |||||||  
 RESULT 13  
 ID R70108 standard; Protein; 309 AA.  
 AC R70108.  
 DT 10-NOV-1995 (first entry)  
 DE TNF-R-GBP fusion protein.  
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
 KW red blood cell; cytokine receptor; glycophorin binding peptide 130;  
 KW GBP 130; GBPH; glycophorin binding peptide homologue; glycophorin A;  
 KW tumour necrosis factor receptor; TNF-R.  
 OS Chimeric Homo sapiens.  
 OS Chimeric Plasmodium falciparum.  
 PN WO9506737-A.  
 PD 09-MAR-1995.  
 PF 01-SEP-1994; G01900.  
 PR 03-SEP-1993; GB-018350.  
 PR 23-AUG-1994; GB-017021.  
 PA (PREN) PRENDERGAST K F.  
 PT New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PT malaria parasite peptide capable of binding a red blood cell and  
 PT a receptor peptide.  
 PS Example A: Page 54-55; 93pp: English.  
 CC Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood



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\*\*\*\*\*  
MUSE (TM)  
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MParch\_dp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed May 6 09:05:45 1998; Maspar time 14.61 seconds  
Tabular output not generated. 839.893 Million cell updates/sec

Title: >US-08-804-166-8  
Description: (1-336) from US08804166.pep  
Perfect Score: 2541  
Sequence: 1 SRTSLILAFGLCLCPWLQEG.....PSLSPSRKPGSPDPIILPQ 336

Scoring table: PAM 150  
Gap 11

Searched: 120446 segs, 36531193 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: p1r56  
1:par1 2:par2 3:par3 4:par4 5:n13d

Statistics: Mean 42.414; Variance 82.038; scale 0.517

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1322	52.0	455	1	GOHUT1 tumor necrosis factor	9.45e-253
2	1257	49.5	160	5	LEXTA tumor necrosis factor	1.30e-238
3	1238	48.7	158	5	LEXTB tumor necrosis factor	1.74e-234
4	1121	44.1	142	5	INCFB tumor necrosis factor	4.07e-209
5	1105	43.5	139	5	INCFB tumor necrosis factor	1.18e-205
6	1098	43.2	140	5	INCFB tumor necrosis factor	3.86e-204
7	1030	40.5	145	2	IT7412 beta-gonadotropin - h	1.88e-189
8	1030	40.5	165	1	KTHUB choriongonadotropin be	5.08e-189
9	1028	40.5	461	1	JC4302 beta-gonadotropin - h	3.70e-188
10	1024	40.3	145	2	IT7231 tumor necrosis factor	2.26e-174
11	960	37.8	454	1	GOMST1 tumor necrosis factor	2.26e-174
12	960	37.8	454	2	IT57826 tumor necrosis factor	2.26e-174
13	944	37.2	461	1	GORT1L tumor necrosis factor	6.21e-171
14	857	33.7	165	1	KTBAB choriongonadotropin be	2.82e-152
15	803	31.6	110	5	IXULB chorionic gonadotropi	9.67e-141
16	803	31.6	110	5	IXULB Human chorionic gonad	9.67e-141
17	803	31.6	110	5	IXULB Human chorionic gonad	9.67e-141
18	740	29.1	121	2	IT3794 beta-h - human (frag	2.46e-127
19	709	27.9	115	1	UTRUB lutropin beta chain -	9.18e-121
20	614	24.2	141	1	UTBOB lutropin beta chain p	9.77e-101
21	614	24.2	141	1	IT6949 lutelizing hormone b	1.58e-100
22	613	24.1	169	1	KTHOB choriongonadotropin be	1.58e-100
23	596	23.5	119	2	A61465 lutropin beta chain -	5.78e-97

RESULT	ENTRY	1	GOHUT1	#type complete	ALIGNMENTS
24	598	23.5	141	1	UTRUB lutropin beta chain p
25	597	23.5	141	1	UTRUB lutropin beta chain p
26	595	23.4	141	1	PN0139 lutropin beta chain p
27	594	23.4	141	1	UTRUB lutropin beta chain p
28	587	23.1	138	2	S00512 lutropin beta chain p
29	585	22.9	141	2	PN0141 lutropin beta chain p
30	582	22.9	141	2	JC4527 lutelizing hormone b
31	430	16.9	141	2	UTCAR gonadotropin beta cha
32	427	16.8	141	2	B60626 gonadotropin beta cha
33	426	16.8	146	2	S16763 gonadotropin beta cha
34	420	16.5	119	2	S09344 gonadotropin II beta
35	416	16.4	142	2	S36179 gonadotropin II beta
36	411	16.2	142	2	I51232 gonadotropin beta cha
37	407	16.0	113	2	S07092 gonadotropin beta cha
38	405	15.9	112	2	S21196 lutropin beta chain -
39	403	15.9	140	2	A48166 gonadotropin II beta
40	398	15.7	142	2	A25800 gonadotropin beta cha
41	388	15.3	142	2	I50143 gonadotropin II beta
42	368	14.5	158	2	A61091 lutropin beta chain p
43	366	14.4	166	2	I51242 lutelizing hormone b
44	361	14.2	147	2	I50994 gonadotropin II beta
45	352	13.9	159	2	I51373 lutelizing hormone b

REFERENCE #authors Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Fiebich, H.; Lesslauer, W.  
#journal Cell (1990) 61:351-359  
#title Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.  
#accession M34899  
#molecule-type mRNA  
#residues 1-455 #label LOE  
##cross-references GB:M58286; GB:M33480; NID:g339753; PID:g339754  
##experimental\_source placenta  
##note part of this sequence, including the amino end of the mature protein, confirmed by protein sequencing

REFERENCE #authors Schnall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab, H.; Kohr, W.J.; Goeddel, D.V.  
#journal Cell (1990) 61:361-370  
#title Molecular cloning and expression of a receptor for human tumor necrosis factor.  
#cross-references M34900  
#accession A34900  
#molecule-type mRNA  
#residues 1-455 #label SCH  
##cross-references GB:M33294; NID:g339744; PID:g339745

REFERENCE  
#authors A36555  
#journal Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.; Stratowa, C.; Adolf, G.R.  
#title DNA Cell Biol. (1990) 9:705-715  
Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.

#cross-references M01D:91090841  
#accession A36555  
#molecule-type mRNA  
#residues 1-455 ##label HIM  
#cross-references GB:M63121; NID:g339755; PID:g339756  
#accession C36555  
#molecule-type protein  
#residues 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104; 107-128;162-167,'X',169-201 ##label HIT  
the purified protein, called tumor necrosis factor binding protein, is a soluble derivative of the receptor

REFERENCE  
#authors A38281  
Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384  
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein.  
#cross-references M01D:91017509  
#accession A38281  
#molecule-type mRNA  
#residues 1-455 ##label GRA  
#cross-references GB:M37764  
#note The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Leu, and GAC for residue 477 as Asn

REFERENCE  
#authors S12057  
Nopnar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, H.; Wallach, D.  
#journal EMBO J. (1990) 9:3269-3278  
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.  
#cross-references M01D:91006021  
#accession S12057  
#molecule-type mRNA  
#residues 1-455 ##label NOP  
#cross-references EMBL:X55313; NID:g37223; PID:g37224  
#note parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were confirmed by protein sequencing

REFERENCE  
#authors J07058  
Kemper, O.; Wallach, D.  
#journal Gene (1993) 134:209-216  
#title Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor (TNF) receptor.  
#accession J07058  
#molecule-type DNA  
#residues 1-13 ##label KEM

REFERENCE  
#authors A60231  
Secklinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
#journal J. Immunol. (1990) 20:1167-1174  
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence and evidence for anti-inflammatory and immunomodulatory activities.  
#cross-references M01D:90292116  
#accession A60231  
#molecule-type protein  
#residues 41-43,'X',45-53,'X',55-57 ##label SEC

REFERENCE  
#authors A38258  
Gatanga, T.; Huang, C.; Kohr, W.; Capuccini, F.; Luccl III, J.A.; Jeffes, E.W.B.; Lantz, R.; Tomlich, J.; Yamamoto, R.S.; Granger, G.A.

#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784  
#title Purification and characterization of an inhibitor (soluble tumor necrosis factor receptor) for tumor necrosis factor and lymphotoxin obtained from the serum ultrafiltrates of human cancer patients.  
#cross-references M01D:91062364  
#accession A38258  
#molecule-type protein  
#residues 41-60 ##label GAT  
#experimental\_source cancer patient serum

REFERENCE  
#authors A60594  
Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
#journal Eur. J. Haematol. (1989) 42:270-275  
#title Isolation and characterization of a tumor necrosis factor binding protein from urine.  
#accession A60594  
#molecule-type protein  
#residues 41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS  
#experimental\_source renal failure patient urine

REFERENCE  
#authors A35010  
Engelmann, H.; Novick, D.; Wallach, D.  
#journal J. Biol. Chem. (1990) 265:1531-1536  
#title Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.  
#cross-references M01D:90110215  
#accession A35010  
#molecule-type protein  
#residues 41-45 ##label ENG  
#experimental\_source normal urine

REFERENCE  
#authors J02404  
Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
#journal Biosci. Biotechnol. Biochem. (1994) 58:2266-2268  
#title Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.  
#accession J02404  
#molecule-type protein  
#residues 41-53,'X',55-144,'X',146-150,'X',152-166,'X',188-201 ##label KAU  
#experimental\_source urine

COMMENT This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).

GENETICS  
#gene GDB:TNFR1  
#map\_position 12p13.2-12p13.2  
#inons 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
#superfamily tumor necrosis factor receptor type 1; NGR  
CLASSIFICATION  
#duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS  
#domain signal sequence #status predicted #label SIG  
#product tumor necrosis factor receptor type 1 #status predicted #label MAT  
#domain extracellular #status predicted #label EXT  
#alpha inhibitor) #status experimental #label TBPI  
#domain NGF receptor repeat homology #label NG1  
#domain NGF receptor repeat homology #label NG2  
#domain NGF receptor repeat homology #label NG3  
#domain NGF receptor repeat homology #label NG4  
#domain transmembrane #status predicted #label MEM  
#domain intracellular #status predicted #label INT  
#binding\_site carbohydrate (Asn) (covalent) #status predicted

SUMMARY  
#length 455 #molecular\_weight 50494 #checksum 153

Query Match 52.0%; Score 1322; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 9,456-253;  
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 41 DSVCPGKXIIHPNNSICTCKCHKGYLYNDPCPGPQDTRCEGSGSTASENHLRCL 100

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Qy 23 DSVCPQGIYHPNNNSICCKCHKGYLYNDPCPGDDTDCRECESSGFASENHLRHCL 82
Db 101 CSCKRKGQVEISSCTVDRTVCGCRKNQRYHYSENFLQCFNCSLCNGTVHLSCOE 160
Qy 83 CSCKRKGQVEISSCTVDRTVCGCRKNQRYHYSENFLQCFNCSLCNGTVHLSCOE 142
Db 161 KONTVCTCHAGFLRENECVSCSNCKKSECTKCLPQIENVGTEDSGTT 211
Qy 143 KONTVCTCHAGFLRENECVSCSNCKKSECTKCLPQIENVGTEDSGTT 193

RESULT 2
ENTRY 1EXTB #type complete

TITLE
PDB_TITLE tumor necrosis factor receptor extracellular domain, chain A
ORGANISM receptor, crystallized at pH3.7 in p 21 21 21.
#formal_name Homo sapiens #common_name man
expressed in Escherichia coli, the construct contains
residues 12 to 172 of the mature sequence of the entire
receptor. residue 11 is mutated to met as a result of the
expression system

REFERENCE
#authors Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
TNO26248
#journal Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal J. Biol. Chem. (1995) 270:13303
#title Crystallographic evidence for dimerization of unliganded
tumor necrosis factor receptor.
TNO26249
#authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
K.; Naismith, J.H.; Sprang, S.R.
#journal J. Mol. Biol. (1994) 239:332
#title Two crystal forms of the extracellular domain of type 1 tumor
necrosis factor receptor.
A40737
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal Cell (1993) 73:431-445
#title Crystal structure of the soluble human 55 kd TNF
receptor-human TNFbeta complex: implications for TNF
receptor activation.
COMMENT Resolution: 1.85 angstroms
Determination: X-ray diffraction
KEYWORDS R-value: no refinement
binding protein; cytokine; signalling protein
FEATURE
66-68 #region helix (right hand 3-10)\
14-143 #region helix (right hand 3-10)\
151-154 #region helix (right hand alpha)\
7-9,17-19 #region beta sheet\
131-134,137-140 #region beta sheet\
25-29,39-42 #region beta sheet\
71-74,83-85 #region beta sheet\
90-96,99-104 #region beta sheet\
111-115,124-127 #region beta sheet\
3-17 #disulfide_bonds\
18-31 #disulfide_bonds\
21-40 #disulfide_bonds\
43-58 #disulfide_bonds\
61-76 #disulfide_bonds\
64-84 #disulfide_bonds\
86-102 #disulfide_bonds\
105-117 #disulfide_bonds\
108-125 #disulfide_bonds\
127-138 #disulfide_bonds\
141-154 #disulfide_bonds\
144-150 #disulfide_bonds\
SUMMARY #length 160 #molecular-weight 18065 #checksum 2297

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Query Match 49.5%; Score 1257; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 1,30e-238;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SVCPQGIYHPNNNSICCKCHKGYLYNDPCPGDDTDCRECESSGFASENHLRHCLS 60
Qy 24 SVCPQGIYHPNNNSICCKCHKGYLYNDPCPGDDTDCRECESSGFASENHLRHCLS 83
Db 61 CSCKRKGQVEISSCTVDRTVCGCRKNQRYHYSENFLQCFNCSLCNGTVHLSCOE 120
Qy 84 CSCKRKGQVEISSCTVDRTVCGCRKNQRYHYSENFLQCFNCSLCNGTVHLSCOE 143
Db 121 QNTVCTCHAGFLRENECVSCSNCKKSECTKCLPQIEN 160
Qy 144 QNTVCTCHAGFLRENECVSCSNCKKSECTKCLPQIEN 183

RESULT 3
ENTRY 1EXTB #type complete

TITLE
PDB_TITLE tumor necrosis factor receptor extracellular domain, chain B
ORGANISM receptor, crystallized at pH3.7 in p 21 21 21.
#formal_name Homo sapiens #common_name man
expressed in Escherichia coli, the construct contains
residues 12 to 172 of the mature sequence of the entire
receptor. residue 11 is mutated to met as a result of the
expression system

REFERENCE
#authors Naismith, J.H.; Sprang, S.R.
#submission submitted to the Brookhaven Protein Data Bank, July 1996
#cross-references PDB:1EXT
TNO26251
#journal Naismith, J.H.; Devine, T.Q.; Brandhuber, B.J.; Sprang, S.R.
#journal J. Biol. Chem. (1995) 270:13303
#title Crystallographic evidence for dimerization of unliganded
tumor necrosis factor receptor.
TNO26252
#authors Rodseth, L.E.; Brandhuber, B.; Devine, T.Q.; Eck, M.J.; Hale,
K.; Naismith, J.H.; Sprang, S.R.
#journal J. Mol. Biol. (1994) 239:332
#title Two crystal forms of the extracellular domain of type 1 tumor
necrosis factor receptor.
A40737
#authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal Cell (1993) 73:431-445
#title Crystal structure of the soluble human 55 kd TNF
receptor-human TNFbeta complex: implications for TNF
receptor activation.
COMMENT Resolution: 1.85 angstroms
Determination: X-ray diffraction
KEYWORDS R-value: no refinement
binding protein; cytokine; signalling protein
FEATURE
68-70 #region helix (right hand 3-10)\
143-145 #region helix (right hand 3-10)\
9-11,19-21 #region beta sheet\
133-136,139-142 #region beta sheet\
27-31,41-44 #region beta sheet\
73-76,85-87 #region beta sheet\
92-98,101-106 #region beta sheet\
113-117,126-129 #region beta sheet\
5-19 #disulfide_bonds\
20-33 #disulfide_bonds\
23-42 #disulfide_bonds\
45-60 #disulfide_bonds\
63-78 #disulfide_bonds\
66-86 #disulfide_bonds\
88-104 #disulfide_bonds\
107-119 #disulfide_bonds\
110-127 #disulfide_bonds\
129-140 #disulfide_bonds\

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143-156 #disulfide\_bonds\  
146-152 #disulfide\_bonds  
SUMMARY #length 158 #molecular-weight 17827 #checksum 5022

Query Match 48.7%; Score 1238; DB 5; Length 158;  
Best Local Similarity 100.0%; Pred. No. 1.74e-234;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 DSVCPGKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCL 61  
QY 23 DSVCPGKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCL 82

Db 62 SCSCRKEMGVEISSCTVDRTVCGCRKNQRYHYSSENLFQCFNCSLCNGTVHLSQOE 121  
QY 83 SCSCRKEMGVEISSCTVDRTVCGCRKNQRYHYSSENLFQCFNCSLCNGTVHLSQOE 142

Db 122 KONTVCTCHAGFFLRENECVSCSNCKSLLECTKICLP 158  
QY 143 KONTVCTCHAGFFLRENECVSCSNCKSLLECTKICLP 179

RESULT 4 INCFB #type complete  
ENTRY  
TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
chain B - hu  
#formal\_name Homo sapiens #common\_name man  
#note expressed in Baculovirus cell, residue 11 is mutated to met  
as a result of the expression system

REFERENCE #authors Naismith, J.H.; Sprang, S.R.  
#journal J. Mol. Biol. (1994) 239:332  
#title Two crystal forms of the extracellular domain of type 1 tumor  
necrosis factor receptor.  
A40737  
Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
Cell (1993) 73:431-445  
Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
binding protein: cytokine; signalling protein

COMMENT Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
binding protein: cytokine; signalling protein

KEYWORDS  
FEATURE  
2-16 #disulfide\_bonds\  
17-30 #disulfide\_bonds\  
20-39 #disulfide\_bonds\  
42-57 #disulfide\_bonds\  
60-75 #disulfide\_bonds\  
63-83 #disulfide\_bonds\  
85-101 #disulfide\_bonds\  
104-116 #disulfide\_bonds\  
107-124 #disulfide\_bonds\  
126-137 #disulfide\_bonds\  
SUMMARY #length 142 #molecular-weight 16046 #checksum 1225

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Best Local Similarity 100.0%; Pred. No. 4.07e-209;  
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VCPGKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCLSC 60  
QY 25 VCPGKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCLSC 84

Db 61 SKCRKEMGVEISSCTVDRTVCGCRKNQRYHYSSENLFQCFNCSLCNGTVHLSQOEKQ 120  
QY 85 SKCRKEMGVEISSCTVDRTVCGCRKNQRYHYSSENLFQCFNCSLCNGTVHLSQOEKQ 144

Db 121 NTVCTCHAGFFLRENECVSCSN 142  
QY 145 NTVCTCHAGFFLRENECVSCSN 166

RESULT 5 ITNRR #type complete  
ENTRY  
TITLE tumor necrosis factor receptor type 1 (p55 extracellular  
#formal\_name Homo sapiens #common\_name man  
#note recombinant form expressed in Baculovirus Sf9  
A52442  
REFERENCE #authors Banner, D.W.  
#submission submitted to the Brookhaven Protein Data Bank, May 1994  
#cross-references PDB:ITNR  
A40737  
REFERENCE #authors Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
Cell (1993) 73:431-445  
Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
TN034093  
D'Arcy, A.; Banner, D.W.; Janes, W.; Winkler, F.K.;  
Loetscher, H.; Schoenfeld, H.J.; Zulauf, M.; Gentz, R.;  
Lesslauer, W.  
J. Mol. Biol. (1993) 229:555  
Crystallization and preliminary analysis of tnfbeta and a  
tnfbeta-55 kd tnfr receptor complex.  
Resolution: 2.85 angstroms  
Determination: X-ray diffraction  
Complex(lymphokineRECEPTOR)

COMMENT Resolution: 2.85 angstroms  
Determination: X-ray diffraction  
Complex(lymphokineRECEPTOR)

KEYWORDS  
FEATURE  
1-15 #disulfide\_bonds\  
16-29 #disulfide\_bonds\  
19-38 #disulfide\_bonds\  
41-56 #disulfide\_bonds\  
59-74 #disulfide\_bonds\  
62-82 #disulfide\_bonds\  
84-100 #disulfide\_bonds\  
103-115 #disulfide\_bonds\  
106-123 #disulfide\_bonds\  
125-136 #disulfide\_bonds\  
SUMMARY #length 139 #molecular-weight 15746 #checksum 5235

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Best Local Similarity 100.0%; Pred. No. 1.18e-205;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CPQKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCLSCS 60  
QY 26 CPQKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCLSCS 85

Db 61 KCRKEMGVEISSCTVDRTVCGCRKNQRYHYSSENLFQCFNCSLCNGTVHLSQOEKON 120  
QY 86 KCRKEMGVEISSCTVDRTVCGCRKNQRYHYSSENLFQCFNCSLCNGTVHLSQOEKON 145

Db 121 TVCTCHAGFFLRENECVSC 139  
QY 146 TVCTCHAGFFLRENECVSC 164

RESULT 6 INCFB #type complete  
ENTRY  
TITLE tumor necrosis factor receptor 55 kd extracellular domain  
contains residues 12 172 of the mature receptor sequence,  
chain A - hu  
#formal\_name Homo sapiens #common\_name man  
#note expressed in Baculovirus cell, residue 11 is mutated to met  
as a result of the expression system

REFERENCE #authors Naismith, J.H.; Sprang, S.R.  
#journal J. Mol. Biol. (1994) 239:332  
#title Two crystal forms of the extracellular domain of type 1 tumor  
necrosis factor receptor.  
A40737  
Banner, D.W.; D'Arcy, A.; Janes, W.; Gentz, R.; Schoenfeld,  
H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.  
Cell (1993) 73:431-445  
Crystal structure of the soluble human 55 kd TNF  
receptor-human TNFbeta complex: implications for TNF  
receptor activation.  
Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
binding protein: cytokine; signalling protein

COMMENT Resolution: 2.25 angstroms  
Determination: X-ray diffraction  
R-value: no refinement  
binding protein: cytokine; signalling protein

KEYWORDS  
FEATURE  
2-16 #disulfide\_bonds\  
17-30 #disulfide\_bonds\  
20-39 #disulfide\_bonds\  
42-57 #disulfide\_bonds\  
60-75 #disulfide\_bonds\  
63-83 #disulfide\_bonds\  
85-101 #disulfide\_bonds\  
104-116 #disulfide\_bonds\  
107-124 #disulfide\_bonds\  
126-137 #disulfide\_bonds\  
SUMMARY #length 142 #molecular-weight 16046 #checksum 1225

Query Match 44.1%; Score 1121; DB 5; Length 142;  
Best Local Similarity 100.0%; Pred. No. 4.07e-209;  
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VCPGKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCLSC 60  
QY 25 VCPGKXIHPPNNISCTCKHKGTYLYNDCCPGPQDTPDCRECSGSFTASENHLRHCLSC 84

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ORGANISM      #formal_name Homo sapiens #common_name man
#note         expressed in Escherichia coli, residue 11 is mutated to met
              as a result of the expression system
REFERENCE     A66195
#authors      Naismith, J.H.; Sprang, S.R.
#submission   submitted to the Brookhaven Protein Data Bank, October 1994
#cross-references PDB:1NCF
REFERENCE     TN029039
#authors      Rodestch, L.E.; Brandhuber, B.; Devine, T.O.; Eck, M.J.; Hale,
              K.; Naismith, J.H.; Sprang, S.R.
#journal      J. Mol. Biol. (1994) 239:332
#title        Two crystal forms of the extracellular domain of type 1 tumor
              necrosis factor receptor.
REFERENCE     A40737
#authors      Banner, D.W.; D'Arcy, A.; Jones, W.; Gentz, R.; Schoenfeld,
              H.J.; Broger, C.; Loetscher, H.; Lesslauer, W.
#journal      Cell (1993) 73:431-445
#title        Crystal structure of the soluble human 55 kd TNF
              receptor-human TNFbeta complex: implications for TNF
              receptor activation.
COMMENT       Resolution: 2.25 angstroms
COMMENT       Determination: X-ray diffraction
COMMENT       R-value: no refinement
KEYWORDS      binding protein; cytokine; signaling protein
FEATURE       5-19          #disulfide_bonds\
20-33          #disulfide_bonds\
23-42          #disulfide_bonds\
45-60          #disulfide_bonds\
63-78          #disulfide_bonds\
66-86          #disulfide_bonds\
88-104         #disulfide_bonds\
107-119        #disulfide_bonds\
110-127        #disulfide_bonds\
129-140        #disulfide_bonds\
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Best Local Similarity 100.0%; Pred. No. 3,86e-204;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 DSVCPQGYIHHQNNSSICCTCKHKGTYLYLNDPCPGPDQDCCRCESGSGTASNNHLRCL 61
    |||
Oy 23 DSVCPQGYIHHQNNSSICCTCKHKGTYLYLNDPCPGPDQDCCRCESGSGTASNNHLRCL 82
    |||
Db 62 SCSKCRKEMGVYEISCTYDRDTCGCRKNQYRHVSENLFCQFNCSLCLNGTVHLSCE 121
    |||
Oy 83 SCSKCRKEMGVYEISCTYDRDTCGCRKNQYRHVSENLFCQFNCSLCLNGTVHLSCE 142
    |||
Db 122 KONTVCTCHAGFLRENEC 140
    |||
Oy 143 KONTVCTCHAGFLRENEC 161

RESULT 7
ENTRY 137412 #type fragment
TITLE beta-gonadotropin - human (fragment)ORGANISM #formal_name Homo
DATE 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
ACCESSIONS 137412
REFERENCE 137231
#authors Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
#journal Nature (1984) 307:37-40
#title Evolution of the genes for the beta subunits of human
        Chorionic gonadotropin and luteinizing hormone.
#cross-references MUID:84093590
#accession 137412
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-145 ##label RES
##cross-references EMBL:X00265; NID:931719
GENETICS

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CLASSIFICATION	41/3	#superfamily	pituitary	glycoprotein	hormone	beta chain
SUMMARY	#length 145	#checksum 2358				
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Best Local Similarity	100.0%	Pred. No. 1,886-189;				
Matches 133;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
Db	7	PROCRINATLAVEKEGCGVCITVNTTICAGYCPMTIRVLOGLVLPALPOVCNRYDVERES	66			
Oy	198	PROCRINATLAVEKEGCGVCITVNTTICAGYCPMTIRVLOGLVLPALPOVCNRYDVERES	257			
Db	67	IRLPCCPGVNPVSYANALSCOCALCRRTTDCGGPRDHPDLTCDPPFDSSSSKAPP	126			
Oy	258	IRLPCCPGVNPVSYANALSCOCALCRRTTDCGGPRDHPDLTCDPPFDSSSSKAPP	317			
Db	127	SLPSPRLPGSPDPIPLPQ	145			
Oy	318	SLPSPRLPGSPDPIPLPQ	336			
RESULT	8	KTIDB	#type complete			
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TITLE		choriogonadotropin beta chain precursor - human	ALTERNATE_NAMES			
ORGANISM		#formal_name Homo sapiens	#common_name man			
DATE		23-Oct-1981	#sequence_revision 23-Oct-1981	#text_change		
ACCESSIONS		A93320: 169972; I55224; I55250; I70007; I70008; A92303; A92181; A92142; PC1016; A61097; B56873; A01502				
REFERENCE		A93320				
#authors		Fiddes, J. C.; Goodman, H. M.				
#journal		Nature (1980) 286:684-687				
#title		The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution of a gene by readthrough into the 3'-untranslated region.				
#cross-references		MUID:81012134				
#accession		A93320				
#molecule_type		mRNA				
#residues		1-165	#label	FTD		
#cross-references		GB:J00117; GB:M58559; GB:M54563; NID:9180436; PID:9180437				
REFERENCE		I55224				
#authors		Policastro, P.; Ovilt, C. E.; Hoshina, M.; Fukuoaka, H.; Boothby, M. R.; Bolme, I.				
#journal		J. Biol. Chem. (1983) 258:11497-11499				
#title		The beta subunit of human chorionic gonadotropin is encoded by multiple genes.				
#cross-references		MUID:84008141				
#accession		I69972				
#status		translated from GB/EMBL/DBJ				
#molecule_type		DNA				
#residues		1-165	#label	POL		
#cross-references		GB:K03189; NID:9180450; PID:9180453				
#note		clone CG-beta-e				
#accession		I55224				
#status		translated from GB/EMBL/DBJ				
#molecule_type		DNA				
#residues		1-23, 'M', 25-136, 'A', 138-165	#label	PO2		
#cross-references		GB:K03183; NID:9180442; PID:9180444				
#note		clone CG-beta-a				
REFERENCE		I55250				
#authors		Policastro, P. F.; Daniels-McQueen, S.; Carle, G.; Bolme, I.				
#journal		J. Biol. Chem. (1986) 261:5907-5916				
#title		A map of the hCG beta-LH beta gene cluster.				
#cross-references		MUID:86195987				
#accession		I55250				
#status		preliminary; translated from GB/EMBL/DBJ				
#molecule_type		DNA				
#residues		1-5	#label	PO3		
#cross-references		GB:M1504; NID:9180419; PID:946308				
#note		CG-beta-3 gene				
#accession		I70007				

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##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues    1-5 ##label PQ4
##cross-references GB:M13505; NID:g180429; PID:g463089
##note        CG-beta-6 gene
#accession    I70008
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues    1-5 ##label RS5
##cross-references GB:M13503; NID:g180432; PID:g463090
##note        CG-beta-7 gene
#accession    A92303
#authors      Birken, S.; Fetherston, J.; Canfield, R.; Bolme, I.
#journal      J. Biol. Chem. (1981) 256:1816-1823
#title        The amino acid sequences of the prepeptides contained in the
               alpha and beta subunits of human choriongonadotropin.
#cross-references M13503; NID:g18117268
#accession    A92303
##molecule_type protein
##residues    1-20 ##label BIR
##note        The identity of the residue at position 19 could not be
               determined
#accession    A92181
#authors      Morgan, F.J.; Birken, S.; Canfield, R.E.
#journal      J. Biol. Chem. (1975) 250:5247-5258
#title        The amino acid sequence of human chorionic gonadotropin. The
               alpha subunit and beta subunit.
#cross-references M13503
#accession    A92181
##molecule_type protein
##residues    21-165 ##label MOR
#accession    A92142
#authors      Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
#journal      J. Biol. Chem. (1973) 248:6810-6827
#cross-references M13503; NID:g1811267
#accession    A92142
##molecule_type protein
##residues    21-22,'Q',24-73,'ZL',76-140,142-157,'PB',160-165,'SLP'
               ##label CAR
#accession    PC1016
#authors      Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.;
               Wang, Y.
#journal      Chinese Biochem. J. (1990) 6:558-562
#title        The immunological characteristics of the enzymatic fragments
               of human chorionic gonadotropin beta-subunit.
#accession    PC1016
##molecule_type protein
##residues    21-165 ##label SHI
##note        article in Chinese with English abstract
#accession    A61097
#authors      Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.;
               Agosto, G.M.; Krichevsky, A.; Valicakaitis, J.L.; Canfield,
               R.E.
#journal      Endocrinology (1988) 123:572-583
#title        Structure of the human chorionic gonadotropin beta-subunit
               fragment from pregnancy urine.
#accession    A61097
##molecule_type protein
##residues    26-32,'X',34-49,'X',51-60;75-112 ##label B12
##note        this material from pregnancy urine lacks sialic acid in
               its carbohydrate and has been processed further from
               the mature form into two chains linked by disulfide
               bonds
#accession    A56873
#authors      Kardana, A.; Bagshawe, K.D.; Coles, B.; Reed, D.; Taylor, M.
#journal      Br. J. Cancer (1993) 67:686-692
#title        Characterisation of UGP and its relationship with beta-core
               fragment.
#cross-references M13503; NID:g1811267
#accession    B56873
##molecule_type protein
##residues    26-28,'X',30-32,'X',34-42,'X',44-45,'X',47-48;75-76,'X',
               78-91,'G',93-102 ##label KAR

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##experimental_source urine
##note        sequence modified after extraction from NCBI backbone
##note        this material was designated urinary gonadotropin
               peptide (peak 2)
#accession    A44674
#authors      Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader,
               J.W.; Canfield, R.E.; Machin, K.D.; Morgan, F.J.; Isaacs,
               N.W.
#journal      Nature (1994) 369:455-461
#title        Crystal structure of human chorionic gonadotropin.
               annotation; X-ray crystallography, 3.0 angstroms; correction
               of disulfide bonds
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#GENETICS
#gene          GDB:GDB
#cross-references GDB:119055; OMIM:118860
#map_position  19q13.3-19q13.3
#introns       5/3; 61/3
#note          the choriongonadotropin beta chain locus contains six genes
               (or pseudogenes)
               #superfamily pituitary glycoprotein hormone beta chain
               glycoprotein; hormone; pituitary
#CLASSIFICATION
#KEYWORDS      #domain signal sequence #status experimental #label SIG\
               #product choriongonadotropin beta chain #status
               experimental #label MAT\
#FEATURE
#1-20          #disulfide_bonds #status experimental\
               #binding_site carbohydrate (Asn) (covalent) #status
               experimental\
               #binding_site carbohydrate (Ser) (covalent) #status
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#DB 27 PROCPINATLAVEKECCPCITVNTTICAGCYCPTMTRVAGVLPALPOVCNTRDYRFS 86
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#QY 198 PROCPINATLAVEKECCPCITVNTTICAGCYCPTMTRVAGVLPALPOVCNTRDYRFS 257
               |||||||
#DB 87 IRUPGCPGVNPVSYAVVNLSCCALCRSTDCGSPKHPRLTCDPRDSSSKAPP 146
               |||||||
#QY 258 IRUPGCPGVNPVSYAVVNLSCCALCRSTDCGSPKHPRLTCDPRDSSSKAPP 317
               |||||||
#DB 147 SLSPSRRLPGPSDPTPLPQ 165
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#QY 318 SLSPSRRLPGPSDPTPLPQ 336
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#RESULT 9
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#DATE 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
#ACCESSIONS JC4302; PC4093
#REFERENCE JC4302
#authors Suter, B.; Pauli, U.
#journal Gene (1995) 163:263-266
#title Cloning of the cDNA encoding the porcine p55 tumor necrosis
               factor receptor.
#accession JC4302
##molecule_type mRNA
##residues 1-461 ##label SUNT
##cross-references GB:U19944; NID:g1141752; PID:g1141753
#accession PC4093
##molecule_type protein
##residues 1-7 ##label SU2
##experimental_source kidney cell line 15

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GENETICS	trnf
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KEYWORDS	
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1-29	#domain signal sequence #status predicted #label SIG\
30-461	#product tumor necrosis factor receptor p55 #status predicted #label MAT\
44-194	#domain extracellular cysteine rich #status predicted #label EXT\
44-82	#domain NGF receptor repeat homology #label NG1\
211-231	#domain transmembrane #status predicted #label TM\
361-447	#domain signal transduction #status predicted #label SIT\
54,145,151	#binding_site carbohydrate (asn) (covalent) #status predicted
SUMMARY	#length 461 #molecular-weight 50696 #checksum 8079
Query Match	40.5%; Score 1028; DB 2; Length 461;
Best Local Similarity	73.1%; Pred. No. 5,08e-189;
Matches 125; Conservative	24; Mismatches 1; Indels 1; Gaps 1;
Db	41 ES1LPGGKSHQNSICTCKCHKGYLLHNDCLGPELDTCRECDNGTFETASENHLTQCL 100
Qy	23 DSVCCGKGIHQNSICTCKCHKGYLLHNDCLGPELDTCRECDNGTFETASENHLTQCL 82
Db	101 SCSKCRSEMSQVEISPCYTDVDRDTCGCRKNOYRKYRSETLFOCLNCLCPNGTVQDLPCE 160
Qy	83 SCSKCRKEMGOYEISCTYDTRDTCGCRKNOYRHYSENLFOCFNCSLGLNGVHLSCQE 142
Db	161 KQDTICNCHSGFFLRDKECVSCVNCNA-DCKNLCPATSETRNDPQDTGT 210
Qy	143 KQNTCTCHAGFELRENECVSCSNCKRSLCTKLPQIEENKGTEDSGTT 193
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DATE	21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
ACCESSIONS	137231
REFERENCE	137231
#authors	Talmadge, K.; Yamvakopoulos, N.C.; Fiddes, J.C.
#journal	Nature (1984) 307:37-40
#title	Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone.
#cross-references	MUID:84093590
#accession	I37231
#status	Preliminary; translated from GB/EMBL/DBJ
#molecule_type	DNA
#residues	1-145 #label RES
#cross-references	EMBL:X00266; NID:929907
GENETICS	
#introns	41/3
CLASSIFICATION	#superfamily pituitary glycoprotein hormone beta chain
SUMMARY	#length 145 #checksum 2349
Query Match	40.3%; Score 1024; DB 2; Length 145;
Best Local Similarity	99.3%; Pred. No. 3,70e-188;
Matches 138; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Db	7 PRCRPNATLAKEKCCPCITVNTTICAGYCTPTMRYGVLPALPOVYCNTRYRFS 66
Qy	198 PRCRPNATLAKEKCCPCITVNTTICAGYCTPTMRYGVLPALPOVYCNTRYRFS 257
Db	67 IRLPGCGVNPVSYAVALLSCGALCRSTDCGGPKDHLPCDDPRFOASSSKAPP 126
Qy	258 IRLPGCGVNPVSYAVALLSCGALCRSTDCGGPKDHLPCDDPRFOASSSKAPP 317
Db	127 SLPSRKLPGSPSTPLPQ 145

RESULT	11	QOMST1	#type complete
TITLE		tumor necrosis factor receptor type 1 precursor - mouse	ALTERNATE_NAME
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Sep-1997	
ACCESSIONS		A38634; B40254; S16677; S19021; I54532	
REFERENCE		A38634	
#authors		Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.R.W.; Chen, E.Y.; Goeddel, D.V.	
#journal		Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834	
#title		Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate that one receptor is species specific.	
#cross-references		MUID:91187885	
#accession		A38634	
#molecule_type		mRNA	
#residues		1-454 #label IEM	
#cross-references		GB:M60468; NID:9199825; PID:9199826	
REFERENCE		A40254	
#authors		Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.	
#journal		Mol. Cell. Biol. (1991) 11:3020-3026	
#title		Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.	
#cross-references		MUID:91246168	
#accession		B40254	
#molecule_type		mRNA	
#residues		1-454 #label G02	
#cross-references		GB:M60468; NID:9199825; PID:9199826	
REFERENCE		S16677	
#authors		Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.	
#journal		Eur. J. Immunol. (1991) 21:1649-1656	
#title		Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.	
#cross-references		MUID:91285014	
#accession		S16677	
#molecule_type		mRNA	
#residues		1-454 #label BAR	
#cross-references		EMBL:X59238; NID:953578; PID:953579	
REFERENCE		S19021	
#authors		Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.	
#journal		Immunogenetics (1991) 34:338-340	
#title		Molecular cloning and expression of the mouse Tnf receptor type b.	
#cross-references		MUID:92039815	
#accession		S19021	
#molecule_type		mRNA	
#residues		1-454 #label ROT	
#cross-references		EMBL:X57796; NID:954848; PID:954849	
REFERENCE		I54532	
#authors		Bebo, B.F.	
#journal		Immunogenetics (1994) 39:450-451	
#title		Nucleotide sequence of the TNF type I receptor from a mouse endometrial cell line.	
#cross-references		MUID:94245292	
#accession		I54532	
#status		translated from GB/EMBL/DBJ	
#molecule_type		mRNA	
#residues		1-454 #label RES	
#cross-references		GB:U26349; NID:9430732; PID:9430733	
COMMENT		This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).	
CLASSIFICATION		superfamily tumor necrosis factor receptor type I; NCF receptor repeat homology duplication; glycoprotein; receptor; transmembrane protein	
KEYWORDS		#domain signal sequence #status predicted #label SIG\	
FEATURE		1-29	





#cross-references WTID:87106851      beta-subunit genes have diverged from the human.

#accession A25808  
##molecule\_type mRNA

COMMENT There are at least five copies of CG-related genes and at least two of these are expressed in the baboon placenta.  
CLASSIFICATION #superfamily pituitary glycoprotein hormone beta chain  
KEYWORDS glycoprotein; hormone; placenta; pregnancy maintenance  
FEATURE  
  1-20  
  21-165  
  
29-77,43-92,46-130,  
54-108,58-110,  
113-120  
33,50  
140,147,152

SUMMARY  
#length 165 #molecular-weight 17592 #checksum 4960

Query Match                 33.7%; Score 857; DB 1; Length 165;  
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Matches 113; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Db 27 PLCRPINATLAERKACPCVCTVTITICAGYCPTMRYIAQVALPPVPQVCNRYREVRES 86  
| | | | |  
Oy 198 PCRPI NATLAEKEGCPCTIVNTTICAGYCPMTBVLQGLPALPQVVCNRYRDVFES 257  
| | | | |  
Db 87 IRLPGCPGVDPWAVSVFALSCRCALCRRSTDCGGPRDHPILTCDDPNIQASSSSKDPPP 146  
| | | | |  
Oy 258 IRLPGCPRGVNPAVSVAVALSCOCALCRCRSTRDCGGPRDHPILTCDDPNQSSSKRAAPP 317  
| | | | |  
Db 147 SPSPSRLLPEACTGFPLPO 165  
| | | | | : : : : :  
Oy 318 SLPSPSRLPEPSDTFILPO 336

RESULT 15  
ENTRY 1XULB #type complete

TITLE chorionic gonadotropin, chain B - humanPDB\_TITLE theoretical mod  
ORGANISM receptor complexed with human chorionic gonadotropin  
REFERENCE #formal\_name Homo sapiens #common\_name man  
A66957  
#authors Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Teyar, N.  
#submission submitted to the Brookhaven Protein Data Bank, December 1996  
REFERENCE #cross-references PDB:1XUL TN032625

#authors Jiang, X.; Dreano, M.; Buckler, D.R.; Cheng, S.; Ythier, A.; Wu, H.; Hendrickson, W.A.; El Teyar, N.  
#journal Structure (London) (1996) 3:1341  
#title Structural predictions for the ligand-binding region of glycoprotein hormone receptors and the nature of hormone-receptor interactions structure.  
TN032626

REFERENCE #authors Wu, H.; Lustbader, J.W.; Liu, Y.; Canfield, R.E.; Hendrickson, W.A.  
#journal Structure (London) (1994) 2:545  
#title Structure of human chorionic gonadotropin at 2.6 Å resolution from mad analysis of the selenomethionyl protein.  
COMMENT Resolution: not applicable  
COMMENT Determination: theoretical model  
KEYWORDS complex; glycoprotein hormone receptor glycoprotein; hormone; phosphorylation; receptor

FEATURE  
97-101,26-39,9-17 #region beta sheet\  
54-59,86-91 #region beta sheet\  
61-67,78-84 #region beta sheet\  
8-56 #disulfide\_bonds\  
22-71 #disulfide\_bonds\  
#disulfide\_bonds\

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25-109      #disulfide_bonds\
33-87      #disulfide_bonds\
37-88      #disulfide_bonds\
92-99      #disulfide_bonds\

SUMMARY      #length 110 #molecular-weight 11906 #checksum 6414

Query Match      31.6%; Score 803; DB 5; Length 110;
Best Local Similarity 100.0%; Pred. No. 9,67e-141;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      6      PRCRPINATLAVEGGPVCTIVTTTCAGCGPTMTVLGGVLPALPQVVCNTRDYREFS 65
QY      198     PRCRPINATLAVEGGPCVCTIVTTTCAGCGCPMTNVLGGVLPALPQVVCNTRDYREFS 257
Db      66      IRLPGCPRGVNPVVSVAVALSCCQALCRSTTDDCGGPKDHPITCD 110
QY      258     IRLPGCPRGVNPVVSVAVALSCCQALCRSTTDDCGGPKDHPITCD 302

Search completed: Wed May 6 09:06:41 1998
Job time : 56 secs.

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RL GENOMICS 13:219-224(1992).  
 RN [7]  
 RP SEQUENCE OF 41-45.  
 RX MEDLINE: 90110215.  
 RA ENGELMANN H., NOVICK D., WALLACH D.;  
 RL J. BIOL. CHEM. 265:1531-1536(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
 RX MEDLINE: 93258809.  
 RA BANNER D.W., D'ARCY A., JAMES W., GENTZ R., SCHOENFELD H.-J.,  
 RL CELL 73:431-445(1993).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE: 97094982.  
 RA NAIMUTH J.H., DEVINE T.O., KHONO H., SPRANG S.R.;  
 RL STRUCTURE 4:1251-1262(1996).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS.  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: X55313; G37224; -.  
 DR EMBL: M33294; G339745; -.  
 DR EMBL: M58286; G339754; -.  
 DR EMBL: M63121; G339756; -.  
 DR EMBL: M75866; G339750; -.  
 DR EMBL: M75864; G339750; JOINED.  
 DR EMBL: M75865; G339750; JOINED.  
 DR EMBL: M60275; G339760; -.  
 DR EMBL: A21522; G579600; -.  
 DR PIR: A34899; GQHUT1.  
 DR PIR: A35010; A35010.  
 DR PIR: S12057; S12057.  
 DR PIR: A38208; A38208.  
 DR PDB: 1TNR; 31-JUL-94.  
 DR PDB: 1NCF; 07-DEC-95.  
 DR PDB: 1EXT; 11-JAN-97.  
 DR MIM: 191190; -.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS;  
 KW 3D-STRUCTURE.  
 FT SIGNAL 1 21  
 FT CHAIN 22 455  
 FT CHAIN 41 291  
 FT DOMAIN 22 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 455  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 356 441  
 FT DOMAIN 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125

FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 191  
 FT DISULFID 185 195  
 FT CARBOHYD 54 54  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 FT CONFLICT 412 412  
 FT CONFLICT 443 446  
 SQ SEQUENCE 455 AA; 50494 MW; CDEDA00F CRC32;  
 Query Match 52.0%; Score 1322; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 6,45e-296;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 41 D5VCPGKTIHPONNSICTCKHKGTLYNDGPGQDPTDCRCESGSTASBNHRL 100  
 Qy 23 D5VCPGKTIHPONNSICTCKHKGTLYNDGPGQDPTDCRCESGSTASBNHRL 82  
 Db 101 SCSKCRKRGVEISSCTVDPRDTCGCRKNOYRHWSENLFQCFNCSLGLNGTVHLSOE 160  
 Qy 83 SCSKCRKRGVEISSCTVDPRDTCGCRKNOYRHWSENLFQCFNCSLGLNGTVHLSOE 142  
 Db 161 KONTVCTCHAGFLRENECVSCNCKRSLECKRLCPQIENKGTEDSGTT 211  
 Qy 143 KONTVCTCHAGFLRENECVSCNCKRSLECKRLCPQIENKGTEDSGTT 193  
 RESULT 2  
 ID CGHB\_HUMAN STANDARD; PRT; 165 AA.  
 AC P01233;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE CHORIOGONADOTROPHIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPHIN BETA  
 DE SUBUNIT).  
 GN CGB.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 81012134.  
 RA FIDDES J.C., GOODMAN H.M.;  
 RL NATURE 286:684-687(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 84093590.  
 RA TALMADGE K., VAMVAKOPOULOS N.C., FIDDES J.C.;  
 RL NATURE 307:37-40(1984).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 8408141.  
 RA POLICASTRO P., OVIATT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,  
 RA BOIME I.;  
 RL J. BIOL. CHEM. 258:11492-11499(1983).  
 RN [4]  
 RP SEQUENCE OF 1-20.  
 RX MEDLINE: 81117268.  
 RA BIRKEN S., FETHERSTON J., CANFIELD R.E., BOIME I.;  
 RL J. BIOL. CHEM. 256:1816-1823(1981).  
 RN [5]  
 RP SEQUENCE OF 21-165.  
 RX MEDLINE: 7521304.  
 RA MORGAN F.J., BIRKEN S., CANFIELD R.E.;  
 RL J. BIOL. CHEM. 250:5247-5258(1975).  
 RN [6]  
 RP PRELIMINARY SEQUENCE OF 21-165.  
 RX MEDLINE: 74011267.  
 RA CARLSEN R.B., BAHL O.P., SWAMINATHAN N.;  
 RL J. BIOL. CHEM. 248:6810-6827(1973).





AC	P22934	(REL. 19, CREATED)
DT	01-AUG-1991	(REL. 21, LAST SEQUENCE UPDATE)
DT	01-MAR-1992	(REL. 35, LAST ANNOTATION UPDATE)
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P50) (TNF-R1) (P55).	
GN	TNFR1 OR TNFR-1.	
OS	RATTUS NORVEGICUS (RAT).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.	
CC	EUTHERIA; RODENTIA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 91090841.	
RA	HIMMLER A., MAUERER-FOG I., KROENKE M., SCHEURICH P., PEIZENMAIER K.,	
RA	LAUTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;	
RL	DNA CELL. BIOL. 9:705-715(1990).	
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD	
CC	RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING	
CC	AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)	
CC	PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE	
CC	SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE	
CC	PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).	
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO	
CC	HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS	
CC	PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY	
CC	WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING	
CC	PROTEINS SUCH AS TRAF6, RIP AND POSSIBLY FADD, ARE RECRUITED TO	
CC	TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX	
CC	ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND	
CC	NF-KAPPA B SIGNALING (BY SIMILARITY).	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
DR	EMBL; M63122; G407362; -.	
DR	PIR; B36555; B36555.	
DR	HSSP; P19438; 1TNR.	
DR	PROSITE; PS00652; TNFR_NGFR.1; 3.	
DR	PROSITE; PS50050; TNFR_NGFR.2; 3.	
DR	PROSITE; PS50017; DEATH_DOMAIN.1.	
KM	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL; APOPTOSIS.	
FT	SIGNAL	1
FT	CHAIN	22
FT	DOMAIN	22
FT	TRANSMEM	212
FT	DOMAIN	235
FT	DOMAIN	43
FT	REPEAT	43
FT	REPEAT	83
FT	REPEAT	126
FT	REPEAT	167
FT	DOMAIN	363
FT	DISULFID	44
FT	DISULFID	59
FT	DISULFID	62
FT	DISULFID	84
FT	DISULFID	102
FT	DISULFID	105
FT	DISULFID	127
FT	DISULFID	146
FT	DISULFID	149
FT	DISULFID	168
FT	DISULFID	182
FT	DISULFID	185
FT	CARBOHYD	54
FT	CARBOHYD	151
FT	CARBOHYD	201
SO	SEQUENCE	461 AA; 50969 MW; 82F6B08 CRC32;

Query Match 37.2%; Score 944; DB 1; Length 461;

Best Local Similarity 67.3%; Pred. No. 5.76e-200;

Matches 115; Conservative 25; Mismatches 31; Indels 0; Gaps 0;

41 DNLCPGKYAPRPNKNSICTCKHGTYLVSPGPGGTGVEDCKGTFPASNQHVQCL 100

1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

23 DSVCPGKYITPNNNSICTCKHGTYLVNDCPGGGDDTCRCESSSFTASENHLHACL 82

D <sub>b</sub>	Q <sub>Y</sub>	D <sub>b</sub>	Q <sub>Y</sub>
101	SCSKCREMGEFVEI.SPKCADMDYTGKGGKNOFFYLETHFOCVDCSPYCNQATYICKE	160	
83	SCSKCREMGEVLSCTVBDYDTVCGCRKNGYRIYHSEBNLFQFCNGLCLNGTYHLSQCE	142	
161	KONTVCCHAGFETLSGNECPFSKCKNOCKMCKLCPVANNYNTNPOSSGA	211	
143	KONTVCCHAGFETLRNDCVSCSKCKSLKCTKCLQOIEKVTGKEDSGIT	193	

RESULT	6
ID	CGHB_PAPAN
	STANDARD;
	PRT;
	165 AA

DT	01-APR-1988	(REL. 07, CREATED)
DT	01-APR-1988	(REL. 07, LAST SEQUENCE UPDATE)
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)
DE	CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (CHORIONIC GONADOTROPIN BETA SUBUNIT).	
GN	CSB.	
OS	PAPIO ANUBIS (OLIVE BABOON).	
OC	EUKARIOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
OC	[1]	
RP	SEQUENCE FROM N.A.	
RA	MEDLINE; 87106851.	
RX	CRAWFORD R.J., TREGGAR G.W., NIALL H.D.;	
RL	GENE 46:161-169(1986).	
CC	-1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.	
CC	-1- ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.	
CC	-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.	
CC	-1- TISSUE SPECIFICITY: PLACENTA.	
CC	-1- THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.	
DR	EMBL; M1966; G176573; -	
DR	PIR; A25808; KTBAB.	
DR	HSSP; P01233; 1HCB.	
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.	
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.	
KW	HORMONE; GLYCOPROTEIN; SIGNAL.	
FT	SIGNAL	1 20 BY SIMILARITY.
FT	CHAIN	21 165 CHORIOGONADOTROPIN BETA CHAIN.
FT	DISULFID	29 77 BY SIMILARITY.
FT	DISULFID	43 92 BY SIMILARITY.
FT	DISULFID	46 130 BY SIMILARITY.
FT	DISULFID	54 108 BY SIMILARITY.
FT	DISULFID	58 110 BY SIMILARITY.
FT	DISULFID	113 120 BY SIMILARITY.
FT	CARBOHYD	33 33 BY SIMILARITY.
FT	CARBOHYD	50 50 BY SIMILARITY.
FT	CARBOHYD	141 141 BY SIMILARITY.
FT	CARBOHYD	147 147 BY SIMILARITY.
FT	CARBOHYD	152 152 BY SIMILARITY.
FT	CARBOHYD	165 AA; 17592 MW; 78987D30 CRC32; SEQUENCE

	Query Match	33.7%	Score 857;	DB 1;	Length 165;
	Best Local Similarity	81.3%;	Prod. No. 4.26e-178;		
	Matches 113;	Conservative 14;	Mismatches 12;	Indels 0;	Gaps 0
Db	27	PLCRPINALTAEREACVCVTVNTTICAGCYCPMMRRLQAVLPVPVQVNCNREVFEES	86		
Qy	198	PCRPRINNTLAVNEKEGCGVCCTITVNTTICAGCYCPMMRRLQAVLPVPVQVNCNREVFEES	257		
Db	87	IRLPCCPGVUPPMVSPVPAALSCRCALCRRTSIDCGGPRDHPDLTDDPMLQASSSSKODPP	146		
Qy	258	IRLPCCPGVUPPMVSPVPAALSCRCALCRRTSIDCGGPRDHPDLTDDPFDODSSSSSKAPP	317		
Db	147	SPSPSRLELPAGTPELPQ	165		
Qy	318	SLPSPSRLELPAGTPELPQ	336		







RX MEDLINE; 92357035.  
 RA SHERMAN G.B., WOLFE M.W., FARMERIE T.A., CLAY C.M.,  
 RA THREAGILL D.S., SHARP D.C., NILSON J.H.;  
 RL MOL. ENDOCRINOL. 6:951-959(1992).  
 RN [2]  
 RP SEQUENCE OF 21-169.  
 RX MEDLINE; 87250476.  
 RA BOUSFIELD G.R., LIU W.-K., SUGINO H., WARD D.N.;  
 RL J. BIOL. CHEM. 262:8610-8620(1987).  
 RN [3]  
 RP SEQUENCE OF 21-169.  
 RX MEDLINE; 87250475.  
 RA SUGINO H., BOUSFIELD G.R., MOORE W.T. JR., WARD D.N.;  
 RL J. BIOL. CHEM. 262:8603-8609(1987).  
 RN [4]  
 RP CHORIOGONADOTROPIN, PARTIAL SEQUENCE.  
 RA WARD D.N., MOORE W.T. JR., BURLEIGH B.D.;  
 RL J. PROTEIN CHEM. 1:263-280(1982).  
 RN [5]  
 RP STRUCTURE OF CARBOHYDRATES.  
 RX MEDLINE; 90235854.  
 RA DAMM J.B.L., HARD K., KAMERLING J.P., VAN DEDEM G.W.K.,  
 RA VILGENTHART J.F.G.;  
 RL EUR. J. BIOCHEM. 189:175-183(1990).  
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC -1- PTM: AT LEAST FOUR O-GLYCOSYLATION SITES ARE PRESENT.  
 DR EMBL; S41704; G252741; -.  
 DR PIR; A01503; KTHOB.  
 DR PIR; A29304; A29304.  
 DR PIR; A29305; A29305.  
 DR PIR; A41917; A41917.  
 DR HSP; P01233; IHGN.  
 DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE; PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 KW HORMONE; GLYCOPROTEIN; SIGNAL.  
 FT CHAIN 1 20  
 FT SIGNAL 21 20  
 FT DISULFID 29 169 LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.  
 FT DISULFID 43 92 BY SIMILARITY.  
 FT DISULFID 46 130 BY SIMILARITY.  
 FT DISULFID 54 108 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 113 120 BY SIMILARITY.  
 FT CARBOHYD 33 33 GLYCAN SHOWING A REMARKABLY STRUCTURAL  
 FT HETEROGENEITY.  
 SQ SEQUENCE 169 AA; 17865 MW; 9AB1CAA3 CRC32;  
 Query Match 24.1%; Score 613; DB 1; Length 169;  
 Best Local Similarity 62.7%; Pred. No. 1.77e-117; Indels 5; Gaps 4;  
 Matches 84; Conservative 22; Mismatches 23;






DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).  
 GN LSH.  
 OS OVIS ARIES (SHEEP).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 9331742.  
 RA BROWN P., MCNEILLY J.R., WALLACE R.M., MCNEILLY A.S., CLARK A.J.;  
 RL MOL. CELL. ENDOCRINOL. 93:157-165(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-PITUITARY;  
 RX MEDLINE; 90245669.  
 RA D'ANGELO-BERNARD G., MODUNT M., JUTISZ M., COUNIS R.;  
 RL NUCLEIC ACIDS RES. 18:2175-2175(1990).  
 RN [3]  
 RP SEQUENCE OF 21-139.  
 RX MEDLINE; 7221145.  
 RA LIU W.-K., NAHM H.S., SWEENEY C.M., HOLCOMB G.N., WARD D.N.;  
 RL J. BIOL. CHEM. 247:4365-4381(1972).  
 RN [4]  
 RP SEQUENCE OF 21-139.  
 RX MEDLINE; 73190035.  
 RA SAIRAM M.R., SAMT T.S.A., PAPROFF H., LI C.H.;  
 RL ARCH. BIOCHEM. BIOPHYS. 153:572-586(1972).  
 RN [5]  
 RP STRUCTURE OF CARBOHYDRATE.  
 RX MEDLINE; 91006170.  
 RA WEISSSHAAR G., HIYAMA J., REMNICK A.G.C.;  
 RL EUR. J. BIOCHEM. 192:741-751(1990).  
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING  
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.  
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA  
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,  
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.  
 CC EMBL; S64695; G408241; -.  
 DR EMBL; X52488; G1320; -.  
 DR PIR; A01500; UTSBH.  
 DR PIR; S09232; S09232.  
 DR HSP; P01233; IHGN.  
 DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; 1.  
 DR PROSITE; PS00689; GLYCO\_HORMONE\_BETA\_2; 1.  
 KW HORMONE; SIGNAL; GLYCOPROTEIN.  
 FT CHAIN 1 20  
 FT SIGNAL 21 20  
 FT DISULFID 29 141 LUTROPIN BETA CHAIN.  
 FT DISULFID 43 92 BY SIMILARITY.  
 FT DISULFID 46 130 BY SIMILARITY.  
 FT DISULFID 54 108 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 113 120 BY SIMILARITY.  
 FT MOD\_RES 21 21 BLOCKED.  
 FT CARBOHYD 33 33 MISSING (IN SOME MOLECULES).  
 FT VARIANT 138 141  
 FT CONFLICT 30 30 O -> E (IN REF. 4).  
 FT CONFLICT 59 59 L -> P (IN REF. 1).  
 FT CONFLICT 63 63 R -> Q (IN REF. 2).  
 FT CONFLICT 71 72 PM -> PPM (IN REF. 4).  
 FT CONFLICT 81 81 E -> Q (IN REF. 4).  
 FT CONFLICT 122 123 GP -> PG (IN REF. 3 AND 4).  
 FT CONFLICT 126 126 Q -> E (IN REF. 3 AND 4).  
 SQ SEQUENCE 141 AA; 15184 MW; BA2C0204 CRC32;  
 Query Match 23.7%; Score 602; DB 1; Length 141;  
 Best Local Similarity 64.0%; Pred. No. 8.87e-115;  
 Matches 71; Conservative 22; Mismatches 18; Indels 0; Gaps 0;

RESULT 12  
 ID LSHB SHEEP STANDARD: PRT: 141 AA.  
 AC P01231.  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)

DB	87	VLRLCPGPGVDPNVSFPVALSCHGPGPRLSTDCGGRTPLACDHPPLD	137
Qy	258	IRLPCPGVNPVVSIVAVALSQCQALCRSTTDCGGFADHPDLTCDPFPD	308
RESULT	13	STANDARD:	PRT: 141 AA.
OC	13	LSH, PIG	
AC	21	JUL-1986 (REL. 01, CREATED)	
DT	01-NOV-1980	(REL. 16, LAST SEQUENCE UPDATE)	
DE	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)	
GN	148	LUTEALIN BETA CHAIN PRECURSOR (LUTEALIZING HORMONE) (LSH-B) (LH-B).	
OS	SUS SCROFA (PIG).		
OC	EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA,		
OC	EUTHERIA, ARTIODACTYLA.		
RA	SEQUENCE FROM N.A.		
RX	MEDLINE: 91063934.		
RA	EZASHI T., HIRAI T., KATO T., WAKABAYASHI K., KATO Y.,		
RL	J. MOL. ENDOCRINOL. 5:137-146(1990).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE: 89306142.		
RA	KATO Y., HIRAI T.,		
RL	MOL. CELL. ENDOCRINOL. 62:47-53(1989).		
RL	[3]		
RP	SEQUENCE OF 21-139.		
RX	MEDLINE: 74075724.		
RA	MAGHUIR-ROGISTER G., HENNEN G.,		
RL	EUR. J. BIOCHEM. 39:235-253(1973).		
CC	-1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING		
CC	THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.		
CC	-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA		
CC	CHAIN WHICH CONTERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,		
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.		
DR	EMBL: D00579; G217694; -		
DR	PIR: A30332; UTRGB.		
DR	PIR: A48170; A48170.		
DR	HSSP: P01233; 1HCN.		
DR	PROSITE: PS00261; GLYCO-HORMONE, BETA_1; 1.		
DR	PROSITE: PS00689; GLYCO-HORMONE, BETA_2; 1.		
KV	HORMONE; SIGNAL; GLYCOPROTEIN.		
FT	SIGNAL	1	20
FT	CHAIN	21	141
FT	DISULFID	29	77
FT	DISULFID	43	92
FT	DISULFID	46	130
FT	DISULFID	54	108
FT	DISULFID	58	110
FT	DISULFID	113	120
FT	CARBOHYD	33	33
FT	MOD_RES	21	21
FT	VARIANT	30	30
FT	CONFLICT	40	40
FT	CONFLICT	62	62
FT	CONFLICT	83	83
FT	CONFLICT	87	87
FT	CONFLICT	122	123
FT	CONFLICT	141 AA;	14889 MW; DA2EF539 CRC32;
SO	SEQUENCE		
Query Match	23.5%;	Score 598;	DB 1; Length 141;
Best Local Similarity	66.4%;	Pred. No. 8.48e-114;	
Matches	71;	Conservative 19;	Mismatches 17; Indels 0; Gaps 0;
DB	27	PLCRPINTLAENACFCVCTFTTSCAGYCPSMRVLPALPAPVDPQVCTYRELSFAS	86
Qy	198	PCRCPINTLAENACFCVCTFTTSCAGYCPSMRVLPALPAPVDPQVCTYRELSFAS	257
DB	87	IRLPCPGVDPNVSFPVALSCHGPGPRLSTDCGGRTPLACDHPPLD	137
Qy	258	IRLPCPGVNPVVSIVAVALSQCQALCRSTTDCGGFADHPDLTCDPFPD	308

ID	RESULT	14	STANDARD;	PRT;	141 AA.
AC	LSHB_RAT	P01230;			
DT		21-JUL-1986 (REL. 01, CREATED)			
DT		21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT		01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE) (LSH-B) (LH-B).				
GN	LHB.				
OS	RATTUS NORVEGICUS (RAT).				
OC	EUTARCTA; METAFOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-SPRAGUE-DAWLEY;				
RX	MEDLINE; 83273673.				
RA	CHIN W.W., GODINE J.E., KLEIN D.R., CHANG A.S., TAN L.K.,				
RA	HAEBENER J.F.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 80:4649-4653(1983).				
RN	(2)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 85080043.				
RA	JAMESON L., CHIN W.W., HOLLENBERG A.N., CHANG A.S., HAEBENER J.F.;				
RL	J. BIOL. CHEM. 259:15474-15480(1984).				
RN	(3)				
RP	SEQUENCE OF 4-141 FROM N.A.				
RC	STRAIN-WISTAR-IMMACHI; TISSUE-ANTERIOR PITUITARY;				
RA	KATO Y., EZASHI T., HIRAI T., KATO T.;				
RL	ZOOL. SCI. 7:877-885(1990).				
CC	-1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING				
CC	THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.				
CC	-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA				
CC	CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,				
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.				
DR	EMBL; V01542; G758262; -				
DR	EMBL; J00749; G205176; -				
DR	EMBL; D00576; G220808; -				
DR	PIR; A01498; UTRTB.				
DR	PIR; S42527; S42527.				
DR	HSSP; P01233; IHCN.				
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.				
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.				
KW	HORMONE; SIGNAL; GLYCOPROTEIN.				
FT	SIGNAL	1	20		
FT	CHAIN	21	141		
FT	DISULFID	29	77		
FT	DISULFID	43	92		
FT	DISULFID	46	130		
FT	DISULFID	54	108		
FT	DISULFID	58	110		
FT	DISULFID	113	120		
FT	CARBOHYD	33	33		
FT	SEQUENCE	141 AA;	15177 MW;	6E0C19BA CRC32;	
QY	Query Match	23.5%;	Score 597;	DB 11;	Length 141;
	Best Local Similarity	64.2%;	Pred. No. 1.49e-113;		
	Matches	70;	Conservative	23;	Mismatches 16; Indels 0; Gaps 0;
Db	27	PLCRPVNATLAENEFCEVCITFTTSICAGYCSPMVNLPAALPVPVQVCTYRELRFAS	86		
QY	198	PCRIRINTLAVEEGCEVCITVTNTTICAGYCSPTMTINLGVGVPALPQVVCNRYDAVFES	257		
Db	87	VRLEPCPGVDPIVSEPAVASCRCGRCRLSSDCGGRTPQVPCMDPHL	135		
QY	238	IRLPCPGVNPVSVAYALSCQALCRKRTTDCGGFKDPLTCDPDRF	306		
RESULT	15	STANDARD;	PRT;	118 AA.	
ID	LSHB_BALAC				
AC	P33088;				
DT	01-OCT-1993 (REL. 27, CREATED)				
DT	01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)				



DE CHORIONIC GONADOTROPIN BETA SUBUNIT.  
GN CGB.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 84008141.  
RA POLICASTRO P., OVITT C.E., HOSHINA M., FUKUOKA H., BOOTHBY M.R.,  
RA BOIME I.,  
RL J. BIOL. CHEM. 258:11492-11499(1983).  
DR EMBL: K03183; G180444; -  
DR EMBL: K00092; G180444; JOINED.  
DR EMBL: K03182; G180444; JOINED.  
SO SEQUENCE 165 AA; 17729 MW; B1CA0A0B1 CRC32;

Query Match	40.3%	Score 1024;	DB 2	Length 165;
Best Local Similarity	99.3%	Pred. No. 1,188-204;		
Matches 138; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Db	27	PCRPRINATLAVEKEGCPVCTIVNTTICAGYCPMTTRVLQGVLPALPQVVCNRYDVFRES	86	
QY	198	PCRPRINATLAVEKEGCPVCTIVNTTICAGYCPMTTRVLQGVLPALPQVVCNRYDVFRES	257	
Db	87	IRLPCCPGVNPPVYSYAALSCQCALCKRSTTDDGGPRDHLTLCDDRFQASSSSKAPP	146	
QY	258	IRLPCCPGVNPPVYSYAALSCQCALCKRSTTDDGGPRDHLTLCDDRFQASSSSKAPP	317	
Db	147	SLPSPSRLLPGPSDPTILPQ	165	
QY	318	SLPSPSRLLPGPSDPTILPQ	336	

AC 019131.  
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  
DE TUMOR NECROSIS FACTOR-RECEPTOR 1.  
GN TNF-RI.  
OS BOS TAURUS (BOVINE).  
CC EUCHARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA  
OC EUHERERA; ARTIODACTYLA.  
RN [1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=AORTA;  
RC LEE E.-K., TALYOR M.J., KEHLRI M.E.;  
RL SUBMITTED (AUG1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; U90937; G2290393.  
DR PROSITE: PS00652; TNFR-CFR.1; 3.  
SO SEQUENCE 471 AA; 51368 MW; 1D60FF4A CRC32;

[illegible]

AC Q95185; 01-FEB-1997 (TREMBL;REL. 02, CREATED)  
DT 01-FEB-1997 (TREMBL;REL. 02, LAST SEQUENCE UPDATE)  
DT 01-FEB-1997 (TREMBL;REL. 02, LAST SEQUENCE UPDATE)  
DT 01-JAN-1998 (TREMBL;REL. 05, LAST ANNOTATION UPDATE)  
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).  
GN TNFR-1  
OS FELIS SILVESTRIS CATUS (CAT).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; CARNIVORA.  
RN [1]  
RP  
RA DUTHIE S., NASIR L., ECKERSALL P.D.;  
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; U72344; G1618880; -  
DR PROSITE; PS00653; TNFR\_NGFR\_1; 3.  
FT  
FT NON\_TER 1  
FT NON\_TER 180  
FT SEQUENCE 180 AA; 20399 MW; 54526682 CRC32;

Query Match	37.2%	Score 945;	DB 4;	Length 180;
Best Local Similarity	86.0%	Pred. No. 3,956-186;		
Matches 117;	Conservative	9;	Mismatches 10;	Indels 0; Gaps 0;
Db	45	CPGCKYIHPDONSICCTCKCHKGYILYNDACAGPGIDTDCRECENGTPTASENYLRQCLSCS	104	
Oy	26	CPGCKYIHPDONSICCTCKCHKGYILYNDACAPGQDPTDRCESGSPFASENHLRLCLSCS	85	
Db	105	KCKRMIVVELSPCTVYADYVCGCRKNQYRIYRSETHFPQCLNCSLCLNGYQISCKETLN	164	
Oy	86	KCKRMGVVELSSCTVDRDVTGCGCRKNQYRIYRSENFPOCFNCSLCLNGYVHLSCQEKON	145	
Db	165	TYVCTCHAGFLRGNDG	180	
Oy	146	TYVCTCHAGFLRENDG	161	

AC 01-102; (CREATED)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
 DE LOEINIZING HORMONE BETA SUBUNIT (FRAGMENT).  
 OC CERCATOTHEIUM STMUM (WHITE RHINOCEROS). (SQUARE-LIPPED RHINOCEROS).  
 OC EURAROTATA METAASA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:  
 OC EUTHERIA: PERISSODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PITUITARY GLAND;  
 RX MEDLINE; 97449288.  
 RA SHERMAN G.B.; LUND L.A.; BUNICK D.; WINN R.J.;  
 RL GENE 195:131-139(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PITUITARY GLAND;  
 RA SHERMAN G.B.; LUND L.A.;  
 RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: U72659; G246279; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 135 AA; 14212 MW; F4F196D2 CRC32;

[illegible]

QY 258 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 304

RESULT 6 PRELIMINARY; PRT; 139 AA.

AC 062778;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE TESTICULAR LUTEINIZING HORMONE BETA-SUBUNIT.  
 GN TLHBL.  
 OS RATIUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAQUE DAWLEY;  
 RX MEDLINE: 95283549.  
 RA ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).  
 DR EMBL: U25653; G915217; -.  
 SQ SEQUENCE 139 AA; 14880 MW; 5B2E7DBF CRC32;

Query Match 23.4%; Score 595; DB 10; Length 139;  
 Best Local Similarity 63.3%; Pred. No. 3,86e-105;  
 Matches 69; Conservative 24; Mismatches 16; Indels 0; Gaps 0;

DB 25 PLCPFNATLAENEFPCVITFTTSCAGYCPSPMVLPAALPPVQPVCTRELSPAS 84  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 257

DB 85 VRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 133  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 306

RESULT 7 PRELIMINARY; PRT; 141 AA.

AC 060844;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE LUTEINIZING HORMONE BETA (LUTEINIZING HORMONE BETA-SUBUNIT).  
 GN LHB.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129 SVEV;  
 RA KAPUR V., MATZOK M.M.;  
 RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: U25145; G930345; -.  
 MD: MGI:96782; LHB.  
 SQ SEQUENCE 141 AA; 15028 MW; BE50AB2B CRC32;

Query Match 22.9%; Score 582; DB 10; Length 141;  
 Best Local Similarity 62.4%; Pred. No. 3,51e-102;  
 Matches 68; Conservative 24; Mismatches 17; Indels 0; Gaps 0;

DB 27 PLCPFNATLAENEFPCVITFTTSCAGYCPSPMVLPAALPPVQPVCTRELSPAS 86  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 257

DB 87 VRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 133  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 306

RESULT 8 PRELIMINARY; PRT; 140 AA.

AC 098849;  
 DT 01-FEB-1997 (TREMBLREL. 02, CREATED)  
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  
 DE GONADOTROPIN II BETA SUBUNIT PRECURSOR.  
 OS CARASSIUS AURATUS (GOLDFISH).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;  
 OC OSTEICHTHYES; ACTINOPTERIGII; CYPRINIFORMES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PITUITARY GLAND;  
 RA YOSHIDA Y., KOBAYASHI M., KATO Y., AIDA K.;  
 RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL: D88024; G1644243; -.  
 KW SIGNAL.  
 FT SIGNAL 1 23  
 FT CHAIN 24 140  
 SQ SEQUENCE 140 AA; 15533 MW; 7205FD03 CRC32;

Query Match 16.9%; Score 430; DB 12; Length 140;  
 Best Local Similarity 50.0%; Pred. No. 4,94e-68;  
 Matches 54; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

DB 27 PCEPVNTEVAVEKEGCKVLTOTTCGCLTKEPVKSPSTVYQVCTRYVET 86  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 257

QY 198 PRCPFNATLAENEFPCVITFTTSCAGYCPSPMVLPAALPPVQPVCTRELSPAS 84  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 305

DB 87 VRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 134  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 306

RESULT 9 PRELIMINARY; PRT; 80 AA.

AC 063013;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)  
 DE TESTICULAR LUTEINIZING HORMONE BETA SUBUNIT.  
 GN TLHBL.  
 OS RATIUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAQUE DAWLEY;  
 RX MEDLINE: 95283549.  
 RA ZHANG F.P., RANNIKKO A., HUHTANIEMI I.;  
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 210:858-865(1995).  
 DR EMBL: U25803; G904026; -.  
 SQ SEQUENCE 80 AA; 8515 MW; 74FA772D CRC32;

Query Match 15.4%; Score 391; DB 10; Length 80;  
 Best Local Similarity 60.0%; Pred. No. 1,91e-59;  
 Matches 45; Conservative 18; Mismatches 11; Indels 1; Gaps 1;

DB 1 MVRVLPALPPVQPVCTRELSPAS 59  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 291

QY 232 MVRVLPALPPVQPVCTRELSPAS 59  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 306

DB 60 GGPRTQPMTCDDP 74  
 IRLPGCRGVNPNVSVAVALSOCALCRSTTDCGGPKDHPDLCDDP 306

RESULT 10 PRELIMINARY; PRT; 147 AA.

AC 091121;  
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)







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